



SEQUENCE LISTING

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DEC - 4 2001

TECH CENTER 1600/2900

a1

<110> Pompejus, Markus
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Zelder, Oskar
Haberhauer, Gregor

<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
INVOLVED IN DNA REPLICATION, PROTEIN SYNTHESIS,
AND PATHOGENESIS

<130> BGI-130CP

<140> US 09/604,693

<141> 2000-06-27

<160> 430

<210> 1

<211> 965

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(942)

<223> RXN00625

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Thr Val Lys Pro Val Gly Glu Ser Arg Ile Phe Asp Asp Ala Ala Phe
20 25 30

acc ggc acc gca cgc cag cca ctc gca cag gaa ttc cag cca ctc aac 144
Thr Gly Thr Ala Arg Gln Pro Leu Ala Gln Glu Phe Gln Pro Leu Asn
35 40 45

gac agc gag aaa tcc ttc gtc ggc gta gtc aac cac ttc aag tcc aag 192
Asp Ser Glu Lys Ser Phe Val Gly Val Val Asn His Phe Lys Ser Lys
50 55 60

ggc tct gtc act cgt gga gac gcc gac acc ggc gac ggc caa ggc aac 240
Gly Ser Val Thr Arg Gly Asp Ala Asp Thr Gly Asp Gly Gln Gly Asn
65 70 75 80

aac gcc aac gtt cgc gtc gca cag gca cag gca ctc atc gac cac ctg 288
Asn Ala Asn Val Arg Val Ala Gln Ala Gln Ala Leu Ile Asp His Leu
85 90 95

gaa aac cag gac gac tgg gca tcc aag cca atc ttc atc ctc ggc gac 336
Glu Asn Gln Asp Asp Trp Ala Ser Lys Pro Ile Phe Ile Leu Gly Asp
100 105 110

acc aac tcc tac gcc aag gaa acc gcg atg acc acc ctt tac ggc gct 384
Thr Asn Ser Tyr Ala Lys Glu Thr Ala Met Thr Thr Leu Tyr Gly Ala
115 120 125

ggc tac acc aac atc gcc acc gaa ttc gac gct ggc tac agc tac cag 432
 Gly Tyr Thr Asn Ile Ala Thr Glu Phe Asp Ala Gly Tyr Ser Tyr Gln
 130 135 140

ttc tcc ggc cgc att ggc agc ctc gac cac gca ctc ggc aac gaa gca 480
 Phe Ser Gly Arg Ile Gly Ser Leu Asp His Ala Leu Gly Asn Glu Ala
 145 150 155 160

gcc atg aag cac gtc atc gac gcc gag gtc tgg gac atc aac gct gac 528
 Ala Met Lys His Val Ile Asp Ala Glu Val Trp Asp Ile Asn Ala Asp
 165 170 175

gaa gca atc gca ttc gaa tac tcc cgt cga ctc aac aac acc tcc gac 576
 Glu Ala Ile Ala Phe Glu Tyr Ser Arg Arg Leu Asn Asn Thr Ser Asp
 180 185 190

gta ttc gag aac aac gtc ttc cgc tcc tcc gac cac gac ccg atc aag 624
 Val Phe Glu Asn Asn Val Phe Arg Ser Ser Asp His Asp Pro Ile Lys
 195 200 205

gtc gga ttc aac ctc agc gag acc act gag ccc acc att ccg gta gag 672
 Val Gly Phe Asn Leu Ser Glu Thr Thr Glu Pro Thr Ile Pro Val Glu
 210 215 220

ccc act gat cct gca gaa cct acc gat cca act acc cca gtt aag cca 720
 Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Thr Thr Pro Val Lys Pro
 225 230 235 240

act gat ccg gta gag acc acg gat cca tct gag cca acc gac cct gca 768
 Thr Asp Pro Val Glu Thr Thr Asp Pro Ser Glu Pro Thr Asp Pro Ala
 245 250 255

gaa cct act gat cca gct gaa cca act gac cct gag gaa acg aag aag 816
 Glu Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Glu Glu Thr Lys Lys
 260 265 270

cca gag gag ccg aag aac cct ggt tcc tcc aac gga agc tcc caa tac 864
 Pro Glu Glu Pro Lys Asn Pro Gly Ser Ser Asn Gly Ser Ser Gln Tyr
 275 280 285

gcc acc att gca gca atc atc gca gca atc cta ggt gcc att gct ttg 912
 Ala Thr Ile Ala Ala Ile Ile Ala Ala Ile Leu Gly Ala Ile Ala Leu
 290 295 300

gcc ttc cag ttc ttc cat tca agt tct aat taactcttag ggagtaatcc 962
 Ala Phe Gln Phe Phe His Ser Ser Ser Asn
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cct 965

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<211> 314

<212> PRT

<213> Corynebacterium glutamicum

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Thr Gly Thr Ala Arg Gln Pro Leu Ala Gln Glu Phe Gln Pro Leu Asn
35 40 45

Asp Ser Glu Lys Ser Phe Val Gly Val Val Asn His Phe Lys Ser Lys
50 55 60

Gly Ser Val Thr Arg Gly Asp Ala Asp Thr Gly Asp Gly Gln Gly Asn
65 70 75 80

Asn Ala Asn Val Arg Val Ala Gln Ala Gln Ala Leu Ile Asp His Leu
85 90 95

Glu Asn Gln Asp Asp Trp Ala Ser Lys Pro Ile Phe Ile Leu Gly Asp
100 105 110

Thr Asn Ser Tyr Ala Lys Glu Thr Ala Met Thr Thr Leu Tyr Gly Ala
115 120 125

Gly Tyr Thr Asn Ile Ala Thr Glu Phe Asp Ala Gly Tyr Ser Tyr Gln
130 135 140

Phe Ser Gly Arg Ile Gly Ser Leu Asp His Ala Leu Gly Asn Glu Ala
145 150 155 160

Ala Met Lys His Val Ile Asp Ala Glu Val Trp Asp Ile Asn Ala Asp
165 170 175

Glu Ala Ile Ala Phe Glu Tyr Ser Arg Arg Leu Asn Asn Thr Ser Asp
180 185 190

Val Phe Glu Asn Asn Val Phe Arg Ser Ser Asp His Asp Pro Ile Lys
195 200 205

Val Gly Phe Asn Leu Ser Glu Thr Thr Glu Pro Thr Ile Pro Val Glu
210 215 220

Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Thr Thr Pro Val Lys Pro
225 230 235 240

Thr Asp Pro Val Glu Thr Thr Asp Pro Ser Glu Pro Thr Asp Pro Ala
245 250 255

Glu Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Glu Glu Thr Lys Lys
260 265 270

Pro Glu Glu Pro Lys Asn Pro Gly Ser Ser Asn Gly Ser Ser Gln Tyr
275 280 285

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290 295 300

Ala Phe Gln Phe Phe His Ser Ser Ser Asn
305 310

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<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (1)..(339)

<223> FRXA00625

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gag	ccc	acc	att	ccg	gta	gag	ccc	act	gat	cct	gca	gaa	cct	acc	gat	96
Glu	Pro	Thr	Ile	Pro	Val	Glu	Pro	Thr	Asp	Pro	Ala	Glu	Pro	Thr	Asp	
			20					25					30			

cca	act	acc	cca	gtt	aag	cca	act	gat	ccg	gta	gag	acc	acg	gat	cca	144
Pro	Thr	Thr	Pro	Val	Lys	Pro	Thr	Asp	Pro	Val	Glu	Thr	Thr	Asp	Pro	
			35					40					45			

tct	gag	cca	acc	gac	cct	gca	gaa	cct	act	gat	cca	gct	gaa	cca	act	192
Ser	Glu	Pro	Thr	Asp	Pro	Ala	Glu	Pro	Thr	Asp	Pro	Ala	Glu	Pro	Thr	
	50					55					60					

gac	cct	gag	gaa	acg	aag	aag	cca	gag	gag	ccg	aag	aac	cct	ggt	tcc	240
Asp	Pro	Glu	Glu	Thr	Lys	Lys	Pro	Glu	Glu	Pro	Lys	Asn	Pro	Gly	Ser	
65					70					75					80	

tcc	aac	gga	agc	tcc	caa	tac	gcc	acc	att	gca	gca	atc	atc	gca	gca	288
Ser	Asn	Gly	Ser	Ser	Gln	Tyr	Ala	Thr	Ile	Ala	Ala	Ile	Ile	Ala	Ala	
				85					90					95		

atc	cta	ggt	gcc	att	gct	ttg	gcc	ttc	cag	ttc	ttc	cat	tca	agt	tct	336
Ile	Leu	Gly	Ala	Ile	Ala	Leu	Ala	Phe	Gln	Phe	Phe	His	Ser	Ser	Ser	
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aat	taactcttag	ggagtaatcc	cct	362
Asn				

<210> 4

<211> 113

<212> PRT

<213> Corynebacterium glutamicum

<400> 4

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			20					25					30		

Pro	Thr	Thr	Pro	Val	Lys	Pro	Thr	Asp	Pro	Val	Glu	Thr	Thr	Asp	Pro
			35					40					45		

Ser	Glu	Pro	Thr	Asp	Pro	Ala	Glu	Pro	Thr	Asp	Pro	Ala	Glu	Pro	Thr
	50					55				60					

Asp	Pro	Glu	Glu	Thr	Lys	Lys	Pro	Glu	Glu	Pro	Lys	Asn	Pro	Gly	Ser
65					70					75					80

Ser Asn Gly Ser Ser Gln Tyr Ala Thr Ile Ala Ala Ile Ile Ala Ala
85 90 95

Ile Leu Gly Ala Ile Ala Leu Ala Phe Gln Phe Phe His Ser Ser Ser
100 105 110

Asn

<210> 5

<211> 1768

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1768)

<223> RXN02943

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Met Ser Arg Ile Ser
1 5

gcg cgc act ctg gca atc gca ctt gcc ggt gca acc gcg gcc agc ctg 163
Ala Arg Thr Leu Ala Ile Ala Leu Ala Gly Ala Thr Ala Ala Ser Leu
10 15 20

gca gtt gtt cca gca gca aca gct aat cct gcc gga acc gct cct gtc 211
Ala Val Val Pro Ala Ala Thr Ala Asn Pro Ala Gly Thr Ala Pro Val
25 30 35

atc aac gaa atc tac gaa ggc ggt gga aac agc gga tcg ttg ttc tcc 259
Ile Asn Glu Ile Tyr Glu Gly Gly Gly Asn Ser Gly Ser Leu Phe Ser
40 45 50

aac gac ttc att gag ctg tac aac cca acc tca ggg gac att tcc ctg 307
Asn Asp Phe Ile Glu Leu Tyr Asn Pro Thr Ser Gly Asp Ile Ser Leu
55 60 65

gac ggt tgg agc gtt acc tac tac gca gcc aac ggt aac tcc ggc gga 355
Asp Gly Trp Ser Val Thr Tyr Tyr Ala Ala Asn Gly Asn Ser Gly Gly
70 75 80 85

acc aca aac ctg acc gga aac atc cct gcc aac ggt tac tac ctg atc 403
Thr Thr Asn Leu Thr Gly Asn Ile Pro Ala Asn Gly Tyr Tyr Leu Ile
90 95 100

cag caa cgc gca ggc agc aac aac acc ggc gct ctg cct acc cca gac 451
Gln Gln Arg Ala Gly Ser Asn Asn Thr Gly Ala Leu Pro Thr Pro Asp
105 110 115

gcc acc ggt aac ttg gca atg ggt gcc tcc caa gga tca gtt gca ctg 499
Ala Thr Gly Asn Leu Ala Met Gly Ala Ser Gln Gly Ser Val Ala Leu
120 125 130

acc gac aac tct ggc cta acc gct gac ctt gtc gga ttc ggt ggc acg 547

Thr 135	Asp	Asn	Ser	Gly	Leu	Thr 140	Ala	Asp	Leu	Val	Gly 145	Phe	Gly	Gly	Thr	
tcc	atg	ttt	gaa	gga	aca	gct	gct	gca	cct	gag	acc	agc	aac	aaa	ttg	595
Ser 150	Met	Phe	Glu	Gly	Thr 155	Ala	Ala	Ala	Pro	Glu 160	Thr	Ser	Asn	Lys	Leu 165	
tct	gtt	caa	cgc	aaa	gaa	gtt	ggc	gct	gac	tct	gat	aac	aac	tcc	gta	643
Ser	Val	Gln	Arg	Lys 170	Glu	Val	Gly	Ala	Asp 175	Ser	Asp	Asn	Asn	Ser	Val 180	
gac	ttc	gag	act	gga	gct	cca	act	cca	acg	tcc	tcg	gga	gga	tcc	gct	691
Asp	Phe	Glu	Thr 185	Gly	Ala	Pro	Thr	Pro	Thr 190	Ser	Ser	Gly	Gly	Ser	Ala 195	
cct	gtt	gac	cca	ggc	gag	cca	gaa	act	cca	gta	aac	cct	ggg	'gaa	aca	739
Pro	Val	Asp 200	Pro	Gly	Glu	Pro	Glu	Thr 205	Pro	Val	Asn	Pro	Gly	Glu	Thr 210	
gtc	tcc	atc	gca	caa	atc	caa	gga	acc	ggt	ctc	gct	acc	cca	ctc	gag	787
Val	Ser	Ile	Ala	Gln	Ile	Gln	Gly	Thr	Gly	Leu	Ala	Thr	Pro	Leu	Glu 225	
215						220										
ggt	cag	acc	gtc	acc	acc	gaa	ggt	att	gtc	act	gcc	gtt	tac	gca	gaa	835
Gly 230	Gln	Thr	Val	Thr	Thr 235	Glu	Gly	Ile	Val	Thr 240	Ala	Val	Tyr	Ala	Glu 245	
ggt	ggc	ttc	aac	ggt	tac	tac	atc	cag	aca	cct	gga	tct	ggt	act	gca	883
Gly	Gly	Phe	Asn 250	Gly	Tyr	Tyr	Ile	Gln	Thr 255	Pro	Gly	Ser	Gly	Thr	Ala 260	
cca	aag	gtt	gct	ggc	gac	gca	tcc	gac	ggc	atc	ttc	gtc	tac	gtg	gga	931
Pro	Lys	Val	Ala 265	Gly	Asp	Ala	Ser	Asp 270	Gly	Ile	Phe	Val	Tyr	Val	Gly 275	
agc	aat	ggt	tcc	tac	cca	gag	ctc	ggc	gca	tct	gtc	acc	gtc	act	ggc	979
Ser	Asn	Gly 280	Ser	Tyr	Pro	Glu	Leu	Gly 285	Ala	Ser	Val	Thr	Val	Thr	Gly 290	
aag	gcc	acc	gaa	cac	tac	gag	atg	act	cag	cta	ggc	aac	tcc	tcc	ttc	1027
Lys	Ala	Thr	Glu	His	Tyr	Glu	Met	Thr 300	Gln	Leu	Gly 305	Asn	Ser	Ser	Phe	
295						300										
acc	gtt	tcg	gac	acc	gca	ttc	gag	cca	gta	acc	cca	ctc	gaa	ctg	gac	1075
Thr	Val	Ser	Asp	Thr	Ala	Phe	Glu	Pro	Val	Thr 320	Pro	Leu	Glu	Leu	Asp 325	
310					315											
acc	gtt	cct	act	ggc	gat	gac	att	cgc	gaa	gca	tac	gaa	ggc	atg	ctg	1123
Thr	Val	Pro	Thr	Gly 330	Asp	Asp	Ile	Arg	Glu 335	Ala	Tyr	Glu	Gly	Met	Leu 340	
ctg	aag	cca	acc	ggc	gct	cac	acc	gtg	acc	aac	aac	tac	gca	acc	aac	1171
Leu	Lys	Pro	Thr	Gly	Ala	His	Thr	Val 350	Thr	Asn	Asn	Tyr	Ala	Thr	Asn 355	
345																
acc	ttc	ggt	gaa	att	gcc	ctc	gcc	cca	ggt	aac	gag	cct	ttg	tac	cag	1219
Thr	Phe	Gly	Glu	Ile	Ala	Leu	Ala	Pro	Gly	Asn	Glu	Pro	Leu	Tyr	Gln	
360							365					370				
gcc	act	caa	atg	gtg	gca	ccg	gga	gcc	gaa	gcg	att	gcg	tac	gag	gcg	1267
Ala	Thr	Gln	Met	Val	Ala	Pro	Gly	Ala	Glu	Ala	Ile	Ala	Tyr	Glu	Ala	

375	380	385	
gaa aac gtc gca aag caa att acg ctg gat gac gga cgc tcc ggc aac			1315
Glu Asn Val Ala Lys Gln Ile Thr Leu Asp Asp Gly Arg Ser Gly Asn			
390	395	400	405
tac act cgc ggc gac tcc agc acg cct atg gca tgg ctt gtg cag gac			1363
Tyr Thr Arg Gly Asp Ser Ser Thr Pro Met Ala Trp Leu Val Gln Asp			
	410	415	420
ggt ggc gag acc atc aag tcc atc cgc acc ggc gac cag gtg gaa ttc			1411
Gly Gly Glu Thr Ile Lys Ser Ile Arg Thr Gly Asp Gln Val Glu Phe			
	425	430	435
cag gca cca gta atc ttc gat tac cgc tac gac ctg tgg aaa ttc cag			1459
Gln Ala Pro Val Ile Phe Asp Tyr Arg Tyr Asp Leu Trp Lys Phe Gln			
	440	445	450
cca acc acc cct gtc acc ggc aac acc gca agc tcc gac ctt cct atc			1507
Pro Thr Thr Pro Val Thr Gly Asn Thr Ala Ser Ser Asp Leu Pro Ile			
	455	460	465
acc tgg gat gac acc cgc gcg gct gag cta gct tca atc aat gac gtt			1555
Thr Trp Asp Asp Thr Arg Ala Ala Glu Leu Ala Ser Ile Asn Asp Val			
470	475	480	485
gct ggc gaa ttc cac atc gca agc ttc aac gtg ctc aac tac ttc acc			1603
Ala Gly Glu Phe His Ile Ala Ser Phe Asn Val Leu Asn Tyr Phe Thr			
	490	495	500
tct ctc ggc gaa gat gaa cca ggc tgc agc gca tac agg gat atc aac			1651
Ser Leu Gly Glu Asp Glu Pro Gly Cys Ser Ala Tyr Arg Asp Ile Asn			
	505	510	515
aac acc cca gtc acc gcc aac aac tgt aac gtc cgt ggc gct tac acc			1699
Asn Thr Pro Val Thr Ala Asn Asn Cys Asn Val Arg Gly Ala Tyr Thr			
	520	525	530
gaa gaa gca ctc gaa gat cag cag agc aag atc gtc gaa gca atc aac			1747
Glu Glu Ala Leu Glu Asp Gln Gln Ser Lys Ile Val Glu Ala Ile Asn			
	535	540	545
cgc ctt gac gtc gat gtt ctt			1768
Arg Leu Asp Val Asp Val Leu			
550	555		

<210> 6

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<212> PRT

<213> Corynebacterium glutamicum

<400> 6

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Gly	Thr	Ala	Pro	Val	Ile	Asn	Glu	Ile	Tyr	Glu	Gly	Gly	Gly	Asn	Ser
			35				40						45		

Gly Ser Leu Phe Ser Asn Asp Phe Ile Glu Leu Tyr Asn Pro Thr Ser
50 55 60

Gly Asp Ile Ser Leu Asp Gly Trp Ser Val Thr Tyr Tyr Ala Ala Asn
65 70 75 80

Gly Asn Ser Gly Gly Thr Thr Asn Leu Thr Gly Asn Ile Pro Ala Asn
85 90 95

Gly Tyr Tyr Leu Ile Gln Gln Arg Ala Gly Ser Asn Asn Thr Gly Ala
100 105 110

Leu Pro Thr Pro Asp Ala Thr Gly Asn Leu Ala Met Gly Ala Ser Gln
115 120 125

Gly Ser Val Ala Leu Thr Asp Asn Ser Gly Leu Thr Ala Asp Leu Val
130 135 140

Gly Phe Gly Gly Thr Ser Met Phe Glu Gly Thr Ala Ala Ala Pro Glu
145 150 155 160

Thr Ser Asn Lys Leu Ser Val Gln Arg Lys Glu Val Gly Ala Asp Ser
165 170 175

Asp Asn Asn Ser Val Asp Phe Glu Thr Gly Ala Pro Thr Pro Thr Ser
180 185 190

Ser Gly Gly Ser Ala Pro Val Asp Pro Gly Glu Pro Glu Thr Pro Val
195 200 205

Asn Pro Gly Glu Thr Val Ser Ile Ala Gln Ile Gln Gly Thr Gly Leu
210 215 220

Ala Thr Pro Leu Glu Gly Gln Thr Val Thr Thr Glu Gly Ile Val Thr
225 230 235 240

Ala Val Tyr Ala Glu Gly Gly Phe Asn Gly Tyr Tyr Ile Gln Thr Pro
245 250 255

Gly Ser Gly Thr Ala Pro Lys Val Ala Gly Asp Ala Ser Asp Gly Ile
260 265 270

Phe Val Tyr Val Gly Ser Asn Gly Ser Tyr Pro Glu Leu Gly Ala Ser
275 280 285

Val Thr Val Thr Gly Lys Ala Thr Glu His Tyr Glu Met Thr Gln Leu
290 295 300

Gly Asn Ser Ser Phe Thr Val Ser Asp Thr Ala Phe Glu Pro Val Thr
305 310 315 320

Pro Leu Glu Leu Asp Thr Val Pro Thr Gly Asp Asp Ile Arg Glu Ala
325 330 335

Tyr Glu Gly Met Leu Leu Lys Pro Thr Gly Ala His Thr Val Thr Asn
340 345 350

Asn Tyr Ala Thr Asn Thr Phe Gly Glu Ile Ala Leu Ala Pro Gly Asn
355 360 365

Glu Pro Leu Tyr Gln Ala Thr Gln Met Val Ala Pro Gly Ala Glu Ala
 370 375 380
 Ile Ala Tyr Glu Ala Glu Asn Val Ala Lys Gln Ile Thr Leu Asp Asp
 385 390 395 400
 Gly Arg Ser Gly Asn Tyr Thr Arg Gly Asp Ser Ser Thr Pro Met Ala
 405 410 415
 Trp Leu Val Gln Asp Gly Gly Glu Thr Ile Lys Ser Ile Arg Thr Gly
 420 425 430
 Asp Gln Val Glu Phe Gln Ala Pro Val Ile Phe Asp Tyr Arg Tyr Asp
 435 440 445
 Leu Trp Lys Phe Gln Pro Thr Thr Pro Val Thr Gly Asn Thr Ala Ser
 450 455 460
 Ser Asp Leu Pro Ile Thr Trp Asp Asp Thr Arg Ala Ala Glu Leu Ala
 465 470 475 480
 Ser Ile Asn Asp Val Ala Gly Glu Phe His Ile Ala Ser Phe Asn Val
 485 490 495
 Leu Asn Tyr Phe Thr Ser Leu Gly Glu Asp Glu Pro Gly Cys Ser Ala
 500 505 510
 Tyr Arg Asp Ile Asn Asn Thr Pro Val Thr Ala Asn Asn Cys Asn Val
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 545 550 555

<210> 7

<211> 1369

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1369)

<223> FRXA00538

<400> 7

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 Met Ser Arg Ile Ser
 1 5

gcg cgc act ctg gca atc gca ctt gcc ggt gca acc gcg gcc agc ctg 163
 Ala Arg Thr Leu Ala Ile Ala Leu Ala Gly Ala Thr Ala Ala Ser Leu
 10 15 20

gca gtt gtt cca gca gca aca gct aat cct gcc gga acc gct cct gtc 211
 Ala Val Val Pro Ala Ala Thr Ala Asn Pro Ala Gly Thr Ala Pro Val
 25 30 35

atc aac gaa atc tac gaa ggc ggt gga aac agc gga tcg ttg ttc tcc Ile Asn Glu Ile Tyr Glu Gly Gly Gly Asn Ser Gly Ser Leu Phe Ser 40 45 50	259
aac gac ttc att gag ctc tac aac cca acc tca ggg gac att tcc ctc Asn Asp Phe Ile Glu Leu Tyr Asn Pro Thr Ser Gly Asp Ile Ser Leu 55 60 65	307
gac ggt tgg agc gtt acc tac tac gca gcc aac ggt aac tcc ggc gga Asp Gly Trp Ser Val Thr Tyr Tyr Ala Ala Asn Gly Asn Ser Gly Gly 70 75 80 85	355
acc aca aac ctg acc gga aac atc cct gcc aac ggt tac tac ctc atc Thr Thr Asn Leu Thr Gly Asn Ile Pro Ala Asn Gly Tyr Tyr Leu Ile 90 95 100	403
cag caa cgc gca ggc agc aac aac acc ggc gct ctg cct acc cca gac Gln Gln Arg Ala Gly Ser Asn Asn Thr Gly Ala Leu Pro Thr Pro Asp 105 110 115	451
gcc acc ggt aac ttg gca atg ggt gcc tcc caa gga tca gtt gca ctg Ala Thr Gly Asn Leu Ala Met Gly Ala Ser Gln Gly Ser Val Ala Leu 120 125 130	499
acc gac aac tct ggc cta acc gct gac ctt gtc gga ttc ggt ggc acg Thr Asp Asn Ser Gly Leu Thr Ala Asp Leu Val Gly Phe Gly Gly Thr 135 140 145	547
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tct gtt caa cgc aaa gaa gtt ggc gct gac tct gat aac aac tcc gta Ser Val Gln Arg Lys Glu Val Gly Ala Asp Ser Asp Asn Asn Ser Val 170 175 180	643
gac ttc gag act gga gct cca act cca acg tcc tcg gga gga tcc gct Asp Phe Glu Thr Gly Ala Pro Thr Pro Thr Ser Ser Gly Gly Ser Ala 185 190 195	691
cct gtt gac cca ggc gag cca gaa act cca gta aac cct ggg gaa aca Pro Val Asp Pro Gly Glu Pro Glu Thr Pro Val Asn Pro Gly Glu Thr 200 205 210	739
gtc tcc atc gca caa atc caa gga acc ggt ctc gct acc cca ctc gag Val Ser Ile Ala Gln Ile Gln Gly Thr Gly Leu Ala Thr Pro Leu Glu 215 220 225	787
ggt cag acc gtc acc acc gaa ggt att gtc act gcc gtt tac gca gaa Gly Gln Thr Val Thr Glu Gly Ile Val Thr Ala Val Tyr Ala Glu 230 235 240 245	835
ggt ggc ttc aac ggt tac tac atc cag aca cct gga tct ggt act gca Gly Gly Phe Asn Gly Tyr Tyr Ile Gln Thr Pro Gly Ser Gly Thr Ala 250 255 260	883
cca aag gtt gct ggc gac gca tcc gac ggc atc ttc gtc tac gtg gga Pro Lys Val Ala Gly Asp Ala Ser Asp Gly Ile Phe Val Tyr Val Gly 265 270 275	931

agc aat ggt tcc tac cca gag ctc ggc gca tct gtc acc gtc act ggc 979
 Ser Asn Gly Ser Tyr Pro Glu Leu Gly Ala Ser Val Thr Val Thr Gly
 280 285 290

aag gcc acc gaa cac tac gag atg act cag cta ggc aac tcc tcc ttc 1027
 Lys Ala Thr Glu His Tyr Glu Met Thr Gln Leu Gly Asn Ser Ser Phe
 295 300 305

acc gtt tcg gac acc gca ttc gag cca gta acc cca ctc gaa ctg gac 1075
 Thr Val Ser Asp Thr Ala Phe Glu Pro Val Thr Pro Leu Glu Leu Asp
 310 315 320 325

acc gtt cct act ggc gat gac att cgc gaa gca tac gaa ggc atg ctg 1123
 Thr Val Pro Thr Gly Asp Asp Ile Arg Glu Ala Tyr Glu Gly Met Leu
 330 335 340

ctg aag cca acc ggc gct cac acc gtg acc aac aac tac gca acc aac 1171
 Leu Lys Pro Thr Gly Ala His Thr Val Thr Asn Asn Tyr Ala Thr Asn
 345 350 355

acc ttc ggt gaa att gcc ctc gcc cca ggt aac gag cct ttg tac cag 1219
 Thr Phe Gly Glu Ile Ala Leu Ala Pro Gly Asn Glu Pro Leu Tyr Gln
 360 365 370

gcc act caa atg gtg gca ccg gga gcc gaa gcg att gcg tac gag gcg 1267
 Ala Thr Gln Met Val Ala Pro Gly Ala Glu Ala Ile Ala Tyr Glu Ala
 375 380 385

gaa aac gtc gca aag caa att acg ctg gat gac gga cgc tcc ggc aac 1315
 Glu Asn Val Ala Lys Gln Ile Thr Leu Asp Asp Gly Arg Ser Gly Asn
 390 395 400 405

tac act cgc ggc gac tcc agc acg cct atg gca tgg ctt gtg cag gac 1363
 Tyr Thr Arg Gly Asp Ser Ser Thr Pro Met Ala Trp Leu Val Gln Asp
 410 415 420

ggt ggc 1369
 Gly Gly

<210> 8

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 8

Met Ser Arg Ile Ser Ala Arg Thr Leu Ala Ile Ala Leu Ala Gly Ala
 1 5 10 15

Thr Ala Ala Ser Leu Ala Val Val Pro Ala Ala Thr Ala Asn Pro Ala
 20 25 30

Gly Thr Ala Pro Val Ile Asn Glu Ile Tyr Glu Gly Gly Gly Asn Ser
 35 40 45

Gly Ser Leu Phe Ser Asn Asp Phe Ile Glu Leu Tyr Asn Pro Thr Ser
 50 55 60

Gly Asp Ile Ser Leu Asp Gly Trp Ser Val Thr Tyr Tyr Ala Ala Asn
 65 70 75 80

Gly Asn Ser Gly Gly Thr Thr Asn Leu Thr Gly Asn Ile Pro Ala Asn
85 90 95

Gly Tyr Tyr Leu Ile Gln Gln Arg Ala Gly Ser Asn Asn Thr Gly Ala
100 105 110

Leu Pro Thr Pro Asp Ala Thr Gly Asn Leu Ala Met Gly Ala Ser Gln
115 120 125

Gly Ser Val Ala Leu Thr Asp Asn Ser Gly Leu Thr Ala Asp Leu Val
130 135 140

Gly Phe Gly Gly Thr Ser Met Phe Glu Gly Thr Ala Ala Ala Pro Glu
145 150 155 160

Thr Ser Asn Lys Leu Ser Val Gln Arg Lys Glu Val Gly Ala Asp Ser
165 170 175

Asp Asn Asn Ser Val Asp Phe Glu Thr Gly Ala Pro Thr Pro Thr Ser
180 185 190

Ser Gly Gly Ser Ala Pro Val Asp Pro Gly Glu Pro Glu Thr Pro Val
195 200 205

Asn Pro Gly Glu Thr Val Ser Ile Ala Gln Ile Gln Gly Thr Gly Leu
210 215 220

Ala Thr Pro Leu Glu Gly Gln Thr Val Thr Thr Glu Gly Ile Val Thr
225 230 235 240

Ala Val Tyr Ala Glu Gly Gly Phe Asn Gly Tyr Tyr Ile Gln Thr Pro
245 250 255

Gly Ser Gly Thr Ala Pro Lys Val Ala Gly Asp Ala Ser Asp Gly Ile
260 265 270

Phe Val Tyr Val Gly Ser Asn Gly Ser Tyr Pro Glu Leu Gly Ala Ser
275 280 285

Val Thr Val Thr Gly Lys Ala Thr Glu His Tyr Glu Met Thr Gln Leu
290 295 300

Gly Asn Ser Ser Phe Thr Val Ser Asp Thr Ala Phe Glu Pro Val Thr
305 310 315 320

Pro Leu Glu Leu Asp Thr Val Pro Thr Gly Asp Asp Ile Arg Glu Ala
325 330 335

Tyr Glu Gly Met Leu Leu Lys Pro Thr Gly Ala His Thr Val Thr Asn
340 345 350

Asn Tyr Ala Thr Asn Thr Phe Gly Glu Ile Ala Leu Ala Pro Gly Asn
355 360 365

Glu Pro Leu Tyr Gln Ala Thr Gln Met Val Ala Pro Gly Ala Glu Ala
370 375 380

Ile Ala Tyr Glu Ala Glu Asn Val Ala Lys Gln Ile Thr Leu Asp Asp
385 390 395 400

Gly Arg Ser Gly Asn Tyr Thr Arg Gly Asp Ser Ser Thr Pro Met Ala
 405 410 415

Trp Leu Val Gln Asp Gly Gly
 420

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(880)

<223> RXA00823

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 Met Gly Ser Ile Thr
 1 5

ccg cag aag cgg cct cgc gtg ggg tct cac atc gcg aac aag ggt caa 163
 Pro Gln Lys Arg Pro Arg Val Gly Ser His Ile Ala Asn Lys Gly Gln
 10 15 20

gag act gat atc ggg cga aaa cgc cga gct cga cgc atc aat cgc aca 211
 Glu Thr Asp Ile Gly Arg Lys Arg Arg Ala Arg Arg Ile Asn Arg Thr
 25 30 35

ctc acc gtg gca tat ccg gat gcg cac tgc gaa tta gat ttc acc aat 259
 Leu Thr Val Ala Tyr Pro Asp Ala His Cys Glu Leu Asp Phe Thr Asn
 40 45 50

ccg cta gaa ctc acg gtc gcc acc att ttg tcc gcc cag tgc acg gac 307
 Pro Leu Glu Leu Thr Val Ala Thr Ile Leu Ser Ala Gln Cys Thr Asp
 55 60 65

gtt cgc gtg aac cag gtg acg ccc gcg ttg ttc aag cgc tat ccg acg 355
 Val Arg Val Asn Gln Val Thr Pro Ala Leu Phe Lys Arg Tyr Pro Thr
 70 75 80 85

gcc aca gat tac gcc aac gcc gat cgc acg gaa ttg gag gag ttc atc 403
 Ala Thr Asp Tyr Ala Asn Ala Asp Arg Thr Glu Leu Glu Glu Phe Ile
 90 95 100

cgt ccg aca ggc ttt tac cgc aac aag gcc act tct tta atc ggc ctg 451
 Arg Pro Thr Gly Phe Tyr Arg Asn Lys Ala Thr Ser Leu Ile Gly Leu
 105 110 115

ggg gag gca cta att tcg ctt cac gac ggc cag gtc ccc ggt acc ctt 499
 Gly Glu Ala Leu Ile Ser Leu His Asp Gly Gln Val Pro Gly Thr Leu
 120 125 130

gag cag cta gtt gag ctg ccg ggg gtc ggg cgg aaa acc gcc aac gtg 547
 Glu Gln Leu Val Glu Leu Pro Gly Val Gly Arg Lys Thr Ala Asn Val
 135 140 145

gtg ctg gga aat gct ttc ggt gtt ccg gga atc acg gtg gat aca cac 595

Val Leu Gly Asn Ala Phe Gly Val Pro Gly Ile Thr Val Asp Thr His
150 155 160 165

ttt ggc agg ttg gtg cgt cgc ctg aag ctc act gat gaa gaa gat ccc 643
Phe Gly Arg Leu Val Arg Arg Leu Lys Leu Thr Asp Glu Glu Asp Pro
170 175 180

gtc aag gtg gaa aaa gtg atg aac gaa ctc atc gaa aag cct gag tgg 691
Val Lys Val Glu Lys Val Met Asn Glu Leu Ile Glu Lys Pro Glu Trp
185 190 195

acc atg ttt tca cat agg ctg atc ttc cac gga cgt agg ata tgt cat 739
Thr Met Phe Ser His Arg Leu Ile Phe His Gly Arg Arg Ile Cys His
200 205 210

agt cga cgc gcc gcc tgt gga gcc tgc atg ctg gca gct gat tgc cca 787
Ser Arg Arg Ala Ala Cys Gly Ala Cys Met Leu Ala Ala Asp Cys Pro
215 220 225

tcc ttt ggt ttg gag ggg ccg tca gat cca ttt gag gcg caa aaa ctc 835
Ser Phe Gly Leu Glu Gly Pro Ser Asp Pro Phe Glu Ala Gln Lys Leu
230 235 240 245

att aaa agt gat gat agg gag cac ctg ctg aaa atg gca gga atg 880
Ile Lys Ser Asp Arg Glu His Leu Lys Met Ala Gly Met
250 255 260

tagaaaacaa atgacaagca gtg 903

<210> 10

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 10

Met Gly Ser Ile Thr Pro Gln Lys Arg Pro Arg Val Gly Ser His Ile
1 5 10 15

Ala Asn Lys Gly Gln Glu Thr Asp Ile Gly Arg Lys Arg Arg Ala Arg
20 25 30

Arg Ile Asn Arg Thr Leu Thr Val Ala Tyr Pro Asp Ala His Cys Glu
35 40 45

Leu Asp Phe Thr Asn Pro Leu Glu Leu Thr Val Ala Thr Ile Leu Ser
50 55 60

Ala Gln Cys Thr Asp Val Arg Val Asn Gln Val Thr Pro Ala Leu Phe
65 70 75 80

Lys Arg Tyr Pro Thr Ala Thr Asp Tyr Ala Asn Ala Asp Arg Thr Glu
85 90 95

Leu Glu Glu Phe Ile Arg Pro Thr Gly Phe Tyr Arg Asn Lys Ala Thr
100 105 110

Ser Leu Ile Gly Leu Gly Glu Ala Leu Ile Ser Leu His Asp Gly Gln
115 120 125

Val Pro Gly Thr Leu Glu Gln Leu Val Glu Leu Pro Gly Val Gly Arg

130	135	140
Lys Thr Ala Asn Val Val Leu Gly Asn Ala Phe Gly Val Pro Gly Ile		
145	150	155 160
Thr Val Asp Thr His Phe Gly Arg Leu Val Arg Arg Leu Lys Leu Thr		
	165	170 175
Asp Glu Glu Asp Pro Val Lys Val Glu Lys Val Met Asn Glu Leu Ile		
	180	185 190
Glu Lys Pro Glu Trp Thr Met Phe Ser His Arg Leu Ile Phe His Gly		
	195	200 205
Arg Arg Ile Cys His Ser Arg Arg Ala Ala Cys Gly Ala Cys Met Leu		
	210	215 220
Ala Ala Asp Cys Pro Ser Phe Gly Leu Glu Gly Pro Ser Asp Pro Phe		
	225	230 235 240
Glu Ala Gln Lys Leu Ile Lys Ser Asp Asp Arg Glu His Leu Leu Lys		
	245	250 255
Met Ala Gly Met		
	260	

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 <211> 1740
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1717)
 <223> RXA02145

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 tcattgagcc actcgccct gcattctggg agcgtaagtc atg agt cta gct acc 115
 Met Ser Leu Ala Thr
 1 5
 gtg gga aac aat ctt gat tcc cgt tac acc atg gcg tcg ggt atc cgt 163
 Val Gly Asn Asn Leu Asp Ser Arg Tyr Thr Met Ala Ser Gly Ile Arg
 10 15 20
 cgc cag atc aac aag gtc ttc cca act cac tgg tcc ttc atg ctc ggc 211
 Arg Gln Ile Asn Lys Val Phe Pro Thr His Trp Ser Phe Met Leu Gly
 25 30 35
 gag att gcg ctt tac agc ttc atc gtc ttg ctg ctg act ggt gtc tac 259
 Glu Ile Ala Leu Tyr Ser Phe Ile Val Leu Leu Leu Thr Gly Val Tyr
 40 45 50
 ctg acc ctg ttc ttc gac cca tca atc acc aag gtc att tat gac ggc 307
 Leu Thr Leu Phe Phe Asp Pro Ser Ile Thr Lys Val Ile Tyr Asp Gly
 55 60 65
 ggc tac ctc cca ctg aac ggt gtg gag atg tcc cgt gca tac gca act 355

Gly	Tyr	Leu	Pro	Leu	Asn	Gly	Val	Glu	Met	Ser	Arg	Ala	Tyr	Ala	Thr	
70					75					80					85	
gcg	ttg	gat	att	tcc	ttc	gag	gtt	cgc	ggg	ggg	ctg	ttc	atc	cgc	cag	403
Ala	Leu	Asp	Ile	Ser	Phe	Glu	Val	Arg	Gly	Gly	Leu	Phe	Ile	Arg	Gln	
				90					95					100		
atg	cac	cac	tgg	gca	gcc	ctg	ctg	ttc	gtt	gta	tcc	atg	ctg	gtt	cac	451
Met	His	His	Trp	Ala	Ala	Leu	Leu	Phe	Val	Val	Ser	Met	Leu	Val	His	
			105					110					115			
atg	ctc	cgt	att	ttc	ttc	acc	ggg	gcg	ttc	cgt	cgc	cca	cgt	gaa	gca	499
Met	Leu	Arg	Ile	Phe	Phe	Thr	Gly	Ala	Phe	Arg	Arg	Pro	Arg	Glu	Ala	
		120					125					130				
aac	tgg	atc	atc	ggg	gtt	gtt	ctg	atc	atc	ctg	ggg	atg	gct	gaa	ggc	547
Asn	Trp	Ile	Ile	Gly	Val	Val	Leu	Ile	Ile	Leu	Gly	Met	Ala	Glu	Gly	
	135					140					145					
ttc	atg	ggg	tac	tcc	ctg	cct	gat	gac	ctg	ctc	tct	ggg	gtt	ggg	ctt	595
Phe	Met	Gly	Tyr	Ser	Leu	Pro	Asp	Asp	Leu	Leu	Ser	Gly	Val	Gly	Leu	
150					155					160					165	
cga	atc	atg	tcc	gcc	atc	atc	gtt	ggg	ctt	ccg	atc	ata	ggg	acc	tgg	643
Arg	Ile	Met	Ser	Ala	Ile	Ile	Val	Gly	Leu	Pro	Ile	Ile	Gly	Thr	Trp	
				170					175					180		
atg	cac	tgg	ctg	atc	ttc	ggg	gga	gac	ttc	cca	tcc	gat	ctg	atg	ctg	691
Met	His	Trp	Leu	Ile	Phe	Gly	Gly	Asp	Phe	Pro	Ser	Asp	Leu	Met	Leu	
			185					190					195			
gac	cgc	ttc	tac	atc	gca	cac	gtt	cta	atc	atc	cca	gct	atc	ctg	ctt	739
Asp	Arg	Phe	Tyr	Ile	Ala	His	Val	Leu	Ile	Ile	Pro	Ala	Ile	Leu	Leu	
		200					205					210				
ggc	ttg	atc	gca	gct	cac	ctg	gca	ctt	gtt	tgg	tac	cag	aag	cac	acc	787
Gly	Leu	Ile	Ala	Ala	His	Leu	Ala	Leu	Val	Trp	Tyr	Gln	Lys	His	Thr	
	215					220					225					
cag	ttc	cca	ggc	gct	ggc	cgc	act	gag	aac	aac	gtg	atc	ggg	atc	cga	835
Gln	Phe	Pro	Gly	Ala	Gly	Arg	Thr	Glu	Asn	Asn	Val	Ile	Gly	Ile	Arg	
230					235					240					245	
atc	atg	cct	ctg	ttc	gca	gtt	aag	gct	gtt	gct	ttc	ggc	ctc	atc	gtc	883
Ile	Met	Pro	Leu	Phe	Ala	Val	Lys	Ala	Val	Ala	Phe	Gly	Leu	Ile	Val	
				250					255					260		
ttc	ggg	ttc	ctc	gca	ctg	ctt	gct	ggg	gtc	acc	acc	att	aac	gca	att	931
Phe	Gly	Phe	Leu	Ala	Leu	Leu	Ala	Gly	Val	Thr	Thr	Ile	Asn	Ala	Ile	
			265					270					275			
tgg	aat	ctt	gga	ccg	tac	aac	cct	tca	cag	gtg	tct	gct	ggg	tcc	cag	979
Trp	Asn	Leu	Gly	Pro	Tyr	Asn	Pro	Ser	Gln	Val	Ser	Ala	Gly	Ser	Gln	
		280					285					290				
cct	gac	gtt	tac	atg	ctg	tgg	aca	gat	ggg	gct	gct	cgt	gtc	atg	ccg	1027
Pro	Asp	Val	Tyr	Met	Leu	Trp	Thr	Asp	Gly	Ala	Ala	Arg	Val	Met	Pro	
		295				300					305					
gca	tgg	gag	ctc	tac	ctc	ggg	aac	tac	act	att	cca	gca	gtc	ttc	tgg	1075
Ala	Trp	Glu	Leu	Tyr	Leu	Gly	Asn	Tyr	Thr	Ile	Pro	Ala	Val	Phe	Trp	

310	315	320	325	
gtt gct gtg atg ctg ggt atc ctc gtg gtt ctg ctt gtg act tac cca				1123
Val Ala Val Met Leu Gly Ile Leu Val Val Leu Leu Val Thr Tyr Pro				
	330	335	340	
ttc att gag cgt aag ttc acc ggc gac gat gca cac cac aac ttg ctg				1171
Phe Ile Glu Arg Lys Phe Thr Gly Asp Asp Ala His His Asn Leu Leu				
	345	350	355	
cag cgt cct cgc gat gtt cca gtc cgc acc tca ctc ggt gtc atg gcg				1219
Gln Arg Pro Arg Asp Val Pro Val Arg Thr Ser Leu Gly Val Met Ala				
	360	365	370	
ctt gtc ttc tac atc ctg ctt acc gtt tct ggt ggt aac gat gtt tac				1267
Leu Val Phe Tyr Ile Leu Leu Thr Val Ser Gly Gly Asn Asp Val Tyr				
	375	380	385	
gca atg cag ttc cat gtt tca ctg aac gcg atg acc tgg atc ggt cgt				1315
Ala Met Gln Phe His Val Ser Leu Asn Ala Met Thr Trp Ile Gly Arg				
	390	395	400	405
atc ggc ctc atc gtt gga cca gct att gca tac ttc atc act tac cga				1363
Ile Gly Leu Ile Val Gly Pro Ala Ile Ala Tyr Phe Ile Thr Tyr Arg				
	410	415	420	
ctg tgc atc ggc ttg cag cgc tct gac cgc gag gtc ctg gag cac ggc				1411
Leu Cys Ile Gly Leu Gln Arg Ser Asp Arg Glu Val Leu Glu His Gly				
	425	430	435	
atc gag acc ggt atc atc aag cag atg cca aat ggt gcc ttc att gaa				1459
Ile Glu Thr Gly Ile Ile Lys Gln Met Pro Asn Gly Ala Phe Ile Glu				
	440	445	450	
gtt cac cag cca ctt ggc cca gtt gat gac cat ggt cac cca atc cca				1507
Val His Gln Pro Leu Gly Pro Val Asp Asp His Gly His Pro Ile Pro				
	455	460	465	
ctg cca tac gct ggc gct gcg gtt cca aag cag atg aac cag ctt ggt				1555
Leu Pro Tyr Ala Gly Ala Ala Val Pro Lys Gln Met Asn Gln Leu Gly				
	470	475	480	485
tac gct gag gtt gaa acc cgc ggt gga ttc ttc gga cct gat cca gaa				1603
Tyr Ala Glu Val Glu Thr Arg Gly Gly Phe Phe Gly Pro Asp Pro Glu				
	490	495	500	
gac atc cgt gcg aag gct aag gaa att gag cac gca aac cac att gag				1651
Asp Ile Arg Ala Lys Ala Lys Glu Ile Glu His Ala Asn His Ile Glu				
	505	510	515	
gaa gcg aac act ctt cgt gca ctc aac gag gca aac att gag cgt gac				1699
Glu Ala Asn Thr Leu Arg Ala Leu Asn Glu Ala Asn Ile Glu Arg Asp				
	520	525	530	
aag aat gag ggc aag aac tagtttctag gacttcatct ctg				1740
Lys Asn Glu Gly Lys Asn				
	535			

<210> 12

<211> 539

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

Met Ser Leu Ala Thr Val Gly Asn Asn Leu Asp Ser Arg Tyr Thr Met
1 5 10 15

Ala Ser Gly Ile Arg Arg Gln Ile Asn Lys Val Phe Pro Thr His Trp
20 25 30

Ser Phe Met Leu Gly Glu Ile Ala Leu Tyr Ser Phe Ile Val Leu Leu
35 40 45

Leu Thr Gly Val Tyr Leu Thr Leu Phe Phe Asp Pro Ser Ile Thr Lys
50 55 60

Val Ile Tyr Asp Gly Gly Tyr Leu Pro Leu Asn Gly Val Glu Met Ser
65 70 75 80

Arg Ala Tyr Ala Thr Ala Leu Asp Ile Ser Phe Glu Val Arg Gly Gly
85 90 95

Leu Phe Ile Arg Gln Met His His Trp Ala Ala Leu Leu Phe Val Val
100 105 110

Ser Met Leu Val His Met Leu Arg Ile Phe Phe Thr Gly Ala Phe Arg
115 120 125

Arg Pro Arg Glu Ala Asn Trp Ile Ile Gly Val Val Leu Ile Ile Leu
130 135 140

Gly Met Ala Glu Gly Phe Met Gly Tyr Ser Leu Pro Asp Asp Leu Leu
145 150 155 160

Ser Gly Val Gly Leu Arg Ile Met Ser Ala Ile Ile Val Gly Leu Pro
165 170 175

Ile Ile Gly Thr Trp Met His Trp Leu Ile Phe Gly Gly Asp Phe Pro
180 185 190

Ser Asp Leu Met Leu Asp Arg Phe Tyr Ile Ala His Val Leu Ile Ile
195 200 205

Pro Ala Ile Leu Leu Gly Leu Ile Ala Ala His Leu Ala Leu Val Trp
210 215 220

Tyr Gln Lys His Thr Gln Phe Pro Gly Ala Gly Arg Thr Glu Asn Asn
225 230 235 240

Val Ile Gly Ile Arg Ile Met Pro Leu Phe Ala Val Lys Ala Val Ala
245 250 255

Phe Gly Leu Ile Val Phe Gly Phe Leu Ala Leu Leu Ala Gly Val Thr
260 265 270

Thr Ile Asn Ala Ile Trp Asn Leu Gly Pro Tyr Asn Pro Ser Gln Val
275 280 285

Ser Ala Gly Ser Gln Pro Asp Val Tyr Met Leu Trp Thr Asp Gly Ala
290 295 300

Ala Arg Val Met Pro Ala Trp Glu Leu Tyr Leu Gly Asn Tyr Thr Ile
 305 310 315 320

Pro Ala Val Phe Trp Val Ala Val Met Leu Gly Ile Leu Val Val Leu
 325 330 335

Leu Val Thr Tyr Pro Phe Ile Glu Arg Lys Phe Thr Gly Asp Asp Ala
 340 345 350

His His Asn Leu Leu Gln Arg Pro Arg Asp Val Pro Val Arg Thr Ser
 355 360 365

Leu Gly Val Met Ala Leu Val Phe Tyr Ile Leu Leu Thr Val Ser Gly
 370 375 380

Gly Asn Asp Val Tyr Ala Met Gln Phe His Val Ser Leu Asn Ala Met
 385 390 395 400

Thr Trp Ile Gly Arg Ile Gly Leu Ile Val Gly Pro Ala Ile Ala Tyr
 405 410 415

Phe Ile Thr Tyr Arg Leu Cys Ile Gly Leu Gln Arg Ser Asp Arg Glu
 420 425 430

Val Leu Glu His Gly Ile Glu Thr Gly Ile Ile Lys Gln Met Pro Asn
 435 440 445

Gly Ala Phe Ile Glu Val His Gln Pro Leu Gly Pro Val Asp Asp His
 450 455 460

Gly His Pro Ile Pro Leu Pro Tyr Ala Gly Ala Ala Val Pro Lys Gln
 465 470 475 480

Met Asn Gln Leu Gly Tyr Ala Glu Val Glu Thr Arg Gly Gly Phe Phe
 485 490 495

Gly Pro Asp Pro Glu Asp Ile Arg Ala Lys Ala Lys Glu Ile Glu His
 500 505 510

Ala Asn His Ile Glu Glu Ala Asn Thr Leu Arg Ala Leu Asn Glu Ala
 515 520 525

Asn Ile Glu Arg Asp Lys Asn Glu Gly Lys Asn
 530 535

<210> 13

<211> 759

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(736)

<223> RXA01064

<400> 13

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 cttatccact acccagacct ctacaagaaa gttccccaga atg tca cta tct att 115
 Met Ser Leu Ser Ile

1 5

agt ttt cat aaa att gca ctc tct gcc acc acc ttg ctt ggc gct gtc 163
Ser Phe His Lys Ile Ala Leu Ser Ala Thr Thr Leu Leu Gly Ala Val
10 15 20

gca atc tct gcc tgt gcg cta gta act caa gca cct cct att aac gca 211
Ala Ile Ser Ala Cys Ala Leu Val Thr Gln Ala Pro Pro Ile Asn Ala
25 30 35

gcc ccg gtt act ggc agc agc tca tta agc ttc acc ctc gac ctg ggc 259
Ala Pro Val Thr Gly Ser Ser Ser Leu Ser Phe Thr Leu Asp Leu Gly
40 45 50

acc acc acc cct acc agc atc gac aca gta aaa ctc act cag caa gca 307
Thr Thr Thr Pro Thr Ser Ile Asp Thr Val Lys Leu Thr Gln Gln Ala
55 60 65

caa aat caa gcg gca cca cgc gtt gca gcg agc ctg gtg cgc gtg gtt 355
Gln Asn Gln Ala Ala Pro Arg Val Ala Ala Ser Leu Val Arg Val Val
70 75 80 85

gac ggc gac acc att gtc gtg aac tat cag ggt gct cag aaa act gtt 403
Asp Gly Asp Thr Ile Val Val Asn Tyr Gln Gly Ala Gln Lys Thr Val
90 95 100

cgt atg atc ggt att gat tcc ccc gaa acc aaa cac ccc acc aag cct 451
Arg Met Ile Gly Ile Asp Ser Pro Glu Thr Lys His Pro Thr Lys Pro
105 110 115

gtg ggc ttc tac gga cca gaa tct tca cag aat ctc acc acc atg ctg 499
Val Gly Phe Tyr Gly Pro Glu Ser Ser Gln Asn Leu Thr Thr Met Leu
120 125 130

cgc ggt gcc acc atc aca cta gaa ttt gat tcc acc caa gcc cgc gaa 547
Arg Gly Ala Thr Ile Thr Leu Glu Phe Asp Ser Thr Gln Ala Arg Glu
135 140 145

gat caa tac gga cgc ctg ctt gct tat gtc tgg tac acc aag ggc gat 595
Asp Gln Tyr Gly Arg Leu Leu Ala Tyr Val Trp Tyr Thr Lys Gly Asp
150 155 160 165

agc ggt ctt aag ctt gcc aat ttg gaa caa att gcc tca ggc tct gct 643
Ser Gly Leu Lys Leu Ala Asn Leu Glu Gln Ile Ala Ser Gly Ser Ala
170 175 180

gct gaa tac agc ttc gac acc cgc tac aac cac cgc aat att ttc cta 691
Ala Glu Tyr Ser Phe Asp Thr Arg Tyr Asn His Arg Asn Ile Phe Leu
185 190 195

cgt gca caa acc ctt gcc aag gca agc agt cta ggt atg tgg ggt 736
Arg Ala Gln Thr Leu Ala Lys Ala Ser Ser Leu Gly Met Trp Gly
200 205 210

taaaagaaac ccacctatac caa 759

<210> 14

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 14

Met Ser Leu Ser Ile Ser Phe His Lys Ile Ala Leu Ser Ala Thr Thr
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Leu Leu Gly Ala Val Ala Ile Ser Ala Cys Ala Leu Val Thr Gln Ala
 20 25 30

Pro Pro Ile Asn Ala Ala Pro Val Thr Gly Ser Ser Ser Leu Ser Phe
 35 40 45

Thr Leu Asp Leu Gly Thr Thr Thr Pro Thr Ser Ile Asp Thr Val Lys
 50 55 60

Leu Thr Gln Gln Ala Gln Asn Gln Ala Ala Pro Arg Val Ala Ala Ser
 65 70 75 80

Leu Val Arg Val Val Asp Gly Asp Thr Ile Val Val Asn Tyr Gln Gly
 85 90 95

Ala Gln Lys Thr Val Arg Met Ile Gly Ile Asp Ser Pro Glu Thr Lys
 100 105 110

His Pro Thr Lys Pro Val Gly Phe Tyr Gly Pro Glu Ser Ser Gln Asn
 115 120 125

Leu Thr Thr Met Leu Arg Gly Ala Thr Ile Thr Leu Glu Phe Asp Ser
 130 135 140

Thr Gln Ala Arg Glu Asp Gln Tyr Gly Arg Leu Leu Ala Tyr Val Trp
 145 150 155 160

Tyr Thr Lys Gly Asp Ser Gly Leu Lys Leu Ala Asn Leu Glu Gln Ile
 165 170 175

Ala Ser Gly Ser Ala Ala Glu Tyr Ser Phe Asp Thr Arg Tyr Asn His
 180 185 190

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His Ala Val Glu Met Ile Arg Gly Arg Arg Val Phe Val Ala Gly Met	
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Val Ala Lys Phe Ala Ala Thr Leu Gly Leu Ser Leu Lys His Val Val	
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Phe Val Ala Gly Met Leu Ala Leu Lys Pro Ala Thr Val Val Glu Pro
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Glu Val Ser Ile Arg Val Glu Glu Asp Ala Ser Glu Asp Trp Ala Ser
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Arg Gly Ala His Lys Leu Leu Gly Ala Leu Glu Ser Phe Glu Pro Leu
 65 70 75 80

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 85 90 95

Gly Gly Phe Thr Asp Val Leu Leu Arg Arg Glu Ala Ser Glu Val Val
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Ala Val Asp Val Gly Tyr Gly Gln Leu Ile Trp Arg Leu Gln Asn Asp
 115 120 125

Asp Arg Val Arg Val Val Asp Arg Thr Asn Ile Arg Tyr Met Thr Leu
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Glu Asp Thr Gly Gly Glu Cys Asp Met Met Val Gly Asp Leu Ser Phe
 145 150 155 160

Ile Ser Leu Lys Leu Thr Leu Pro Ala Ile Ala Lys Val Leu Ser Asp
 165 170 175

Gly Ala Asp Leu Leu Pro Met Val Lys Pro Gln Phe Glu Val Gly Lys
 180 185 190

Asp Arg Leu Gly Ser Gly Gly Val Val Arg Ser Pro Glu Leu Arg Ala
 195 200 205

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Gln

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Pro		Leu		Gly		Leu		Lys		Val		Lys		Gly		Arg		Arg		Val		Leu		Asp		Ala		Gly		Ala			
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Val		Val		Ala		Val		Asp		Val		Gly		Tyr		Gly		Gln		Leu		Ile		Trp		Arg		Leu		Gln			
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 Gly Lys Asp Arg Leu Gly Ser Gly Gly Val Val Arg Ser Pro Glu Leu
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 Arg Ala Glu Val Thr Ala Asp Val Ala Lys Phe Ala Ala Thr Leu Gly
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 Leu Ser Leu Lys His Val Val Ala Ser Pro Leu Pro Gly Pro Ser Gly
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 Asn Val Glu Tyr Phe Leu Trp Leu Val Lys Asp Gly Gly Ala Ser Met
 215 220 225
 ccg gat gac cag caa ttg tcg gca atg att gac acg gct gta aag gaa 835
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 Gly Pro Gln

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<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45
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 Arg Glu Ala Ser Glu Val Val Ala Val Asp Val Gly Tyr Gly Gln Leu
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 Ile Trp Arg Leu Gln Asn Asp Asp Arg Val Arg Val Val Asp Arg Thr
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 Asn Ile Arg Tyr Met Thr Leu Glu Asp Thr Gly Gly Glu Cys Asp Met
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Met Val Gly Asp Leu Ser Phe Ile Ser Leu Lys Leu Thr Leu Pro Ala
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Ile Ala Lys Val Leu Ser Asp Gly Ala Asp Leu Leu Pro Met Val Lys
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Pro Gln Phe Glu Val Gly Lys Asp Arg Leu Gly Ser Gly Gly Val Val
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Arg Ser Pro Glu Leu Arg Ala Glu Val Thr Ala Asp Val Ala Lys Phe
 180 185 190

Ala Ala Thr Leu Gly Leu Ser Leu Lys His Val Val Ala Ser Pro Leu
 195 200 205

Pro Gly Pro Ser Gly Asn Val Glu Tyr Phe Leu Trp Leu Val Lys Asp
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Thr Ala Val Lys Glu Gly Pro Gln
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 Leu Leu Thr Ala Val
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ttg tct tta att gct ggt ttg gtg gtc att ggg gtg atc atc gtc ctc 163
 Leu Ser Leu Ile Ala Gly Leu Val Val Ile Gly Val Ile Ile Val Leu
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 Asn Gly Tyr Phe Val Ala Gln Glu Phe Ala Tyr Met Ser Val Asp Arg
 25 30 35

aat gag ctg cga gct ctc gct gac tct gga gat aag aag gct cgt cgc 259
 Asn Glu Leu Arg Ala Leu Ala Asp Ser Gly Asp Lys Lys Ala Arg Arg
 40 45 50

gct ctc agc atc act aag cgc aca tcc ttt atg ctt tct ggt gcg caa 307
 Ala Leu Ser Ile Thr Lys Arg Thr Ser Phe Met Leu Ser Gly Ala Gln
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 Leu Gly Ile Thr Val Thr Gly Leu Leu Val Gly Phe Val Ala Glu Pro

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Leu Val Gly Asn Ala Leu Gly Val Leu Leu Gly Gly Val Gly Val Pro				
	90	95	100	
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Ala Ala Val Ser Ile Ser Val Gly Thr Val Leu Ala Leu Ala Ile Ser				
	105	110	115	
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Thr Val Val Gln Met Ile Phe Gly Glu Leu Phe Pro Lys Asn Tyr Thr				
	120	125	130	
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Leu Ala Thr Pro Leu Lys Ser Ala Leu Ala Leu Ala Pro Ser Thr Thr				
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Met Ser Val Asp Arg Asn Glu Leu Arg Ala Leu Ala Asp Ser Gly Asp
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Lys Lys Ala Arg Arg Ala Leu Ser Ile Thr Lys Arg Thr Ser Phe Met
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Leu Ser Gly Ala Gln Leu Gly Ile Thr Val Thr Gly Leu Leu Val Gly
65 70 75 80

Phe Val Ala Glu Pro Leu Val Gly Asn Ala Leu Gly Val Leu Leu Gly
85 90 95

Gly Val Gly Val Pro Ala Ala Val Ser Ile Ser Val Gly Thr Val Leu
100 105 110

Ala Leu Ala Ile Ser Thr Val Val Gln Met Ile Phe Gly Glu Leu Phe
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Leu Glu Gln Leu Glu Lys Glu Asn Val Lys Asn Ala Lys Leu Ala Leu	35	40	45
His Val Thr His His Leu Asp Asn Tyr Leu Ser Ala Ser Gln Leu Gly	50	55	60
Ile Thr Leu Thr Gly Leu Ile Ile Gly Trp Val Gly Glu Gly Ser Val	65	70	75
Ala Ala Leu Leu Glu Pro Val Ile Gly Lys Leu Pro Phe Ser Ser Ala	85	90	95
Ile Ser Ser Thr Ile Ser Val Ala Leu Gly Phe Ile Leu Val Thr Val	100	105	110
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 Met Asp Ala Asp Pro
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 Leu Ile Glu Asp Asp Val Ser Gly Ala Glu Val Lys Asp Ser Ser Asp
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 Glu Pro Leu Leu Ala Leu Thr Arg Tyr Val Phe Asp Arg Gly Glu Arg
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 Pro Val Thr Arg Gly Leu Phe His Gln Val Ala Ala Ile Leu Ser Ile
 40 45 50
 gtg tca ggt tcg gtg ctc tcc acg tat gca tgg atg gaa ctg gtg tgg 307
 Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp Met Glu Leu Val Trp
 55 60 65
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 Trp Gln Ala Leu Gly Val Met Val Tyr Ala Leu Ala Met Leu Gly Leu
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 Phe Ala Val Ser Ala Ala Tyr His Arg Gly Pro Trp Arg Arg Leu His
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 Thr Val Ala Trp Trp Arg Lys Ala Asp His Ser Thr Ile Ala Val Phe
 105 110 115

atc gca gca acc tat acg cca ctg tgc ttg atc gtc tta gag ccc ggt 499
 Ile Ala Ala Thr Tyr Thr Pro Leu Cys Leu Ile Val Leu Glu Pro Gly
 120 125 130

acc gca gca tgg atg tta ggt att gcg tgg gtt ggt gcc att gac agc 547
 Thr Ala Ala Trp Met Leu Gly Ile Ala Trp Val Gly Ala Ile Asp Ser
 135 140 145

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 Val Ile Met Asn Met Val Trp Ile Asn His Pro Arg Trp Leu Ser Val
 150 155 160 165

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 Leu Val Tyr Leu Ala Leu Gly Trp Leu Ile Val Pro Leu Val Pro Gln
 170 175 180

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 Leu Trp Ser Gly Ala Gly Pro Thr Val Val Trp Leu Leu Leu Ala Gly
 185 190 195

ggc atc gtc tac agc gtt ggc gcg ttg gtg tac ggc ttt aaa tgg cca 739
 Gly Ile Val Tyr Ser Val Gly Ala Leu Val Tyr Gly Phe Lys Trp Pro
 200 205 210

gga cgc aac gca cga gtg att ggc tac cac gag cac ttc cac atc gcc 787
 Gly Arg Asn Ala Arg Val Ile Gly Tyr His Glu His Phe His Ile Ala
 215 220 225

acg atc gtc gca gcg att gtc cat ctg gtt gca gtg tgaatggttg 833
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Asp Arg Gly Glu Arg Pro Val Thr Arg Gly Leu Phe His Gln Val Ala
 35 40 45

Ala Ile Leu Ser Ile Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp
 50 55 60

Met Glu Leu Val Trp Trp Gln Ala Leu Gly Val Met Val Tyr Ala Leu
65 70 75 80

Ala Met Leu Gly Leu Phe Ala Val Ser Ala Ala Tyr His Arg Gly Pro
85 90 95

Trp Arg Arg Leu His Thr Val Ala Trp Trp Arg Lys Ala Asp His Ser
100 105 110

Thr Ile Ala Val Phe Ile Ala Ala Thr Tyr Thr Pro Leu Cys Leu Ile
115 120 125

Val Leu Glu Pro Gly Thr Ala Ala Trp Met Leu Gly Ile Ala Trp Val
130 135 140

Gly Ala Ile Asp Ser Val Ile Met Asn Met Val Trp Ile Asn His Pro
145 150 155 160

Arg Trp Leu Ser Val Leu Val Tyr Leu Ala Leu Gly Trp Leu Ile Val
165 170 175

Pro Leu Val Pro Gln Leu Trp Ser Gly Ala Gly Pro Thr Val Val Trp
180 185 190

Leu Leu Leu Ala Gly Gly Ile Val Tyr Ser Val Gly Ala Leu Val Tyr
195 200 205

Gly Phe Lys Trp Pro Gly Arg Asn Ala Arg Val Ile Gly Tyr His Glu
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His Phe His Ile Ala Thr Ile Val Ala Ala Ile Val His Leu Val Ala
225 230 235 240

Val

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Met Asp Ala Asp Pro
1 5

ctg att gag gat gac gtt agt gga gca gaa gta aaa gat agt tcg gat 163
Leu Ile Glu Asp Asp Val Ser Gly Ala Glu Val Lys Asp Ser Ser Asp
10 15 20

gaa ccg ctt ctc gca ctg aca cgt tac gtt ttt gat cgc ggt gag ccg 211
Glu Pro Leu Leu Ala Leu Thr Arg Tyr Val Phe Asp Arg Gly Glu Arg
25 30 35

Asp Arg Gly Glu Arg Pro Val Thr Arg Gly Leu Phe His Gln Val Ala
35 40 45

Ala Ile Leu Ser Ile Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp
 50 55 60

Met Glu Leu Val Trp Trp Gln Ala Leu Gly Val Met Val Tyr Ala Leu
 65 70 75 80

Ala Met Leu Gly Leu Phe Ala Val Ser Ala Ala Tyr His Arg Gly Pro
 85 90 95

Trp Arg Arg Leu His Thr Val Ala Trp Trp Arg Lys Ala Asp His Ser
 100 105 110

Thr Ile Ala Val Phe Ile Ala Ala Thr Tyr Thr Pro Leu Cys Leu Ile
 115 120 125

Val Leu Glu Pro Gly Thr Ala Ala Trp Met Leu Gly Ile Ala Trp Val
 130 135 140

Gly Ala Ile Asp Ser Val Ile Met Asn Met Val Trp Ile Asn His Pro
 145 150 155 160

Arg Trp Leu Ser Val Leu Val Tyr Leu Ala Leu Gly Trp Leu Ile Val
 165 170 175

Pro Leu Val Pro Gln Leu Trp Ser Gly Ala Gly Pro Thr Val Val Trp
 180 185 190

Leu Leu Leu Ala Glu Gly Ile Val Tyr Ser Val Gly Ala Leu Val Tyr
 195 200 205

Gly Phe
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 Leu Ser Ile Ala Thr
 1 5

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 Val Val Ala Leu Leu Phe Ser Gly Leu Leu Gly Ala Val Glu Ser Ala
 10 15 20

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 Leu Ser Ser Val Ser Arg Ala Arg Val Glu Gln Met Leu Lys Asp Glu
 25 30 35

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 Ala Ser Gly Ser Ala Ser Leu Leu Arg Val Ile Asp Glu Arg Ala Leu

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His Ile Asn Met Leu Ile Met Leu Arg Thr Leu Leu Asp Ala Ser Ala			
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Ala Val Phe Ala Gly Ala Ile Ala Val Asn Val Met Asp Ser Trp Ala			
70	75	80	85
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Trp Gly Ile Val Leu Ala Ile Val Val Val Ser Leu Leu Thr Phe Ala			
90	95	100	
gta gtg ggc gtg ttt ggc cgc acc gtt ggc cgc aaa aac cca tat tca			451
Val Val Gly Val Phe Gly Arg Thr Val Gly Arg Lys Asn Pro Tyr Ser			
105	110	115	
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Val Met Leu Arg Ser Ala Val Val Leu Ser Gly Leu Ala Lys Ile Leu			
120	125	130	
ggc ccc att gca cgt ggc ctc atc tgg atc ggc aac atc atc gcg ccc			547
Gly Pro Ile Ala Arg Gly Leu Ile Trp Ile Gly Asn Ile Ile Ala Pro			
135	140	145	
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Gly Pro Gly Phe Arg Asn Gly Pro Tyr Ala Thr Glu Val Glu Leu Arg			
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gag atg gtc gat atc gcc caa gaa cac ggc atc gtg gaa att gaa gag			643
Glu Met Val Asp Ile Ala Gln Glu His Gly Ile Val Glu Ile Glu Glu			
170	175	180	
cgc cgc atg atc cag tcg gtg ttc gac ctg gca tcc acg acg gtt cgc			691
Arg Arg Met Ile Gln Ser Val Phe Asp Leu Ala Ser Thr Thr Val Arg			
185	190	195	
cag gtg atg gtg cca cgt cct gaa atg atc tgg att gaa tct gga aaa			739
Gln Val Met Val Pro Arg Pro Glu Met Ile Trp Ile Glu Ser Gly Lys			
200	205	210	
aca gcc ggg caa gca acc gcg ctg tgc gtg cgc tct ggt cat tcg cgc			787
Thr Ala Gly Gln Ala Thr Ala Leu Cys Val Arg Ser Gly His Ser Arg			
215	220	225	
atc cca gtc atc ggt gaa aac gtc gac gac atc atc ggc atc gtc tac			835
Ile Pro Val Ile Gly Glu Asn Val Asp Asp Ile Ile Gly Ile Val Tyr			
230	235	240	245
ctc aaa gac ttg gtc caa aaa acc tac tac gcc act gat ggc gga aag			883
Leu Lys Asp Leu Val Gln Lys Thr Tyr Tyr Ala Thr Asp Gly Gly Lys			
250	255	260	
tct gtg ctt gta gac gag gtc atg cgc gaa gct acc ttc gtg cca gac			931
Ser Val Leu Val Asp Glu Val Met Arg Glu Ala Thr Phe Val Pro Asp			
265	270	275	
tcc aag tcc ctt gat gcg ctg ctg cag gaa atg cag gaa gac cac aaa			979
Ser Lys Ser Leu Asp Ala Leu Leu Gln Glu Met Gln Glu Asp His Lys			
280	285	290	

cac atc gca atc ctg gtt gat gaa tac ggc ggc gtg gca ggt ctt att 1027
 His Ile Ala Ile Leu Val Asp Glu Tyr Gly Gly Val Ala Gly Leu Ile
 295 300 305

tcc att gag gat att ttg gaa gaa atc gtc ggt gaa atc gct gat gaa 1075
 Ser Ile Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Ala Asp Glu
 310 315 320 325

tat gac gcc cgc gaa gta gcc ccc atc gag aaa atc ggc gac cgc acc 1123
 Tyr Asp Ala Arg Glu Val Ala Pro Ile Glu Lys Ile Gly Asp Arg Thr
 330 335 340

tac cgc gtg gtc tcc cga ctc tcg ctg gaa gat ctc aaa gac cac atc 1171
 Tyr Arg Val Val Ser Arg Leu Ser Leu Glu Asp Leu Lys Asp His Ile
 345 350 355

gaa gaa gaa ctc gac cta gaa atc gaa ttc ggt gat gaa att gaa gat 1219
 Glu Glu Glu Leu Asp Leu Glu Ile Glu Phe Gly Asp Glu Ile Glu Asp
 360 365 370

cag gtc gac act gtc ggt ggc ctt att gcc ttt gaa ctt ggc cga gtg 1267
 Gln Val Asp Thr Val Gly Gly Leu Ile Ala Phe Glu Leu Gly Arg Val
 375 380 385

cct ctg ccg ggt gcc act gtg gaa acc tgc gga cta aag ctc acc gcc 1315
 Pro Leu Pro Gly Ala Thr Val Glu Thr Cys Gly Leu Lys Leu Thr Ala
 390 395 400 405

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 Glu Gly Ala Lys Asn Arg Arg Gly Arg Leu Arg Met His Ser Ala Val
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<213> Corynebacterium glutamicum

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Asp Glu Arg Ala Leu His Ile Asn Met Leu Ile Met Leu Arg Thr Leu
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Leu Asp Ala Ser Ala Ala Val Phe Ala Gly Ala Ile Ala Val Asn Val
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Leu Leu Thr Phe Ala Val Val Gly Val Phe Gly Arg Thr Val Gly Arg
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Lys Asn Pro Tyr Ser Val Met Leu Arg Ser Ala Val Val Leu Ser Gly
115 120 125

Leu Ala Lys Ile Leu Gly Pro Ile Ala Arg Gly Leu Ile Trp Ile Gly
130 135 140

Asn Ile Ile Ala Pro Gly Pro Gly Phe Arg Asn Gly Pro Tyr Ala Thr
145 150 155 160

Glu Val Glu Leu Arg Glu Met Val Asp Ile Ala Gln Glu His Gly Ile
165 170 175

Val Glu Ile Glu Glu Arg Arg Met Ile Gln Ser Val Phe Asp Leu Ala
180 185 190

Ser Thr Thr Val Arg Gln Val Met Val Pro Arg Pro Glu Met Ile Trp
195 200 205

Ile Glu Ser Gly Lys Thr Ala Gly Gln Ala Thr Ala Leu Cys Val Arg
210 215 220

Ser Gly His Ser Arg Ile Pro Val Ile Gly Glu Asn Val Asp Asp Ile
225 230 235 240

Ile Gly Ile Val Tyr Leu Lys Asp Leu Val Gln Lys Thr Tyr Tyr Ala
245 250 255

Thr Asp Gly Gly Lys Ser Val Leu Val Asp Glu Val Met Arg Glu Ala
260 265 270

Thr Phe Val Pro Asp Ser Lys Ser Leu Asp Ala Leu Leu Gln Glu Met
275 280 285

Gln Glu Asp His Lys His Ile Ala Ile Leu Val Asp Glu Tyr Gly Gly
290 295 300

Val Ala Gly Leu Ile Ser Ile Glu Asp Ile Leu Glu Glu Ile Val Gly
305 310 315 320

Glu Ile Ala Asp Glu Tyr Asp Ala Arg Glu Val Ala Pro Ile Glu Lys
325 330 335

Ile Gly Asp Arg Thr Tyr Arg Val Val Ser Arg Leu Ser Leu Glu Asp
340 345 350

Leu Lys Asp His Ile Glu Glu Glu Leu Asp Leu Glu Ile Glu Phe Gly
355 360 365

Asp Glu Ile Glu Asp Gln Val Asp Thr Val Gly Gly Leu Ile Ala Phe
370 375 380

Glu Leu Gly Arg Val Pro Leu Pro Gly Ala Thr Val Glu Thr Cys Gly
385 390 395 400

Leu Lys Leu Thr Ala Glu Gly Ala Lys Asn Arg Arg Gly Arg Leu Arg

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410

415

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<212> DNA

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 Leu Ser Ile Ala Thr
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gtc gtt gcg ttg ctc ttc tcc ggt tta tta ggt gcg gtt gaa tct gcg 163
 Val Val Ala Leu Leu Phe Ser Gly Leu Leu Gly Ala Val Glu Ser Ala
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 Leu Ser Ser Val Ser Arg Ala Arg Val Glu Gln Met Leu Lys Asp Glu
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gcc tcc ggg tcc gcg tcc ttg ctg cga gtc atc gac gaa cgc gca ctc 259
 Ala Ser Gly Ser Ala Ser Leu Leu Arg Val Ile Asp Glu Arg Ala Leu
 40 45 50

cac atc aac atg ctc atc atg ttg cgc acc ttg ctg gat gcc tcc gca 307
 His Ile Asn Met Leu Ile Met Leu Arg Thr Leu Leu Asp Ala Ser Ala
 55 60 65

gca gtc ttc gcc ggg gca atc gca gtc aat gtg atg gac agc tgg gcg 355
 Ala Val Phe Ala Gly Ala Ile Ala Val Asn Val Met Asp Ser Trp Ala
 70 75 80 85

tgg ggc atc gtc ctg gcc atc gtg gtg gtt tcc ctc ctg acc ttc gca 403
 Trp Gly Ile Val Leu Ala Ile Val Val Val Ser Leu Leu Thr Phe Ala
 90 95 100

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 Val Val Gly Val Phe Gly Arg Thr Val Gly Arg Lys Asn Pro Tyr Ser
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gtg atg ctt cgc tcc gca gtc gtg ctg agc ggt tta gct aaa atc ctt 499
 Val Met Leu Arg Ser Ala Val Val Leu Ser Gly Leu Ala Lys Ile Leu
 120 125 130

ggc ccc att gca cgt ggc ctc atc tgg atc ggc aac atc atc gcg ccc 547
 Gly Pro Ile Ala Arg Gly Leu Ile Trp Ile Gly Asn Ile Ile Ala Pro
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gag atg gtc gat atc gcc caa gaa cac ggc atc gtg gaa att gaa gag Glu Met Val Asp Ile Ala Gln Glu His Gly Ile Val Glu Ile Glu Glu 170 175 180	643
cgc cgc atg atc cag tcg gtg ttc gac ctg gca tcc acg acg gtt cgc Arg Arg Met Ile Gln Ser Val Phe Asp Leu Ala Ser Thr Thr Val Arg 185 190 195	691
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 Pro Leu Pro Gly Ala Thr Val Glu Thr Cys Gly Leu Lys Leu Thr Ala
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 35 40 45

Asp Glu Arg Ala Leu His Ile Asn Met Leu Ile Met Leu Arg Thr Leu
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Leu Asp Ala Ser Ala Ala Val Phe Ala Gly Ala Ile Ala Val Asn Val
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Met Asp Ser Trp Ala Trp Gly Ile Val Leu Ala Ile Val Val Val Ser
 85 90 95

Leu Leu Thr Phe Ala Val Val Gly Val Phe Gly Arg Thr Val Gly Arg
 100 105 110

Lys Asn Pro Tyr Ser Val Met Leu Arg Ser Ala Val Val Leu Ser Gly
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Leu Ala Lys Ile Leu Gly Pro Ile Ala Arg Gly Leu Ile Trp Ile Gly
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Asn Ile Ile Ala Pro Gly Pro Gly Phe Arg Asn Gly Pro Tyr Ala Thr
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Glu Val Glu Leu Arg Glu Met Val Asp Ile Ala Gln Glu His Gly Ile
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Val Glu Ile Glu Glu Arg Arg Met Ile Gln Ser Val Phe Asp Leu Ala
 180 185 190

Ser Thr Thr Val Arg Gln Val Met Val Pro Arg Pro Glu Met Ile Trp
 195 200 205

Ile Glu Ser Gly Lys Thr Ala Gly Gln Ala Thr Ala Leu Cys Val Arg
 210 215 220

Ser Gly His Ser Arg Ile Pro Val Ile Gly Glu Asn Val Asp Asp Ile
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Ile Gly Ile Val Tyr Leu Lys Asp Leu Val Gln Lys Thr Tyr Tyr Ala
245 250 255

Thr Asp Gly Gly Lys Ser Val Leu Val Asp Glu Val Met Arg Glu Ala
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Thr Phe Val Pro Asp Ser Lys Ser Leu Asp Ala Leu Leu Gln Glu Met
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Gln Glu Asp His Lys His Ile Ala Ile Leu Val Asp Glu Tyr Gly Gly
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Val Ala Gly Leu Ile Ser Ile Glu Asp Ile Leu Glu Glu Ile Val Gly
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Glu Ile Ala Asp Glu Tyr Asp Ala Arg Glu Val Ala Pro Ile Glu Lys
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Ile Gly Asp Arg Thr Tyr Arg Val Val Ser Arg Leu Ser Leu Glu Asp
340 345 350

Leu Lys Asp His Ile Glu Glu Glu Leu Asp Leu Glu Ile Glu Phe Gly
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Asp Glu Ile Glu Asp Gln Val Asp Thr Val Gly Gly Leu Ile Ala Phe
370 375 380

Glu Leu Gly Arg Val Pro Leu Pro Gly Ala Thr Val Glu Thr Cys Gly
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Met Glu Cys Met Ser
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Ala Gln Gly Leu Ala Phe Glu Lys Leu Met Val Asn Phe Ile Lys Ser	
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Asp Pro Thr Leu Ser Thr Glu Phe Asp Glu Val His Arg Trp Val Asp	
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Trp Pro Tyr Asn Gly Gly Thr Met Asp Thr Gly Ile Asp Leu Val Ala	
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Tyr Asn Lys Asp Asp Asp Ala Tyr Thr Ala Ile Gln Cys Lys Phe Tyr	
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Lys Met Leu Glu Asn Gln Thr Ile Pro Thr Asn Arg Ile Gly Leu Ser	
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Ala Ile Ala Glu Ser Pro Ile Asp Trp Asp Ile Ala Tyr Pro Gly Ser	
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Glu Leu Thr Ile Asn Leu Gln Leu Lys Glu Pro Tyr Ser Pro Arg Pro	
170 175 180	
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His Gln Gln Thr Ala Ile Glu Lys Ala Ile Glu Gly Phe Gln Thr His	
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Arg Ile Leu Phe Leu Val Pro Ser Ile Ser Leu Leu Ser Gln Thr Leu	
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Lys Glu Trp Thr Ala Gln Lys Thr Met Asp Leu Arg Pro Val Ala Val	
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Cys	Ser	Asp	Ser	Lys	Val	Ser	Lys	Ala	Ala	Glu	Asp	Ile	Ala	Ala	Tyr	
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Leu	Glu	His	Arg	Lys	Arg	Ala	Ala	Gly	Leu	Thr	Val	Val	Phe	Ser	Thr	
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Tyr	Gln	Ser	Leu	Pro	Ala	Val	His	Ala	Ala	Gln	Glu	Ala	Gly	Ala	Glu	
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Pro	Phe	Asp	Leu	Val	Ile	Cys	Asp	Glu	Ala	His	Arg	Thr	Thr	Gly	Ile	
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Thr	Leu	Ala	Gly	Glu	Asp	Pro	Ser	Asn	Phe	Thr	Arg	Ile	His	Asp	Ala	
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Ser	Tyr	Ile	Lys	Ala	Ala	Lys	Arg	Leu	Tyr	Met	Thr	Ala	Thr	Pro	Arg	
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ctt	ttc	gac	gac	tcc	gtg	aag	ggc	aag	gct	gca	gat	cat	tca	gct	gaa	1267
Leu	Phe	Asp	Asp	Ser	Val	Lys	Gly	Lys	Ala	Ala	Asp	His	Ser	Ala	Glu	
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Val	Ser	Ser	Met	Asp	Asp	Glu	Ala	Ile	Tyr	Gly	Pro	Glu	Phe	His	Arg	
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Leu	Gly	Phe	Gly	Glu	Ala	Val	Glu	Lys	Gly	Leu	Leu	Thr	Asp	Tyr	Lys	
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gtt	gta	gtg	atg	aca	gtt	gat	gag	caa	gtt	gca	gcc	agt	gcc	tta	act	1411
Val	Val	Val	Met	Thr	Val	Asp	Glu	Gln	Val	Ala	Ala	Ser	Ala	Leu	Thr	
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caa	gac	acc	aag	act	ggg	ttc	tca	agc	tct	gac	gca	gca	atg	gaa	cga	1555
Gln	Asp	Thr	Lys	Thr	Gly	Phe	Ser	Ser	Ser	Asp	Ala	Ala	Met	Glu	Arg	
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gct	gtt	gca	ttt	gcg	cga	gac	att	aag	act	tct	cag	caa	atc	gcg	gag	1603
Ala	Val	Ala	Phe	Ala	Arg	Asp	Ile	Lys	Thr	Ser	Gln	Gln	Ile	Ala	Glu	
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Ser	Phe	Pro	Arg	Val	Val	Asn	Ala	Tyr	Thr	Thr	Glu	Leu	Glu	Val	Lys	

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Phe Val Glu Gly Leu Arg Gly Asn Leu Asn Glu Ser Ile Ser Asp Asp	
760 765 770	
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Glu Ala Ile Ser Met Leu Ser Gln His Leu Ile Thr Ala Pro Val Phe	
775 780 785	
gac gct cta ttt gct gaa tca agc ttc gct aag caa aac cct gtt tcc	2515
Asp Ala Leu Phe Ala Glu Ser Ser Phe Ala Lys Gln Asn Pro Val Ser	
790 795 800 805	
cag gtt atg caa cgc atg gca gat gct ctt aat agt gct gaa ctt aac	2563
Gln Val Met Gln Arg Met Ala Asp Ala Leu Asn Ser Ala Glu Leu Asn	
810 815 820	
tct gaa acg gaa aaa ctt gag aag ttc tat gac tct gtt cgt atc cgt	2611
Ser Glu Thr Glu Lys Leu Glu Lys Phe Tyr Asp Ser Val Arg Ile Arg	
825 830 835	
gct gct gaa gta agc tcc gca gct ggt aaa caa gca gta att aaa gac	2659
Ala Ala Glu Val Ser Ser Ala Ala Gly Lys Gln Ala Val Ile Lys Asp	
840 845 850	
ctc tac gaa cga ttc ttt aaa aag gcc ttt aaa aag caa tct gaa gct	2707
Leu Tyr Glu Arg Phe Phe Lys Lys Ala Phe Lys Lys Gln Ser Glu Ala	
855 860 865	
cta ggt att gtc tat acc cct gtt gag atc gtg gac ttt att ctg cga	2755
Leu Gly Ile Val Tyr Thr Pro Val Glu Ile Val Asp Phe Ile Leu Arg	
870 875 880 885	
gct gcc gat gat gtg tcc aag aag cat ttt ggt cgt gcc tta agc gat	2803
Ala Ala Asp Asp Val Ser Lys Lys His Phe Gly Arg Gly Leu Ser Asp	
890 895 900	
aaa gat gtc cat gtt ctt gat cct ttc acc ggt acg ggt act ttt atg	2851
Lys Asp Val His Val Leu Asp Pro Phe Thr Gly Thr Gly Thr Phe Met	
905 910 915	
gtg cgt tta ttg cag tca ggt cta att aag cct gaa gat ttg gcc cgt	2899
Val Arg Leu Leu Gln Ser Gly Leu Ile Lys Pro Glu Asp Leu Ala Arg	
920 925 930	
aaa tat gcc aat gag ctg cac gct act gag atc atg ttg ctt gcc tat	2947
Lys Tyr Ala Asn Glu Leu His Ala Thr Glu Ile Met Leu Leu Ala Tyr	
935 940 945	
tat gtt gcg gcc gtt aac att gag acc act tat ttt ggt ctc gag gga	2995
Tyr Val Ala Ala Val Asn Ile Glu Thr Thr Tyr Phe Gly Leu Glu Gly	
950 955 960 965	
gag cgt gct ctg cgt aat ggt gaa gat gcg ccg gtc tat gag ccg ttt	3043
Glu Arg Ala Leu Arg Asn Gly Glu Asp Ala Pro Val Tyr Glu Pro Phe	
970 975 980	
gat ggc att gtg ttg ggt gat acc ttc cag atg tat gaa gac gat gac	3091
Asp Gly Ile Val Leu Gly Asp Thr Phe Gln Met Tyr Glu Asp Asp Asp	
985 990 995	

aaa ctc gat cta gat gtt ttt act gct aac aat gac cgt atg gag cgt 3139
 Lys Leu Asp Leu Asp Val Phe Thr Ala Asn Asn Asp Arg Met Glu Arg
 1000 1005 1010

cag aga ctt act cct gta cag gtt att gtg ggt aac ccg cct tac tct 3187
 Gln Arg Leu Thr Pro Val Gln Val Ile Val Gly Asn Pro Pro Tyr Ser
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 Val Gly Gln Ser Ser Ala Asn Asp Asn Asn Ala Asn Leu Lys Tyr Pro
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act ctt gat cga cgt att gaa gat tct tat gcg aag tat tcg acc gca 3283
 Thr Leu Asp Arg Arg Ile Glu Asp Ser Tyr Ala Lys Tyr Ser Thr Ala
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 Thr Asn Lys Asn Ser Leu Tyr Asp Ser Tyr Leu Arg Ala Phe Arg Trp
 1065 1070 1075

gca aca gat cgt att cac aca caa ggg gtt gtt gct ttt gtt tct aac 3379
 Ala Thr Asp Arg Ile His Thr Gln Gly Val Val Ala Phe Val Ser Asn
 1080 1085 1090

aac ggt tgg gtt gac ggc aat acc gct gat ggt gtg cgc cta agt ttg 3427
 Asn Gly Trp Val Asp Gly Asn Thr Ala Asp Gly Val Arg Leu Ser Leu
 1095 1100 1105

gca cag gac ttc tcc gag att tat gtt ttc aac ctt cgt ggc aat tcc 3475
 Ala Gln Asp Phe Ser Glu Ile Tyr Val Phe Asn Leu Arg Gly Asn Ser
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cga aca ggt ggt gat ttg gct aag cgc gag ggc ggc aac gtc ttt aat 3523
 Arg Thr Gly Gly Asp Leu Ala Lys Arg Glu Gly Gly Asn Val Phe Asn
 1130 1135 1140

gtc cgt gtg ggt act caa atc att gtt gcc gtg aaa aac cca caa ttg 3571
 Val Arg Val Gly Thr Gln Ile Ile Val Ala Val Lys Asn Pro Gln Leu
 1145 1150 1155

tct ggt tgc agg att ctt tat aaa gat att ggt gac aat ctc agc gcg 3619
 Ser Gly Cys Arg Ile Leu Tyr Lys Asp Ile Gly Asp Asn Leu Ser Ala
 1160 1165 1170

gat gcg aag ttg aac gag att gcc gtt gcc aca att gag ggc gct gag 3667
 Asp Ala Lys Leu Asn Glu Ile Ala Val Ala Thr Ile Glu Gly Ala Glu
 1175 1180 1185

tgg cag act att tcg cct aat gaa tat gga gat tgg atc agc cag cgc 3715
 Trp Gln Thr Ile Ser Pro Asn Glu Tyr Gly Asp Trp Ile Ser Gln Arg
 1190 1195 1200 1205

tct gta gat ttt gat acc tgg cct gta ctc ggt gat aag aaa aac aaa 3763
 Ser Val Asp Phe Asp Thr Trp Pro Val Leu Gly Asp Lys Lys Asn Lys
 1210 1215 1220

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 Ser Ala Leu Lys Val Phe Gln Thr Phe Ser Ala Gly Leu Lys Thr Gly
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cgc gat gcc tgg tgc tat ggg cca aca tct gcg cag gta aaa act aat 3859

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Ile	Thr	Arg	Leu	Leu	Glu	Thr	Tyr	Glu	Gln	Ala	Gln	Gln	Arg	Phe	Asn	
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tgc	tgg	gtt	gtg	gat	aac	gga	gtg	aca	tct	cct	aag	gaa	gct	gac	gtt	3955
Ser	Trp	Val	Val	Asp	Asn	Gly	Val	Thr	Ser	Pro	Lys	Glu	Ala	Asp	Val	
		1270			1275					1280					1285	
aat	caa	ttc	ctt	aag	cag	aac	cct	gat	tta	gcg	gat	agc	aag	aaa	ata	4003
Asn	Gln	Phe	Leu	Lys	Gln	Asn	Pro	Asp	Leu	Ala	Asp	Ser	Lys	Lys	Ile	
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tcc	tgg	gat	tcc	aat	cta	aaa	atg	tcc	ttg	tca	cgc	ggt	gat	act	ttt	4051
Ser	Trp	Asp	Ser	Asn	Leu	Lys	Met	Ser	Leu	Ser	Arg	Gly	Asp	Thr	Phe	
			1305					1310					1315			
tct	ttt	gat	cca	agc	agc	atc	caa	atg	tcc	ttg	tat	cgt	cca	ttt	ttc	4099
Ser	Phe	Asp	Pro	Ser	Ser	Ile	Gln	Met	Ser	Leu	Tyr	Arg	Pro	Phe	Phe	
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cct	caa	cag	aca	tac	ttc	cat	gtt	tca	ttg	aac	cag	cgt	cga	tac	cag	4147
Pro	Gln	Gln	Thr	Tyr	Phe	His	Val	Ser	Leu	Asn	Gln	Arg	Arg	Tyr	Gln	
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Leu	Pro	Ser	Met	Phe	Pro	Thr	Pro	Glu	His	Asp	Asn	Gln	Gly	Phe	Tyr	
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atc	gtc	aac	cca	ggt	agt	gcc	aag	cca	ttc	tct	acc	ctt	gca	aca	aat	4243
Ile	Val	Asn	Pro	Gly	Ser	Ala	Lys	Pro	Phe	Ser	Thr	Leu	Ala	Thr	Asn	
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cta	ctt	cca	gat	ctt	gct	atg	tgg	ggt	tct	aac	gcc	gga	cag	ttc	ttt	4291
Leu	Leu	Pro	Asp	Leu	Ala	Met	Trp	Gly	Ser	Asn	Ala	Gly	Gln	Phe	Phe	
			1385					1390					1395			
acc	cga	tgg	act	tgg	gaa	ccc	atc	gaa	act	cga	gaa	ggc	gaa	tta	gac	4339
Thr	Arg	Trp	Thr	Trp	Glu	Pro	Ile	Glu	Thr	Arg	Glu	Gly	Glu	Leu	Asp	
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ttc	ggt	aat	gga	ctt	ttc	tcc	aca	acc	cca	aaa	aag	gga	gtt	gaa	ggc	4387
Phe	Gly	Asn	Gly	Leu	Phe	Ser	Thr	Thr	Pro	Lys	Lys	Gly	Val	Glu	Gly	
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gag	atc	ctt	gac	ggt	tac	cgg	cgc	gtc	gat	aac	atc	acc	gac	gag	atc	4435
Glu	Ile	Leu	Asp	Gly	Tyr	Arg	Arg	Val	Asp	Asn	Ile	Thr	Asp	Glu	Ile	
		1430			1435					1440					1445	
tta	aag	ctc	tac	caa	tca	agc	ttg	ggt	gag	gat	gtc	acc	aag	gat	gac	4483
Leu	Lys	Leu	Tyr	Gln	Ser	Ser	Leu	Gly	Glu	Asp	Val	Thr	Lys	Asp	Asp	
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Ile	Phe	Tyr	Phe	Val	Tyr	Ala	Gln	Leu	His	Asp	Pro	Ala	Tyr	Arg	Glu	
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gcc	tat	gcg	gct	gat	cta	aag	aag	atg	ctg	cca	cat	att	gaa	acc	cct	4579
Ala	Tyr	Ala	Ala	Asp	Leu	Lys	Lys	Met	Leu	Pro	His	Ile	Glu	Thr	Pro	

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Thr Asp Arg Ala Arg Phe Asp	His Phe Val Thr Ala	Gly Lys Glu Leu	
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atg gat ctt cat atc aac tat gaa gat gtt gaa	cca tgg gat gtg gag		4675
Met Asp Leu His Ile Asn Tyr Glu Asp Val Glu	Pro Trp Asp Val Glu		
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gta aag gtc aaa gaa aaa gct gat ccc acg	gat cgt gag acc tgg cgt		4723
Val Lys Val Lys Glu Lys Ala Asp Pro Thr	Asp Arg Glu Thr Trp Arg		
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gtt acc aag atg aag tgg gct aag gtt cgt	gat cca gag acc aag aaa		4771
Val Thr Lys Met Lys Trp Ala Lys Val Arg	Asp Pro Glu Thr Lys Lys		
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ttg gtg gag gac cat acc acc ttg att tac aac agc tca	atc acc atc		4819
Leu Val Glu Asp His Thr Thr Leu Ile Tyr Asn Ser Ser	Ile Thr Ile		
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agc ggc atc ccc gaa gaa gct gaa aac tat caa cta	ggg tca cgt tct		4867
Ser Gly Ile Pro Glu Glu Ala Glu Asn Tyr Gln Leu	Gly Ser Arg Ser		
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gcc atc gca tgg ctt att gac cgt tac cag gtg	aag aaa gat aag gcg		4915
Ala Ile Ala Trp Leu Ile Asp Arg Tyr Gln Val	Lys Lys Asp Lys Ala		
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tcc ggc att gtt aat gat ccc aat gat tgg gct	gat gaa gtg ggt aac		4963
Ser Gly Ile Val Asn Asp Pro Asn Asp Trp	Ala Asp Glu Val Gly Asn		
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cct cgc tac att gtg gag ctg att gct aag gtc acc cgc gtt	gcc gtt		5011
Pro Arg Tyr Ile Val Glu Leu Ile Ala Lys Val Thr Arg Val	Ala Val		
1625	1630	1635	
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Glu Thr Met Arg Ile Val Glu Glu Leu			
1640	1645		
tcc			5061

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<212> PRT

<213> Corynebacterium glutamicum

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Leu	Pro	Ser	Gln	Ser	Ala	Gln	Gly	Leu	Ala	Phe	Glu	Lys	Leu	Met	Val
		20					25						30		
Asn	Phe	Ile	Lys	Ser	Asp	Pro	Thr	Leu	Ser	Thr	Glu	Phe	Asp	Glu	Val
	35						40					45			
His	Arg	Trp	Val	Asp	Trp	Pro	Tyr	Asn	Gly	Gly	Thr	Met	Asp	Thr	Gly

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Ile Asp Leu Val Ala Tyr Asn Lys Asp Asp Asp Ala Tyr Thr Ala Ile 65 70 75 80		
Gln Cys Lys Phe Tyr Leu Pro Thr Thr Ser Leu Ala Lys Gly Gln Leu 85 90 95		
Asp Ser Phe Phe Glu Ala Ser Gly Arg Thr Phe Glu Thr Pro Glu Gly 100 105 110		
Thr Arg Ser Phe Ser Asn Arg Leu Val Ile Ser Thr Thr Asp Lys Trp 115 120 125		
Ser Ser Asn Ala Glu Lys Met Leu Glu Asn Gln Thr Ile Pro Thr Asn 130 135 140		
Arg Ile Gly Leu Ser Ala Ile Ala Glu Ser Pro Ile Asp Trp Asp Ile 145 150 155 160		
Ala Tyr Pro Gly Ser Glu Leu Thr Ile Asn Leu Gln Leu Lys Glu Pro 165 170 175		
Tyr Ser Pro Arg Pro His Gln Gln Thr Ala Ile Glu Lys Ala Ile Glu 180 185 190		
Gly Phe Gln Thr His Asp Arg Gly Lys Leu Ile Met Ala Cys Gly Thr 195 200 205		
Gly Lys Thr Phe Thr Ala Leu Arg Leu Ser Glu Glu Val Ala Arg Leu 210 215 220		
Asn Gly Asn Lys Ala Arg Ile Leu Phe Leu Val Pro Ser Ile Ser Leu 225 230 235 240		
Leu Ser Gln Thr Leu Lys Glu Trp Thr Ala Gln Lys Thr Met Asp Leu 245 250 255		
Arg Pro Val Ala Val Cys Ser Asp Ser Lys Val Ser Lys Ala Ala Glu 260 265 270		
Asp Ile Ala Ala Tyr Asp Leu Glu Val Pro Val Ser Thr Asp Gly Ala 275 280 285		
Leu Ile Ala Glu Lys Leu Glu His Arg Lys Arg Ala Ala Gly Leu Thr 290 295 300		
Val Val Phe Ser Thr Tyr Gln Ser Leu Pro Ala Val His Ala Ala Gln 305 310 315 320		
Glu Ala Gly Ala Glu Pro Phe Asp Leu Val Ile Cys Asp Glu Ala His 325 330 335		
Arg Thr Thr Gly Ile Thr Leu Ala Gly Glu Asp Pro Ser Asn Phe Thr 340 345 350		
Arg Ile His Asp Ala Ser Tyr Ile Lys Ala Ala Lys Arg Leu Tyr Met 355 360 365		
Thr Ala Thr Pro Arg Leu Phe Asp Asp Ser Val Lys Gly Lys Ala Ala 370 375 380		

Asp His Ser Ala Glu Val Ser Ser Met Asp Asp Glu Ala Ile Tyr Gly
 385 390 395 400
 Pro Glu Phe His Arg Leu Gly Phe Gly Glu Ala Val Glu Lys Gly Leu
 405 410 415
 Leu Thr Asp Tyr Lys Val Val Val Met Thr Val Asp Glu Gln Val Ala
 420 425 430
 Ala Ser Ala Leu Thr Val Leu Gly Ser Thr Pro Gly Glu Glu Leu Thr
 435 440 445
 Leu Asp Met Thr Ser Ala Ile Ile Gly Ala Trp Asn Gly Leu Ala Lys
 450 455 460
 Arg Ser Gly Lys Glu Gln Asp Thr Lys Thr Gly Phe Ser Ser Ser Asp
 465 470 475 480
 Ala Ala Met Glu Arg Ala Val Ala Phe Ala Arg Asp Ile Lys Thr Ser
 485 490 495
 Gln Gln Ile Ala Glu Ser Phe Pro Arg Val Val Asn Ala Tyr Thr Thr
 500 505 510
 Glu Leu Glu Val Lys Asn Asp Asp Val Asp Glu His Asn Leu Asn Leu
 515 520 525
 Ser Val Ala Cys Gln His Val Asp Gly Ser Met Asn Ala Leu Glu Arg
 530 535 540
 Asn Ser Arg Leu Thr Trp Leu Lys Ala Pro Thr Gln Ser Met Glu Thr
 545 550 555 560
 Lys Ile Leu Thr Asn Ala Arg Cys Leu Ser Glu Gly Val Asp Val Pro
 565 570 575
 Ala Leu Asp Ser Val Ile Phe Phe Asn Pro Arg Asn Ser Met Val Asp
 580 585 590
 Val Val Gln Ser Val Gly Arg Val Met Arg Lys Ser Pro Gly Lys Asn
 595 600 605
 Tyr Gly Tyr Ile Ile Leu Pro Val Ala Val Pro Pro Gly Val Ala Pro
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 Ser Ala Ala Leu Asn Asp Ser Arg Arg Phe Lys Val Val Trp Gln Val
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 Leu Asn Ala Leu Arg Ala His Asp Asp Arg Phe Asn Ala Met Val Asn
 645 650 655
 Ser Ile Ala Leu Asn Glu Gly Asn Ile Lys Asp Leu Pro Val Glu Thr
 660 665 670
 Glu His Thr Gly Pro Thr Ser Lys Asp Arg Asp Asn Ala Pro Tyr Asp
 675 680 685
 Ser Ala Glu Ser Ala Thr Gln Tyr Val Leu Phe Ser Leu Glu Gln Trp
 690 695 700

Gln Glu Ala Ile Tyr Thr Lys Leu Val Asp Lys Val Gly Thr Arg Thr
705 710 715 720

Tyr Trp Glu Asp Trp Ala Asp Asp Val Ala Asp Ile Ala Gln Ala Gln
725 730 735

Ile Thr Arg Ile Lys Ala Leu Leu Asp Asn Ala Ser Pro Thr Ile Lys
740 745 750

Glu Glu Phe Glu Arg Phe Val Glu Gly Leu Arg Gly Asn Leu Asn Glu
755 760 765

Ser Ile Ser Asp Asp Glu Ala Ile Ser Met Leu Ser Gln His Leu Ile
770 775 780

Thr Ala Pro Val Phe Asp Ala Leu Phe Ala Glu Ser Ser Phe Ala Lys
785 790 795 800

Gln Asn Pro Val Ser Gln Val Met Gln Arg Met Ala Asp Ala Leu Asn
805 810 815

Ser Ala Glu Leu Asn Ser Glu Thr Glu Lys Leu Glu Lys Phe Tyr Asp
820 825 830

Ser Val Arg Ile Arg Ala Ala Glu Val Ser Ser Ala Ala Gly Lys Gln
835 840 845

Ala Val Ile Lys Asp Leu Tyr Glu Arg Phe Phe Lys Lys Ala Phe Lys
850 855 860

Lys Gln Ser Glu Ala Leu Gly Ile Val Tyr Thr Pro Val Glu Ile Val
865 870 875 880

Asp Phe Ile Leu Arg Ala Ala Asp Asp Val Ser Lys Lys His Phe Gly
885 890 895

Arg Gly Leu Ser Asp Lys Asp Val His Val Leu Asp Pro Phe Thr Gly
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Thr Gly Thr Phe Met Val Arg Leu Leu Gln Ser Gly Leu Ile Lys Pro
915 920 925

Glu Asp Leu Ala Arg Lys Tyr Ala Asn Glu Leu His Ala Thr Glu Ile
930 935 940

Met Leu Leu Ala Tyr Tyr Val Ala Ala Val Asn Ile Glu Thr Thr Tyr
945 950 955 960

Phe Gly Leu Glu Gly Glu Arg Ala Leu Arg Asn Gly Glu Asp Ala Pro
965 970 975

Val Tyr Glu Pro Phe Asp Gly Ile Val Leu Gly Asp Thr Phe Gln Met
980 985 990

Tyr Glu Asp Asp Asp Lys Leu Asp Leu Asp Val Phe Thr Ala Asn Asn
995 1000 1005

Asp Arg Met Glu Arg Gln Arg Leu Thr Pro Val Gln Val Ile Val Gly
1010 1015 1020

Asn Pro Pro Tyr Ser Val Gly Gln Ser Ser Ala Asn Asp Asn Asn Ala

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Asn Leu Lys Tyr Pro	Thr Leu Asp Arg Arg	Ile Glu Asp Ser Tyr	Ala
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Lys Tyr Ser Thr	Ala Thr Asn Lys Asn	Ser Leu Tyr Asp Ser	Tyr Leu
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Arg Ala Phe	Arg Trp Ala Thr Asp	Arg Ile His Thr Gln	Gly Val Val
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Ala Phe Val Ser Asn	Asn Gly Trp Val Asp	Gly Asn Thr Ala Asp	Gly
1090	1095	1100	
Val Arg Leu Ser Leu	Ala Gln Asp Phe Ser	Glu Ile Tyr Val Phe	Asn
1105	1110	1115	1120
Leu Arg Gly Asn Ser	Arg Thr Gly Gly Asp	Leu Ala Lys Arg Glu	Gly
1125	1130	1135	
Gly Asn Val Phe	Asn Val Arg Val Gly	Thr Gln Ile Ile Val	Ala Val
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Lys Asn Pro	Gln Leu Ser Gly Cys	Arg Ile Leu Tyr Lys	Asp Ile Gly
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Asp Asn Leu Ser Ala	Asp Ala Lys Leu Asn	Glu Ile Ala Val Ala	Thr
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Ile Glu Gly Ala Glu	Trp Gln Thr Ile Ser	Pro Asn Glu Tyr Gly	Asp
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Trp Ile Ser Gln Arg	Ser Val Asp Phe Asp	Thr Trp Pro Val Leu	Gly
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Asp Lys Lys Asn	Lys Ser Ala Leu Lys	Val Phe Gln Thr Phe	Ser Ala
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Gly Leu Lys Thr Gly	Arg Asp Ala Trp Cys Tyr	Gly Pro Thr Ser Ala	
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Gln Val Lys Thr Asn	Ile Thr Arg Leu Leu	Glu Thr Tyr Glu Gln	Ala
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Gln Gln Arg Phe Asn	Ser Trp Val Val Asp	Asn Gly Val Thr Ser	Pro
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Lys Glu Ala Asp Val	Asn Gln Phe Leu Lys	Gln Asn Pro Asp Leu	Ala
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Asp Ser Lys Lys	Ile Ser Trp Asp Ser	Asn Leu Lys Met Ser	Leu Ser
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Arg Gly Asp Thr Phe	Ser Phe Asp Pro Ser	Ser Ile Gln Met Ser	Leu
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Tyr Arg Pro Phe Phe	Pro Gln Gln Thr Tyr	Phe His Val Ser Leu	Asn
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Gln Arg Arg Tyr Gln	Leu Pro Ser Met Phe	Pro Thr Pro Glu His	Asp
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Thr Leu Ala Thr Asn Leu Leu Pro Asp Leu Ala Met Trp Gly Ser Asn
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Ala Gly Gln Phe Phe Thr Arg Trp Thr Trp Glu Pro Ile Glu Thr Arg
1395 1400 1405

Glu Gly Glu Leu Asp Phe Gly Asn Gly Leu Phe Ser Thr Thr Pro Lys
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Lys Gly Val Glu Gly Glu Ile Leu Asp Gly Tyr Arg Arg Val Asp Asn
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Ile Thr Asp Glu Ile Leu Lys Leu Tyr Gln Ser Ser Leu Gly Glu Asp
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Val Thr Lys Asp Asp Ile Phe Tyr Phe Val Tyr Ala Gln Leu His Asp
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Pro Ala Tyr Arg Glu Ala Tyr Ala Ala Asp Leu Lys Lys Met Leu Pro
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His Ile Glu Thr Pro Thr Asp Arg Ala Arg Phe Asp His Phe Val Thr
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Ala Gly Lys Glu Leu Met Asp Leu His Ile Asn Tyr Glu Asp Val Glu
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Pro Trp Asp Val Glu Val Lys Val Lys Glu Lys Ala Asp Pro Thr Asp
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Arg Glu Thr Trp Arg Val Thr Lys Met Lys Trp Ala Lys Val Arg Asp
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Pro Glu Thr Lys Lys Leu Val Glu Asp His Thr Thr Leu Ile Tyr Asn
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Ser Ser Ile Thr Ile Ser Gly Ile Pro Glu Glu Ala Glu Asn Tyr Gln
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Leu Gly Ser Arg Ser Ala Ile Ala Trp Leu Ile Asp Arg Tyr Gln Val
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1605 1610 1615

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Ser Lys Lys His Phe Gly Arg Gly Leu Ser Asp Lys Asp Val His Val	
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Leu Asp Pro Phe Thr Gly Thr Gly Thr Phe Met Val Arg Leu Leu Gln	
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Ser Gly Leu Ile Lys Pro Glu Asp Leu Ala Arg Lys Tyr Ala Asn Glu	
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ctg cac gct act gag atc atg ttg ctt gcc tat tat gtt gcg gcc gtt	288
Leu His Ala Thr Glu Ile Met Leu Leu Ala Tyr Tyr Val Ala Ala Val	
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Asn Ile Glu Thr Thr Tyr Phe Gly Leu Glu Gly Glu Arg Ala Leu Arg	
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Asn Gly Glu Asp Ala Pro Val Tyr Glu Pro Phe Asp Gly Ile Val Leu	
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Lys Ala Ala Ala Glu Thr Leu Lys Gln Glu Ala Leu Arg Arg Gln Asn	
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acc tcc atc ggc gac gaa cct acc caa ccc gcc atg cgt cta atc aac	1075
Thr Ser Ile Gly Asp Glu Pro Thr Gln Pro Ala Met Arg Leu Ile Asn	
310 315 320 325	
gtg ctg gcc cgc ttc gac caa acc gaa acc atc acg ccc gaa gaa cgc	1123
Val Leu Ala Arg Phe Asp Gln Thr Glu Thr Ile Thr Pro Glu Glu Arg	
330 335 340	
gcc cgc cgc acc cgc gtc atc gac tac gta gaa cac ata ccc cca agc	1171
Ala Arg Arg Thr Arg Val Ile Asp Tyr Val Glu His Ile Pro Pro Ser	
345 350 355	
ctc gac ccc tac atc gtc atc aac cca gca acg cct gag ttc aac aac	1219
Leu Asp Pro Tyr Ile Val Ile Asn Pro Ala Thr Pro Glu Phe Asn Asn	
360 365 370	
ttc acc gac gac ctc cgc tgg atc gac gca aac ccc aac ctc ttc cac	1267
Phe Thr Asp Asp Leu Arg Trp Ile Asp Ala Asn Pro Asn Leu Phe His	
375 380 385	
cca caa aca atc acc acc cca ccc gcc gac atc tgg gac gac tac atc	1315
Pro Gln Thr Ile Thr Thr Pro Pro Ala Asp Ile Trp Asp Asp Tyr Ile	
390 395 400 405	
tcc cgt ccc gct cac tac caa ggc ctg cta gcc acg ctg ctc ggc cgc	1363
Ser Arg Pro Ala His Tyr Gln Gly Leu Leu Ala Thr Leu Leu Gly Arg	
410 415 420	
gac atc gaa ggc gca gac gaa ctc ctc gac gcc acc acc ctc caa aaa	1411
Asp Ile Glu Gly Ala Asp Glu Leu Leu Asp Ala Thr Thr Leu Gln Lys	
425 430 435	
atc aga gac ctc acc ctc gac aaa act cat ctc acc gac ctc cac ctc	1459

Ile Arg Asp Leu Thr Leu Asp Lys Thr His Leu Thr Asp Leu His Leu	
440 445 450	
cgc gga tac caa tca ttc ggc gcc cgc ttc gcc atc atc caa aag aaa	1507
Arg Gly Tyr Gln Ser Phe Gly Ala Arg Phe Ala Ile Ile Gln Lys Lys	
455 460 465	
acc ctc ctc ggc gac gac atg gga ctc ggc aaa aca gtc caa gcc ctc	1555
Thr Leu Leu Gly Asp Met Gly Leu Gly Lys Thr Val Gln Ala Leu	
470 475 480 485	
tcc gca gct gca cac ctt gcc gcc acc gaa aaa gac ttc cgc acc ctc	1603
Ser Ala Ala Ala His Leu Ala Ala Thr Glu Lys Asp Phe Arg Thr Leu	
490 495 500	
gtc gtc gta ccc gca tcc gtc att gtt aac tgg acc cgc gaa tgc aaa	1651
Val Val Val Pro Ala Ser Val Ile Val Asn Trp Thr Arg Glu Cys Lys	
505 510 515	
cgc ttc ctc aac ctc ccc gta ttc atc gcc cac gga gac aac aaa caa	1699
Arg Phe Leu Asn Leu Pro Val Phe Ile Ala His Gly Asp Asn Lys Gln	
520 525 530	
gac gcc atc aac gcc tgg tct aac acc aac gga atc gca atc tgc acc	1747
Asp Ala Ile Asn Ala Trp Ser Asn Thr Asn Gly Ile Ala Ile Cys Thr	
535 540 545	
tac gac ggc gtc cgc acc atg gac atc ccc gcg ccg ggt ctg gtc att	1795
Tyr Asp Gly Val Arg Thr Met Asp Ile Pro Ala Pro Gly Leu Val Ile	
550 555 560 565	
gcc gat gaa gcc cac ctg atc aaa aac ccc tcc acc aaa cgc acc caa	1843
Ala Asp Glu Ala His Leu Ile Lys Asn Pro Ser Thr Lys Arg Thr Gln	
570 575 580	
gca ctg cgc aaa ctt atc gac gcc gcc cca tac acc ctt ctg atg acc	1891
Ala Leu Arg Lys Leu Ile Asp Ala Ala Pro Tyr Thr Leu Leu Met Thr	
585 590 595	
ggc aca cca cta gaa aac aaa gtg gaa gag ttt gta aat ctc gtg cgc	1939
Gly Thr Pro Leu Glu Asn Lys Val Glu Glu Phe Val Asn Leu Val Arg	
600 605 610	
tac atc caa ccg gag ctg atc acc cgt ggc atg tcc aaa atg cag gcc	1987
Tyr Ile Gln Pro Glu Leu Ile Thr Arg Gly Met Ser Lys Met Gln Ala	
615 620 625	
gag aat ttc cgc gag cgc atc gca cca gcc tat ctg cgc aga aat caa	2035
Glu Asn Phe Arg Glu Arg Ile Ala Pro Ala Tyr Leu Arg Arg Asn Gln	
630 635 640 645	
gct gat gtg ctt gac gaa ctc cca gag cgc acc gac tcc atc gac tgg	2083
Ala Asp Val Leu Asp Glu Leu Pro Glu Arg Thr Asp Ser Ile Asp Trp	
650 655 660	
atc gac ctc acc cca gaa gac cgc agc gcc tac gac gac caa gtc cgc	2131
Ile Asp Leu Thr Pro Glu Asp Arg Ser Ala Tyr Asp Asp Gln Val Arg	
665 670 675	
caa ggc agc tgg atg ggc atg cgc cgc tcc gcc atg ctc tca cca aca	2179
Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala Met Leu Ser Pro Thr	

680	685	690	
cca cgc cta act tcc gca aaa atg caa cgc atc cta gaa ctc ttc gaa			2227
Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile Leu Glu Leu Phe Glu			
695	700	705	
gaa gca gaa gaa cac ggc cgc aaa gcc ctc atc ttc acc tac ttc ctc			2275
Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile Phe Thr Tyr Phe Leu			
710	715	720	725
gac gtc ctc gac gaa ctg gaa aag cat cta ggc gag cgc gtc atc ggc			2323
Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly Glu Arg Val Ile Gly			
730	735	740	
cgc att tcc ggc gac gtg cca gcc acc aag cgc caa ttg ctt gtc gac			2371
Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg Gln Leu Leu Val Asp			
745	750	755	
gcc ctg tcc cac tcc aaa ccc gga tcc gcc ctc att gcc caa atc acc			2419
Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu Ile Ala Gln Ile Thr			
760	765	770	
gcc ggg gga gta ggc cta aac atc caa tcc gcg agc cta tgc att att			2467
Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala Ser Leu Cys Ile Ile			
775	780	785	
tgt gaa cct caa gta aag cca acc atc gaa cag cag gcc gtc gcc cga			2515
Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln Gln Ala Val Ala Arg			
790	795	800	805
gtc cac cgc atg ggc caa acc gcc acc gtc caa gtc cac cga ctc atc			2563
Val His Arg Met Gly Gln Thr Ala Thr Val Gln Val His Arg Leu Ile			
810	815	820	
ggc gac gaa acc gca gac gaa cgc atg cta gaa atc ctg gca ggc aaa			2611
Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu Ile Leu Ala Gly Lys			
825	830	835	
act cac gtc ttc gac gtc tac gcc cgg cta tct gaa acc gca gag att			2659
Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser Glu Thr Ala Glu Ile			
840	845	850	
cca gat gct gtg gat atc act gaa tca cag ctg gca gca cgg gtt att			2707
Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu Ala Ala Arg Val Ile			
855	860	865	
gat gag gag cgt gca cgg tta ggg ctt act gaa tcc act ggc cct aaa			2755
Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu Ser Thr Gly Pro Lys			
870	875	880	885
gat gaa gaa acg gcc tta agc tagttgccta aggccggaat taa			2799
Asp Glu Glu Thr Ala Leu Ser			
890			

<210> 38

<211> 892

<212> PRT

<213> Corynebacterium glutamicum

<400> 38

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 20 25 30
 Leu Arg Leu Leu Lys Thr Pro Gly Thr Ala Thr Val Gly Asp Asn Gly
 35 40 45
 Thr Leu Gly Thr Asp Thr Tyr Leu Ile Pro Ser Arg Asn Ile Thr Trp
 50 55 60
 Pro Asp Asn Leu Tyr Val Asn Val Phe Leu Asp Gly Met Asn Ala Glu
 65 70 75 80
 Ala Thr Leu Thr Asp Tyr Val Ala Ser Val Ala Ser Ile Pro Arg Leu
 85 90 95
 Cys Gln Ile Ile Asn Glu Gly Gln Gly Gly Met Phe Arg Arg Leu Phe
 100 105 110
 Asn Pro Thr Lys Val Gln Ala Gly Asp Gln Ala Val Phe Asp Leu Met
 115 120 125
 Val Lys Leu Asp Glu Ile Ser Ser Thr Thr His Glu Val Ser Arg Met
 130 135 140
 Leu Glu Gly Val His Ala Ala Arg Thr Arg Gln Gln Gln Gly Val Ala
 145 150 155 160
 Leu Phe Pro Gly Ile His Gly Val Gly Glu Arg Tyr Ile Glu Arg Ala
 165 170 175
 Gln Gln Val Leu Ala Ser Ala Leu Gly Ile Ala Gly Phe Gly Ala Glu
 180 185 190
 Pro Trp Asp Gly His Thr Leu Ala Gln Ala Arg Arg Val Val Gln Arg
 195 200 205
 Tyr Ala Gln Asp Pro Asn Ser Glu Tyr Arg Leu Lys Ser Glu Ala Glu
 210 215 220
 Lys His Leu Thr Ser Ile Asn Glu Leu Arg Val Gln Ile Leu Leu Glu
 225 230 235 240
 Gln Leu Pro Val Asp Ala Leu Arg Met Ala Thr Asp His Arg Leu Arg
 245 250 255
 Phe Gly Ser Leu Asp Ser Ile His Val Ala Thr Val Ala Asp Val Leu
 260 265 270
 Lys Thr His Thr Ser Ile Leu Thr Thr Val Gln Gly Ile Gly Ala Gln
 275 280 285
 Thr Ala Gly Arg Met Lys Ala Ala Ala Glu Thr Leu Lys Gln Glu Ala
 290 295 300
 Leu Arg Arg Gln Asn Thr Ser Ile Gly Asp Glu Pro Thr Gln Pro Ala
 305 310 315 320
 Met Arg Leu Ile Asn Val Leu Ala Arg Phe Asp Gln Thr Glu Thr Ile

325								330				335			
Thr	Pro	Glu	Glu	Arg	Ala	Arg	Arg	Thr	Arg	Val	Ile	Asp	Tyr	Val	Glu
			340								345			350	
His	Ile	Pro	Pro	Ser	Leu	Asp	Pro	Tyr	Ile	Val	Ile	Asn	Pro	Ala	Thr
		355					360					365			
Pro	Glu	Phe	Asn	Asn	Phe	Thr	Asp	Asp	Leu	Arg	Trp	Ile	Asp	Ala	Asn
		370				375					380				
Pro	Asn	Leu	Phe	His	Pro	Gln	Thr	Ile	Thr	Thr	Pro	Pro	Ala	Asp	Ile
385					390				395						400
Trp	Asp	Asp	Tyr	Ile	Ser	Arg	Pro	Ala	His	Tyr	Gln	Gly	Leu	Leu	Ala
				405					410					415	
Thr	Leu	Leu	Gly	Arg	Asp	Ile	Glu	Gly	Ala	Asp	Glu	Leu	Leu	Asp	Ala
			420						425					430	
Thr	Thr	Leu	Gln	Lys	Ile	Arg	Asp	Leu	Thr	Leu	Asp	Lys	Thr	His	Leu
		435					440					445			
Thr	Asp	Leu	His	Leu	Arg	Gly	Tyr	Gln	Ser	Phe	Gly	Ala	Arg	Phe	Ala
	450					455					460				
Ile	Ile	Gln	Lys	Lys	Thr	Leu	Leu	Gly	Asp	Asp	Met	Gly	Leu	Gly	Lys
465					470					475					480
Thr	Val	Gln	Ala	Leu	Ser	Ala	Ala	Ala	His	Leu	Ala	Ala	Thr	Glu	Lys
				485					490					495	
Asp	Phe	Arg	Thr	Leu	Val	Val	Val	Pro	Ala	Ser	Val	Ile	Val	Asn	Trp
			500						505				510		
Thr	Arg	Glu	Cys	Lys	Arg	Phe	Leu	Asn	Leu	Pro	Val	Phe	Ile	Ala	His
		515					520					525			
Gly	Asp	Asn	Lys	Gln	Asp	Ala	Ile	Asn	Ala	Trp	Ser	Asn	Thr	Asn	Gly
	530					535					540				
Ile	Ala	Ile	Cys	Thr	Tyr	Asp	Gly	Val	Arg	Thr	Met	Asp	Ile	Pro	Ala
545					550					555					560
Pro	Gly	Leu	Val	Ile	Ala	Asp	Glu	Ala	His	Leu	Ile	Lys	Asn	Pro	Ser
				565					570					575	
Thr	Lys	Arg	Thr	Gln	Ala	Leu	Arg	Lys	Leu	Ile	Asp	Ala	Ala	Pro	Tyr
			580						585				590		
Thr	Leu	Leu	Met	Thr	Gly	Thr	Pro	Leu	Glu	Asn	Lys	Val	Glu	Glu	Phe
		595					600					605			
Val	Asn	Leu	Val	Arg	Tyr	Ile	Gln	Pro	Glu	Leu	Ile	Thr	Arg	Gly	Met
	610					615						620			
Ser	Lys	Met	Gln	Ala	Glu	Asn	Phe	Arg	Glu	Arg	Ile	Ala	Pro	Ala	Tyr
625					630					635					640
Leu	Arg	Arg	Asn	Gln	Ala	Asp	Val	Leu	Asp	Glu	Leu	Pro	Glu	Arg	Thr
				645					650					655	

Asp Ser Ile Asp Trp Ile Asp Leu Thr Pro Glu Asp Arg Ser Ala Tyr
 660 665 670
 Asp Asp Gln Val Arg Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala
 675 680 685
 Met Leu Ser Pro Thr Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile
 690 695 700
 Leu Glu Leu Phe Glu Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile
 705 710 715 720
 Phe Thr Tyr Phe Leu Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly
 725 730 735
 Glu Arg Val Ile Gly Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg
 740 745 750
 Gln Leu Leu Val Asp Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu
 755 760 765
 Ile Ala Gln Ile Thr Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala
 770 775 780
 Ser Leu Cys Ile Ile Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln
 785 790 795 800
 Gln Ala Val Ala Arg Val His Arg Met Gly Gln Thr Ala Thr Val Gln
 805 810 815
 Val His Arg Leu Ile Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu
 820 825 830
 Ile Leu Ala Gly Lys Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser
 835 840 845
 Glu Thr Ala Glu Ile Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu
 850 855 860
 Ala Ala Arg Val Ile Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu
 865 870 875 880
 Ser Thr Gly Pro Lys Asp Glu Glu Thr Ala Leu Ser
 885 890

<210> 39

<211> 731

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(708)

<223> FRXA01797

<400> 39

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 Gly Ser Ile Ala Trp Ile Asp Leu Thr Pro Glu Asp Arg Ser Ala Tyr
 1 5 10 15

48

gac gac caa gtc cgc caa ggc agc tgg atg ggc atg cgc cgc tcc gcc	96
Asp Asp Gln Val Arg Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala	
20 25 30	
atg ctc tca cca aca cca cgc cta act tcc gca aaa atg caa cgc atc	144
Met Leu Ser Pro Thr Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile	
35 40 45	
cta gaa ctc ttc gaa gaa gca gaa gaa cac ggc cgc aaa gcc ctc atc	192
Leu Glu Leu Phe Glu Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile	
50 55 60	
ttc acc tac ttc ctc gac gtc ctc gac gaa ctg gaa aag cat cta ggc	240
Phe Thr Tyr Phe Leu Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly	
65 70 75 80	
gag cgc gtc atc ggc cgc att tcc ggc gac gtg cca gcc acc aag cgc	288
Glu Arg Val Ile Gly Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg	
85 90 95	
caa ttg ctt gtc gac gcc ctg tcc cac tcc aaa ccc gga tcc gcc ctc	336
Gln Leu Leu Val Asp Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu	
100 105 110	
att gcc caa atc acc gcc ggg gga gta ggc cta aac atc caa tcc gcg	384
Ile Ala Gln Ile Thr Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala	
115 120 125	
agc cta tgc att att tgt gaa cct caa gta aag cca acc atc gaa cag	432
Ser Leu Cys Ile Ile Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln	
130 135 140	
cag gcc gtc gcc cga gtc cac cgc atg ggc caa acc gcc acc gtc caa	480
Gln Ala Val Ala Arg Val His Arg Met Gly Gln Thr Ala Thr Val Gln	
145 150 155 160	
gtc cac cga ctc atc ggc gac gaa acc gca gac gaa cgc atg cta gaa	528
Val His Arg Leu Ile Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu	
165 170 175	
atc ctg gca ggc aaa act cac gtc ttc gac gtc tac gcc cgg cta tct	576
Ile Leu Ala Gly Lys Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser	
180 185 190	
gaa acc gca gag att cca gat gct gtg gat atc act gaa tca cag ctg	624
Glu Thr Ala Glu Ile Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu	
195 200 205	
gca gca cgg gtt att gat gag gag cgt gca cgg tta ggg ctt act gaa	672
Ala Ala Arg Val Ile Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu	
210 215 220	
tcc act ggc cct aaa gat gaa gaa acg gcc tta agc tagttgccta	718
Ser Thr Gly Pro Lys Asp Glu Glu Thr Ala Leu Ser	
225 230 235	
aggccggaat taa	731

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

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Asp Asp Gln Val Arg Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala
20 25 30

Met Leu Ser Pro Thr Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile
35 40 45

Leu Glu Leu Phe Glu Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile
50 55 60

Phe Thr Tyr Phe Leu Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly
65 70 75 80

Glu Arg Val Ile Gly Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg
85 90 95

Gln Leu Leu Val Asp Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu
100 105 110

Ile Ala Gln Ile Thr Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala
115 120 125

Ser Leu Cys Ile Ile Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln
130 135 140

Gln Ala Val Ala Arg Val His Arg Met Gly Gln Thr Ala Thr Val Gln
145 150 155 160

Val His Arg Leu Ile Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu
165 170 175

Ile Leu Ala Gly Lys Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser
180 185 190

Glu Thr Ala Glu Ile Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu
195 200 205

Ala Ala Arg Val Ile Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu
210 215 220

Ser Thr Gly Pro Lys Asp Glu Glu Thr Ala Leu Ser
225 230 235

<210> 41

<211> 1299

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1276)

<223> RXN01030

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gtattaatcc cctctttgtg cagcatagga gactactgct atg acc tca aca acc 115
Met Thr Ser Thr Thr
1 5

caa cct ggc aca aca cct gag ctc agc gca gac act cat tct gag ccc 163
Gln Pro Gly Thr Thr Pro Glu Leu Ser Ala Asp Thr His Ser Glu Pro
10 15 20

tgg gat gtc gtc atc gaa aac acc ctt gaa cct ttt caa aaa gtc gtt 211
Trp Asp Val Val Ile Glu Asn Thr Leu Glu Pro Phe Gln Lys Val Val
25 30 35

cgt caa ttt att att gac cgc ccc tat tcc ggc att ttc ctc acc atg 259
Arg Gln Phe Ile Ile Asp Arg Pro Tyr Ser Gly Ile Phe Leu Thr Met
40 45 50

ggg ggc ggc aaa aca ctc act acc ctc tcc gca ttg acc tat atc cag 307
Gly Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala Leu Thr Tyr Ile Gln
55 60 65

cca cct gga cac att ctg gtt gtc gcg cct cta aat atc tct cga ctc 355
Pro Pro Gly His Ile Leu Val Val Ala Pro Leu Asn Ile Ser Arg Leu
70 75 80 85

acc tgg ccc gaa gag gtt cgc aag tgg aat atc cct gtt aac gca atc 403
Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile Pro Val Asn Ala Ile
90 95 100

tcg ctg atc acc aat gag cgc ggc acc aaa ctc acc cgc gcc aaa cgc 451
Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu Thr Arg Ala Lys Arg
105 110 115

ctc aaa ctc tat gag gaa aca gcg acc aca cca cca acg ctg tat tac 499
Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro Pro Thr Leu Tyr Tyr
120 125 130

atc acc att aat ctg ctc gaa gat att gtc aat tac ttt ggt gat agg 547
Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn Tyr Phe Gly Asp Arg
135 140 145

tgg ccg ttt tgg aca gtc att att gat gag tca cag aca atc tct gat 595
Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser Gln Thr Ile Ser Asp
150 155 160 165

ata tcc tcc aag cgc act aga gcg ctc ttt tct gtg cga ccc tat atc 643
Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser Val Arg Pro Tyr Ile
170 175 180

ggc aga cta att ctg ctc acc gga acc ccc agc gcc aac aag ttc gac 691
Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser Ala Asn Lys Phe Asp
185 190 195

tcc att tac gcc caa gtc gca gtg cta gat tat ggt gcc agc ctg ggt 739
Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr Gly Ala Ser Leu Gly
200 205 210

gac aac atc gac gta ttc cga gcc aga tgg tgt gcg ccc gac att att 787
Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys Ala Pro Asp Ile Ile

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215	220	225	
acc gat aaa caa gtg cgt cgc tgg aag ccg gct aac aag cag gct gaa			835
Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala Asn Lys Gln Ala Glu			
230	235	240	245
gca gag gtg tac cgc act att agc cac ctg gtc atg tct gcc gtc aac			883
Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val Met Ser Ala Val Asn			
	250	255	260
acg gat att aag ctg cca ccg ctg cat ttt gtt gat cac gag gta cac			931
Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val Asp His Glu Val His			
	265	270	275
atg agc gac gat gag cac cgc gac tac gag ctc ttc aaa aag gac gcg			979
Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu Phe Lys Lys Asp Ala			
	280	285	290
gtg ctt gct gca ttg ctc gat atg gct gaa gag aat gag ggt ggc gaa			1027
Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu Asn Glu Gly Gly Glu			
	295	300	305
ggc gct gat gac act gac gct gct gat tca gcg aca acg acc cca cct			1075
Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala Thr Thr Thr Pro Pro			
310	315	320	325
gcg tca tca cag cca aca aac cct gcc atc ccc gct gga ctg ctt cag			1123
Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro Ala Gly Leu Leu Gln			
	330	335	340
gca ata caa caa acc cag gac acc aat ggt cgc gcc atc gcg cct gtg			1171
Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg Ala Ile Ala Pro Val			
	345	350	355
acc aca gct gaa ctt gat cat ttt gat gat ctg cca gta cag cgc caa			1219
Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu Pro Val Gln Arg Gln			
	360	365	370
gaa gat ctt ggc acc tta gtt gtt atc tct gct gtt cac gca agc gac			1267
Glu Asp Leu Gly Thr Leu Val Val Ile Ser Ala Val His Ala Ser Asp			
	375	380	385
tct gcg gca tgaaactgct gcaatacgca ggt			1299
Ser Ala Ala			
390			

<210> 42

<211> 392

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

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Thr	His	Ser	Glu	Pro	Trp	Asp	Val	Val	Ile	Glu	Asn	Thr	Leu	Glu	Pro
			20					25					30		

Phe	Gln	Lys	Val	Val	Arg	Gln	Phe	Ile	Ile	Asp	Arg	Pro	Tyr	Ser	Gly
		35					40					45			

Ile Phe Leu Thr Met Gly Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala
50 55 60

Leu Thr Tyr Ile Gln Pro Pro Gly His Ile Leu Val Val Ala Pro Leu
65 70 75 80

Asn Ile Ser Arg Leu Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile
85 90 95

Pro Val Asn Ala Ile Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu
100 105 110

Thr Arg Ala Lys Arg Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro
115 120 125

Pro Thr Leu Tyr Tyr Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn
130 135 140

Tyr Phe Gly Asp Arg Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser
145 150 155 160

Gln Thr Ile Ser Asp Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser
165 170 175

Val Arg Pro Tyr Ile Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser
180 185 190

Ala Asn Lys Phe Asp Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr
195 200 205

Gly Ala Ser Leu Gly Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys
210 215 220

Ala Pro Asp Ile Ile Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala
225 230 235 240

Asn Lys Gln Ala Glu Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val
245 250 255

Met Ser Ala Val Asn Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val
260 265 270

Asp His Glu Val His Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu
275 280 285

Phe Lys Lys Asp Ala Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu
290 295 300

Asn Glu Gly Gly Glu Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala
305 310 315 320

Thr Thr Thr Pro Pro Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro
325 330 335

Ala Gly Leu Leu Gln Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg
340 345 350

Ala Ile Ala Pro Val Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu
355 360 365

Pro Val Gln Arg Gln Glu Asp Leu Gly Thr Leu Val Val Ile Ser Ala
 370 375 380

Val His Ala Ser Asp Ser Ala Ala
 385 390

<210> 43

<211> 1299

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1276)

<223> FRXA01030

<400> 43

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 gtattaatcc cctctttgtg cagcatagga gactactgct atg acc tca aca acc 115
 Met Thr Ser Thr Thr
 1 5

caa cct ggc aca aca cct gag ctc agc gca gac act cat tct gag ccc 163
 Gln Pro Gly Thr Thr Pro Glu Leu Ser Ala Asp Thr His Ser Glu Pro
 10 15 20

tgg gat gtc gtc atc gaa aac acc ctt gaa cct ttt caa aaa gtc gtt 211
 Trp Asp Val Val Ile Glu Asn Thr Leu Glu Pro Phe Gln Lys Val Val
 25 30 35

cgt caa ttt att att gac cgc ccc tat tcc ggc att ttc ctc acc atg 259
 Arg Gln Phe Ile Ile Asp Arg Pro Tyr Ser Gly Ile Phe Leu Thr Met
 40 45 50

ggt ggc ggc aaa aca ctc act acc ctc tcc gca ttg acc tat atc cag 307
 Gly Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala Leu Thr Tyr Ile Gln
 55 60 65

cca cct gga cac att ctg gtt gtc gcg cct cta aat atc tct cga ctc 355
 Pro Pro Gly His Ile Leu Val Val Ala Pro Leu Asn Ile Ser Arg Leu
 70 75 80 85

acc tgg ccc gaa gag gtt cgc aag tgg aat atc cct gtt aac gca atc 403
 Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile Pro Val Asn Ala Ile
 90 95 100

tcg ctg atc acc aat gag cgc ggc acc aaa ctc acc cgc gcc aaa cgc 451
 Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu Thr Arg Ala Lys Arg
 105 110 115

ctc aaa ctc tat gag gaa aca gcg acc aca cca cca acg ctg tat tac 499
 Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro Pro Thr Leu Tyr Tyr
 120 125 130

atc acc att aat ctg ctc gaa gat att gtc aat tac ttt ggt gat agg 547
 Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn Tyr Phe Gly Asp Arg
 135 140 145

tgg ccg ttt tgg aca gtc att att gat gag tca cag aca atc tct gat 595

390

<210> 44

<211> 392

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

Met Thr Ser Thr Thr Gln Pro Gly Thr Thr Pro Glu Leu Ser Ala Asp
1 5 10 15

Thr His Ser Glu Pro Trp Asp Val Val Ile Glu Asn Thr Leu Glu Pro
20 25 30

Phe Gln Lys Val Val Arg Gln Phe Ile Ile Asp Arg Pro Tyr Ser Gly
35 40 45

Ile Phe Leu Thr Met Gly Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala
50 55 60

Leu Thr Tyr Ile Gln Pro Pro Gly His Ile Leu Val Val Ala Pro Leu
65 70 75 80

Asn Ile Ser Arg Leu Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile
85 90 95

Pro Val Asn Ala Ile Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu
100 105 110

Thr Arg Ala Lys Arg Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro
115 120 125

Pro Thr Leu Tyr Tyr Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn
130 135 140

Tyr Phe Gly Asp Arg Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser
145 150 155 160

Gln Thr Ile Ser Asp Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser
165 170 175

Val Arg Pro Tyr Ile Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser
180 185 190

Ala Asn Lys Phe Asp Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr
195 200 205

Gly Ala Ser Leu Gly Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys
210 215 220

Ala Pro Asp Ile Ile Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala
225 230 235 240

Asn Lys Gln Ala Glu Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val
245 250 255

Met Ser Ala Val Asn Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val
260 265 270

Asp His Glu Val His Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu

275	280	285
Phe Lys Lys Asp Ala Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu		
290	295	300
Asn Glu Gly Gly Glu Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala		
305	310	315
Thr Thr Thr Pro Pro Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro		
	325	330
Ala Gly Leu Leu Gln Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg		
	340	345
Ala Ile Ala Pro Val Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu		
	355	360
Pro Val Gln Arg Gln Glu Asp Leu Gly Thr Leu Val Val Ile Ser Ala		
	370	375
Val His Ala Ser Asp Ser Ala Ala		
385	390	

<210> 45
 <211> 720
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(697)
 <223> RXA01739

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 Val Ile Asn Leu Gln
 1 5
 gac ctc gac gag gat caa cgc atc gct gct tct gcg cct cgc gga cca 163
 Asp Leu Asp Glu Asp Gln Arg Ile Ala Ala Ser Ala Pro Arg Gly Pro
 10 15 20
 gtg tgc att ctc gcc gga gcc ggc acg ggt aaa act cga acg att act 211
 Val Cys Ile Leu Ala Gly Ala Gly Thr Gly Lys Thr Arg Thr Ile Thr
 25 30 35
 tat cgc atc gcg cat ctg att gat cag ggt ttt gtg agc ccg aat cgt 259
 Tyr Arg Ile Ala His Leu Ile Asp Gln Gly Phe Val Ser Pro Asn Arg
 40 45 50
 gtt ctt gct gtg acg ttt aca tcc cgc gcg gca ggg gag atg cgt cat 307
 Val Leu Ala Val Thr Phe Thr Ser Arg Ala Ala Gly Glu Met Arg His
 55 60 65
 cgc ttg aat ctc atg ggg atc ggt ggc gtg cag gca agg aca ttc cac 355
 Arg Leu Asn Leu Met Gly Ile Gly Gly Val Gln Ala Arg Thr Phe His
 70 75 80 85

<400> 46																
Val	Ile	Asn	Leu	Gln	Asp	Leu	Asp	Glu	Asp	Gln	Arg	Ile	Ala	Ala	Ser	
1				5					10					15		
Ala	Pro	Arg	Gly	Pro	Val	Cys	Ile	Leu	Ala	Gly	Ala	Gly	Thr	Gly	Lys	
			20					25					30			
Thr	Arg	Thr	Ile	Thr	Tyr	Arg	Ile	Ala	His	Leu	Ile	Asp	Gln	Gly	Phe	
		35					40					45				
Val	Ser	Pro	Asn	Arg	Val	Leu	Ala	Val	Thr	Phe	Thr	Ser	Arg	Ala	Ala	
	50					55					60					
Gly	Glu	Met	Arg	His	Arg	Leu	Asn	Leu	Met	Gly	Ile	Gly	Gly	Val	Gln	
65					70					75					80	
Ala	Arg	Thr	Phe	His	Ala	Ala	Ala	Arg	Lys	Gln	Leu	Leu	Tyr	Phe	Trp	
				85					90					95		
Pro	Gln	Val	Ala	Gly	Asn	Leu	Pro	Trp	Arg	Leu	Leu	Asp	Asn	Lys	Phe	
			100					105					110			
Gln	Leu	Val	Gly	Arg	Ala	Val	Arg	Gly	Ala	Arg	Leu	Glu	Ser	Gln	Thr	

115	120	125
Glu Lys Val Arg Asp Ile Leu Gly Glu Ile Glu Trp Ala Lys Ala Ser		
130	135	140
Leu Ile Thr Pro Glu Gln Tyr Pro Asp Arg Leu Gly Thr Arg Thr Pro		
145	150	155
Pro Ala Pro Ala Glu Lys Ile Ala Glu Val Tyr Gln Arg Tyr Glu Asn		
165	170	175
Met Lys Ala Thr Pro Glu Gly Met Leu Leu Asp Phe Asp Asp Leu Leu		
180	185	190
Leu His Thr Ala Gly Ala Leu		
195		

<210> 47
 <211> 1992
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1969)
 <223> RXA02359

<400> 47
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 Val Glu Leu Pro Ser
 1 5

cct ggt gag gcg ctc gca cat gca ggg cac acc cca gaa gtc ctg gaa 163
 Pro Gly Glu Ala Leu Ala His Ala Gly His Thr Pro Glu Val Leu Glu
 10 15 20

gcc gag ctc ggc att gac ccg gct gcc acc cgt att gtg ttg gaa ctt 211
 Ala Glu Leu Gly Ile Asp Pro Ala Ala Thr Arg Ile Val Leu Glu Leu
 25 30 35

gcc tca gag gat gac atc gca gca gcg ctt cct agc agc ccg acg tgg 259
 Ala Ser Glu Asp Asp Ile Ala Ala Ala Leu Pro Ser Ser Pro Thr Trp
 40 45 50

gaa aaa gac gca ctt atc ggc ctt gtc gcc ggt ttg agc att gaa gat 307
 Glu Lys Asp Ala Leu Ile Gly Leu Val Ala Gly Leu Ser Ile Glu Asp
 55 60 65

atc cgc gaa tcg ctc gct atc ccc gca cct tcc aca gag ccg gat acc 355
 Ile Arg Glu Ser Leu Ala Ile Pro Ala Pro Ser Thr Glu Pro Asp Thr
 70 75 80 85

cgc agc gaa gat acc agg ctc att gct ggg ctt aaa acc cca gca gcg 403
 Arg Ser Glu Asp Thr Arg Leu Ile Ala Gly Leu Lys Thr Pro Ala Ala
 90 95 100

caa atg gac ttt gcc tat ttg gat acc cca aat agc aat gac ctg cgc 451
 Gln Met Asp Phe Ala Tyr Leu Asp Thr Pro Asn Ser Asn Asp Leu Arg

105	110	115	
cgc gtt att gaa act gaa ggt ttt gat agc tgg cgc gtg tat atc gac Arg Val Ile Glu Thr Glu Gly Phe Asp Ser Trp Arg Val Tyr Ile Asp 120 125 130			499
ccc agc cag cgc tcc tta gtc acc cgc aac ttc agc gga tcg ggt cgc Pro Ser Gln Arg Ser Leu Val Thr Arg Asn Phe Ser Gly Ser Gly Arg 135 140 145			547
gtt ttt ggt gga gct ggc acc ggc aaa acc gtg gtg gta gtc cac cgt Val Phe Gly Gly Ala Gly Thr Gly Lys Thr Val Val Val Val His Arg 150 155 160 165			595
gcc aac cgc ctg gtc act tct gat gga cac ctt gag acc gac gat aag Ala Asn Arg Leu Val Thr Ser Asp Gly His Leu Glu Thr Asp Asp Lys 170 175 180			643
acg cct cga gtc ctg ctc acc acc tat acc cgc ggt ttg gcc gat gcg Thr Pro Arg Val Leu Leu Thr Thr Tyr Thr Arg Gly Leu Ala Asp Ala 185 190 195			691
ttg aaa tcc tcc atg aac gcg ctt aat ccc act ttc ccc gag gca gaa Leu Lys Ser Ser Met Asn Ala Leu Asn Pro Thr Phe Pro Glu Ala Glu 200 205 210			739
aaa ccc ggt agt cct ggc ttg tgg atc agc gga att gat gcc ttg gca Lys Pro Gly Ser Pro Gly Leu Trp Ile Ser Gly Ile Asp Ala Leu Ala 215 220 225			787
aat aag gtg gtt gcg cta gca aac acc gcc gaa cgt gag gca gca acc Asn Lys Val Val Ala Leu Ala Asn Thr Ala Glu Arg Glu Ala Ala Thr 230 235 240 245			835
act gct atc ttg ggg cgt gca gcc ggc aga atc acc cca ttc atc ggc Thr Ala Ile Leu Gly Arg Ala Ala Gly Arg Ile Thr Pro Phe Ile Gly 250 255 260			883
aac ggc gaa caa gaa ttt tgg atc gac gcg atc att tcc gca gat ccc Asn Gly Glu Gln Glu Phe Trp Ile Asp Ala Ile Ile Ser Ala Asp Pro 265 270 275			931
ggc gat cta tca gaa gaa atc agc aat act gaa ttc ctc gcc caa gag Gly Asp Leu Ser Glu Glu Ile Ser Asn Thr Glu Phe Leu Ala Gln Glu 280 285 290			979
ttt gaa acc gta atc cta gcc cgc gga atc acc caa gaa aag gac tat Phe Glu Thr Val Ile Leu Ala Arg Gly Ile Thr Gln Glu Lys Asp Tyr 295 300 305			1027
ctg cgt gca cct cgt ccc ggc cgt ggt acc cca cta aac cgc gta caa Leu Arg Ala Pro Arg Pro Gly Arg Gly Thr Pro Leu Asn Arg Val Gln 310 315 320 325			1075
cgc aaa aaa gtg tgg gcg att att cag caa ttc atg act tcc tgt gcg Arg Lys Lys Val Trp Ala Ile Ile Gln Gln Phe Met Thr Ser Cys Ala 330 335 340			1123
cgc gaa gga aag atg tcc tgg cca gcg ctt tcc tcc atc gcc gca aac Arg Glu Gly Lys Met Ser Trp Pro Ala Leu Ser Ser Ile Ala Ala Asn 345 350 355			1171

atc ctg gag cag cgc gcc gcc gcc ggc cag ggc cgg cta ttt gac cat	1219
Ile Leu Glu Gln Arg Ala Ala Ala Gly Gln Gly Arg Leu Phe Asp His	
360 365 370	
gtg ctt atc gac gag gcc cag gac ttc cac gcc gga cat tgg ctc tta	1267
Val Leu Ile Asp Glu Ala Gln Asp Phe His Ala Gly His Trp Leu Leu	
375 380 385	
ctc agg gct gcg gta gcc gaa ggt ccc aat gac atc ttc ttg gct gag	1315
Leu Arg Ala Ala Val Ala Glu Gly Pro Asn Asp Ile Phe Leu Ala Glu	
390 395 400 405	
gat tca cac cag cgc atc tac ggc caa cat cat gtg cta agc cgt ttt	1363
Asp Ser His Gln Arg Ile Tyr Gly Gln His His Val Leu Ser Arg Phe	
410 415 420	
ggg att tcc acc cgc ggt cgg gcg tct aag cga ctc acc ctt aac tac	1411
Gly Ile Ser Thr Arg Gly Arg Ala Ser Lys Arg Leu Thr Leu Asn Tyr	
425 430 435	
cgc acc acc gcc gaa aac ctc agt tac gca ctt ggc atg ctc acc ggt	1459
Arg Thr Thr Ala Glu Asn Leu Ser Tyr Ala Leu Gly Met Leu Thr Gly	
440 445 450	
gaa tgg acc gac gcc gaa ggc gaa acg gac aca att gag cac tat cgc	1507
Glu Trp Thr Asp Ala Glu Gly Glu Thr Asp Thr Ile Glu His Tyr Arg	
455 460 465	
tca gcg cgt aag ggc ccc aag cca cac ctc tac caa ttt gaa tct gag	1555
Ser Ala Arg Lys Gly Pro Lys Pro His Leu Tyr Gln Phe Glu Ser Glu	
470 475 480 485	
acc gac gag ttc gaa gca atc gct gag ctc atc aag gtg tgg cag gac	1603
Thr Asp Glu Phe Glu Ala Ile Ala Glu Leu Ile Lys Val Trp Gln Asp	
490 495 500	
agg acc acc gat gta cgc atc ggc att ttg gca cgc acc cgt cct ttg	1651
Arg Thr Thr Asp Val Arg Ile Gly Ile Leu Ala Arg Thr Arg Pro Leu	
505 510 515	
atc aac cgc gtg gtt aat gcg ctc tct gag cag ggc atc gat gcc gtc	1699
Ile Asn Arg Val Val Asn Ala Leu Ser Glu Gln Gly Ile Asp Ala Val	
520 525 530	
aag acg caa aat gcc gaa ctt gca gcc cac gaa act gtc agt gta atg	1747
Lys Thr Gln Asn Ala Glu Leu Ala Ala His Glu Thr Val Ser Val Met	
535 540 545	
aca atg cac gga gct aaa ggc atg gag ttt acc cat gtc atc ttg atc	1795
Thr Met His Gly Ala Lys Gly Met Glu Phe Thr His Val Ile Leu Ile	
550 555 560 565	
gga atg ggc cgt gac ctc att cct ttg caa tac acc atg caa ggt tta	1843
Gly Met Gly Arg Asp Leu Ile Pro Leu Gln Tyr Thr Met Gln Gly Leu	
570 575 580	
ggc gag gcc gag cgt aac gac gcc caa cag cgc gaa cgc tcc ttg ctc	1891
Gly Glu Ala Glu Arg Asn Asp Ala Gln Gln Arg Glu Arg Ser Leu Leu	
585 590 595	

tac gtt gca gct tct cgt gca cgt gat gcc ctt gtt ctc acc acg cat 1939
Tyr Val Ala Ala Ser Arg Ala Arg Asp Ala Leu Val Leu Thr Thr His
600 605 610

act gag cct tcg gag ttg ctg ccg cgg gtt tagagcacca agtaactaaa 1989
Thr Glu Pro Ser Glu Leu Leu Pro Arg Val
615 620

gtt 1992

<210> 48

<211> 623

<212> PRT

<213> Corynebacterium glutamicum

<400> 48

Val Glu Leu Pro Ser Pro Gly Glu Ala Leu Ala His Ala Gly His Thr
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Pro Glu Val Leu Glu Ala Glu Leu Gly Ile Asp Pro Ala Ala Thr Arg
20 25 30

Ile Val Leu Glu Leu Ala Ser Glu Asp Asp Ile Ala Ala Ala Leu Pro
35 40 45

Ser Ser Pro Thr Trp Glu Lys Asp Ala Leu Ile Gly Leu Val Ala Gly
50 55 60

Leu Ser Ile Glu Asp Ile Arg Glu Ser Leu Ala Ile Pro Ala Pro Ser
65 70 75 80

Thr Glu Pro Asp Thr Arg Ser Glu Asp Thr Arg Leu Ile Ala Gly Leu
85 90 95

Lys Thr Pro Ala Ala Gln Met Asp Phe Ala Tyr Leu Asp Thr Pro Asn
100 105 110

Ser Asn Asp Leu Arg Arg Val Ile Glu Thr Glu Gly Phe Asp Ser Trp
115 120 125

Arg Val Tyr Ile Asp Pro Ser Gln Arg Ser Leu Val Thr Arg Asn Phe
130 135 140

Ser Gly Ser Gly Arg Val Phe Gly Gly Ala Gly Thr Gly Lys Thr Val
145 150 155 160

Val Val Val His Arg Ala Asn Arg Leu Val Thr Ser Asp Gly His Leu
165 170 175

Glu Thr Asp Asp Lys Thr Pro Arg Val Leu Leu Thr Thr Tyr Thr Arg
180 185 190

Gly Leu Ala Asp Ala Leu Lys Ser Ser Met Asn Ala Leu Asn Pro Thr
195 200 205

Phe Pro Glu Ala Glu Lys Pro Gly Ser Pro Gly Leu Trp Ile Ser Gly
210 215 220

Ile Asp Ala Leu Ala Asn Lys Val Val Ala Leu Ala Asn Thr Ala Glu
225 230 235 240

Arg Glu Ala Ala Thr Thr Ala Ile Leu Gly Arg Ala Ala Gly Arg Ile
245 250 255

Thr Pro Phe Ile Gly Asn Gly Glu Gln Glu Phe Trp Ile Asp Ala Ile
260 265 270

Ile Ser Ala Asp Pro Gly Asp Leu Ser Glu Glu Ile Ser Asn Thr Glu
275 280 285

Phe Leu Ala Gln Glu Phe Glu Thr Val Ile Leu Ala Arg Gly Ile Thr
290 295 300

Gln Glu Lys Asp Tyr Leu Arg Ala Pro Arg Pro Gly Arg Gly Thr Pro
305 310 315 320

Leu Asn Arg Val Gln Arg Lys Lys Val Trp Ala Ile Ile Gln Gln Phe
325 330 335

Met Thr Ser Cys Ala Arg Glu Gly Lys Met Ser Trp Pro Ala Leu Ser
340 345 350

Ser Ile Ala Ala Asn Ile Leu Glu Gln Arg Ala Ala Ala Gly Gln Gly
355 360 365

Arg Leu Phe Asp His Val Leu Ile Asp Glu Ala Gln Asp Phe His Ala
370 375 380

Gly His Trp Leu Leu Leu Arg Ala Ala Val Ala Glu Gly Pro Asn Asp
385 390 395 400

Ile Phe Leu Ala Glu Asp Ser His Gln Arg Ile Tyr Gly Gln His His
405 410 415

Val Leu Ser Arg Phe Gly Ile Ser Thr Arg Gly Arg Ala Ser Lys Arg
420 425 430

Leu Thr Leu Asn Tyr Arg Thr Thr Ala Glu Asn Leu Ser Tyr Ala Leu
435 440 445

Gly Met Leu Thr Gly Glu Trp Thr Asp Ala Glu Gly Glu Thr Asp Thr
450 455 460

Ile Glu His Tyr Arg Ser Ala Arg Lys Gly Pro Lys Pro His Leu Tyr
465 470 475 480

Gln Phe Glu Ser Glu Thr Asp Glu Phe Glu Ala Ile Ala Glu Leu Ile
485 490 495

Lys Val Trp Gln Asp Arg Thr Thr Asp Val Arg Ile Gly Ile Leu Ala
500 505 510

Arg Thr Arg Pro Leu Ile Asn Arg Val Val Asn Ala Leu Ser Glu Gln
515 520 525

Gly Ile Asp Ala Val Lys Thr Gln Asn Ala Glu Leu Ala Ala His Glu
530 535 540

Thr Val Ser Val Met Thr Met His Gly Ala Lys Gly Met Glu Phe Thr
545 550 555 560

His Val Ile Leu Ile Gly Met Gly Arg Asp Leu Ile Pro Leu Gln Tyr
565 570 575

Thr Met Gln Gly Leu Gly Glu Ala Glu Arg Asn Asp Ala Gln Gln Arg
580 585 590

Glu Arg Ser Leu Leu Tyr Val Ala Ala Ser Arg Ala Arg Asp Ala Leu
595 600 605

Val Leu Thr Thr His Thr Glu Pro Ser Glu Leu Leu Pro Arg Val
610 615 620

<210> 49
<211> 2884
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(2884)
<223> RXN02764

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Met Ser Glu Tyr Lys
1 5

cca ccc att cca tcg gat cca caa gtt cgg ctg att aag cca aca tcc 163
Pro Pro Ile Pro Ser Asp Pro Gln Val Arg Leu Ile Lys Pro Thr Ser
10 15 20

aag ctt cgt cct cgt tcg tgg gag ggc gaa gtt tcg cat tta gtt aaa 211
Lys Leu Arg Pro Arg Ser Trp Glu Gly Glu Val Ser His Leu Val Lys
25 30 35

caa ggc acc ggt ttg tgg cgg gtg act ggt gag gcg ggc tcg ggg gtg 259
Gln Gly Thr Gly Leu Trp Arg Val Thr Gly Glu Ala Gly Ser Gly Val
40 45 50

agc tcc gct gtt gtc gat act gtc ctt gaa cgc att cgc caa ggg tgg 307
Ser Ser Ala Val Val Asp Thr Val Leu Glu Arg Ile Arg Gln Gly Trp
55 60 65

gag ccg tca tcg atg ttg gtt gtc gcc acg tcg aaa gag gcg gcg agt 355
Glu Pro Ser Ser Met Leu Val Val Ala Thr Ser Lys Glu Ala Ala Ser
70 75 80 85

cgc ttg agg caa gag atc tcg gaa tcc gta gcc cag atg gat tat gtg 403
Arg Leu Arg Gln Glu Ile Ser Glu Ser Val Ala Gln Met Asp Tyr Val
90 95 100

tcg gag ggg ccg ttg gtg cga tcg gtg cac tcg gtg gct ttc gcg ctg 451
Ser Glu Gly Pro Leu Val Arg Ser Val His Ser Val Ala Phe Ala Leu
105 110 115

att cgt gat gcg tcg gat gat gat gtg cgg ttg att acg ggc gct gag 499
Ile Arg Asp Ala Ser Asp Asp Asp Val Arg Leu Ile Thr Gly Ala Glu
120 125 130

caa gat gcg gtg att cgg gag ttg ctg cgt ggt cat gct gat gat ggt Gln Asp Ala Val Ile Arg Glu Leu Leu Arg Gly His Ala Asp Asp Gly 135 140 145	547
cgt ggg ggg tgg ccg cag gag cag cgt gag ggt ttg cgg atg gtg ggg Arg Gly Gly Trp Pro Gln Glu Gln Arg Glu Gly Leu Arg Met Val Gly 150 155 160 165	595
ttc gct agg cag ttg cgt gac ttt ttg ctt cgt gcg gtg gag cgt ggt Phe Ala Arg Gln Leu Arg Asp Phe Leu Leu Arg Ala Val Glu Arg Gly 170 175 180	643
gtg ggc cct gat gag ttg gtg gaa ttg ggg gag cga ttt gag cgc gcc Val Gly Pro Asp Glu Leu Val Glu Leu Gly Glu Arg Phe Glu Arg Ala 185 190 195	691
aat tgg gtt gct gcg ggt gag ttc ctt cgt gag tac aag cag gtg atg Asn Trp Val Ala Ala Gly Glu Phe Leu Arg Glu Tyr Lys Gln Val Met 200 205 210	739
aag ctg tcg ggg gcg cat agt ttt tct gcg tct gag ttg gtg act gaa Lys Leu Ser Gly Ala His Ser Phe Ser Ala Ser Glu Leu Val Thr Glu 215 220 225	787
gcg ctg cgt ggt cct gag ccg tcg gtg aag tat cgc ggt gtg ttt att Ala Leu Arg Gly Pro Glu Pro Ser Val Lys Tyr Arg Gly Val Phe Ile 230 235 240 245	835
gat gat gcg cag cat ttg gat ccg aag tcg gcg gaa ctt gtg tcg cgg Asp Asp Ala Gln His Leu Asp Pro Lys Ser Ala Glu Leu Val Ser Arg 250 255 260	883
ttt ttc cct gag gcg gag ttg gct gtg gtg gcg ggt gat ccg cag cag Phe Phe Pro Glu Ala Glu Leu Ala Val Val Ala Gly Asp Pro Gln Gln 265 270 275	931
tcg gtg ttt agg ttc cgt ggt gcg aat ccg gat ttt ctc acc aag ttg Ser Val Phe Arg Phe Arg Gly Ala Asn Pro Asp Phe Leu Thr Lys Leu 280 285 290	979
agt gtg gat cac gag gtg gtg ttg aag ggg agg agg aaa gcg tcg aca Ser Val Asp His Glu Val Val Leu Lys Gly Arg Arg Lys Ala Ser Thr 295 300 305	1027
agc att gtc gtg gca gag acc gag tcg gcg cat gcg gac ctg ctt gct Ser Ile Val Val Ala Glu Thr Glu Ser Ala His Ala Asp Leu Leu Ala 310 315 320 325	1075
gac acg gtg cgg cgc gcg cat ctc att gat ggg cgc agc tgg tcg gag Asp Thr Val Arg Arg Ala His Leu Ile Asp Gly Arg Ser Trp Ser Glu 330 335 340	1123
atc gct gtt atc gtg cgc tcg gcc ggc atg att gcg ccg att tgg cgc Ile Ala Val Ile Val Arg Ser Ala Gly Met Ile Ala Pro Ile Trp Arg 345 350 355	1171
acc ctg ctg gcc gcc ggc gtg ccc gtg cac atc agc ccg act gat gtg Thr Leu Leu Ala Ala Gly Val Pro Val His Ile Ser Pro Thr Asp Val 360 365 370	1219

gtg ctc gcc gaa caa cgt atc gtt gcc gca atg att ctc ggg ctg cgc Val Leu Ala Glu Gln Arg Ile Val Ala Ala Met Ile Leu Gly Leu Arg 375 380 385	1267
gcg ctg acg gaa tcg ctc aac gcc atc gag ttg gag gat ctt ctc cta Ala Leu Thr Glu Ser Leu Asn Ala Ile Glu Leu Glu Asp Leu Leu Leu 390 395 400 405	1315
gga ccg atc ggt ggc gcc gat ccg gtg act ctg cgt cgt ttg ctg cgc Gly Pro Ile Gly Gly Ala Asp Pro Val Thr Leu Arg Arg Leu Leu Arg 410 415 420	1363
ggg ttg cgg cag gcg gag atg aag atg ggt ggg cag agg cga gcg atc Gly Leu Arg Gln Ala Glu Met Lys Met Gly Gly Gln Arg Arg Ala Ile 425 430 435	1411
gag gtg ctc aga agc ctg ctc gca gag tcg gat gcg gag atg ttg ggc Glu Val Leu Arg Ser Leu Leu Ala Glu Ser Asp Ala Glu Met Leu Gly 440 445 450	1459
ttt ttg acc gat cgt gag ctg aat ttg ctc gag cgg gtg cga tct gtg Phe Leu Thr Asp Arg Glu Leu Asn Leu Leu Glu Arg Val Arg Ser Val 455 460 465	1507
ttg gaa gcg ggt cgt gaa gcg ctc gcg gaa cac ggc agt atc gaa gag Leu Glu Ala Gly Arg Glu Ala Leu Ala Glu His Gly Ser Ile Glu Glu 470 475 480 485	1555
gtg ttg tgg gcg ctg tgg tcg gcg acc gat ctg tcg aac tcg ttg tcc Val Leu Trp Ala Leu Trp Ser Ala Thr Asp Leu Ser Asn Ser Leu Ser 490 495 500	1603
gcg atc agc ctt cga ggc ggc gca tcg ggg tcc cag gcc gat cgc gat Ala Ile Ser Leu Arg Gly Gly Ala Ser Gly Ser Gln Ala Asp Arg Asp 505 510 515	1651
ttg gat gcg atg atg gcg ctt ttc gac gcc gcc ggc gac tac gtg gag Leu Asp Ala Met Met Ala Leu Phe Asp Ala Ala Gly Asp Tyr Val Glu 520 525 530	1699
cgc tac ccg tca gcg ggc gtg cgg agt ttc att ctg cat att tct gag Arg Tyr Pro Ser Ala Gly Val Arg Ser Phe Ile Leu His Ile Ser Glu 535 540 545	1747
cag gaa ctt ccg acc ggc atg cgt gag cga cgc ggc gcg atc ccg gag Gln Glu Leu Pro Thr Gly Met Arg Glu Arg Arg Gly Ala Ile Pro Glu 550 555 560 565	1795
gcc gtc gag gtg ctg acg gcg cac gcg acg acg ggt cgt gag tgg aag Ala Val Glu Val Leu Thr Ala His Ala Thr Thr Gly Arg Glu Trp Lys 570 575 580	1843
cgc gtg atc gtt gct gag gtg cag gag ggc agt tgg ccg tcg ctc ggt Arg Val Ile Val Ala Glu Val Gln Glu Gly Ser Trp Pro Ser Leu Gly 585 590 595	1891
gaa act ggc acg ctg ctt ggt cag gaa gag ttc gtc gat ttg gtg gat Glu Thr Gly Thr Leu Leu Gly Gln Glu Glu Phe Val Asp Leu Val Asp 600 605 610	1939
gag ggt att gat ccc gat atc atc att tcc cga tcc gcc gaa cga ctg	1987

Glu Gly Ile Asp Pro Asp Ile Ile Ile Ser Arg Ser Ala Glu Arg Leu 615 620 625	
gcg gag gaa cgc cga ctg ttc tac ctc gcc acc acc aga tcc acc gaa Ala Glu Glu Arg Arg Leu Phe Tyr Leu Ala Thr Thr Arg Ser Thr Glu 630 635 640 645	2035
tcg ctc ctg gtt acc gct gtg aat tcc ccc gac tcc gac gaa gtc cgc Ser Leu Leu Val Thr Ala Val Asn Ser Pro Asp Ser Asp Glu Val Arg 650 655 660	2083
gaa ccc tcc cgg ttt ttg gaa ttg ctg agt caa ccg atc gtt gtt ctc Glu Pro Ser Arg Phe Leu Glu Leu Leu Ser Gln Pro Ile Val Val Leu 665 670 675	2131
gag ggg gag gaa gct tcg gcg atc gcg gaa ccg gag gag att ggg cat Glu Gly Glu Glu Ala Ser Ala Ile Ala Glu Pro Glu Glu Ile Gly His 680 685 690	2179
cgg ttg ttg tcg att cct gcg atg gtt gct gag ttg cgt cgt gtg gtg Arg Leu Leu Ser Ile Pro Ala Met Val Ala Glu Leu Arg Arg Val Val 695 700 705	2227
aat gat ccg cgg gat ccg cgt cgg aag cag gct gcg agg cag ttg tcg Asn Asp Pro Arg Asp Pro Arg Arg Lys Gln Ala Ala Arg Gln Leu Ser 710 715 720 725	2275
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aat ctg cgc act ccg tcg act gat gag gag ttg atc aag ggg gcg gtg Asn Leu Arg Thr Pro Ser Thr Asp Glu Glu Leu Ile Lys Gly Ala Val 745 750 755	2371
tcg ttg tcg ccg tcg cgg att gag cag ttg ttg aat tgt ccg ctg cgc Ser Leu Ser Pro Ser Arg Ile Glu Gln Leu Leu Asn Cys Pro Leu Arg 760 765 770	2419
gct gtg ttg gat cgt ttg gac agt gag gag gaa acg ccg atc gcg atg Ala Val Leu Asp Arg Leu Asp Ser Glu Glu Glu Thr Pro Ile Ala Met 775 780 785	2467
ctc aag ggc acc ttg gtg cac gcg ttt gcg gag gcg gtc gcc ggt ggc Leu Lys Gly Thr Leu Val His Ala Phe Ala Glu Ala Val Ala Gly Gly 790 795 800 805	2515
gtc gat gcg gcg ctc gcc gaa gag aag gtg acc agc gcc tac atg cag Val Asp Ala Ala Leu Ala Glu Glu Lys Val Thr Ser Ala Tyr Met Gln 810 815 820	2563
ctg gcg aac gtg ccg agc tgg tcg cgc gaa agc acc gaa att gct ttt Leu Ala Asn Val Pro Ser Trp Ser Arg Glu Ser Thr Glu Ile Ala Phe 825 830 835	2611
cga cgc atc ctc tca cgt acc gat acc tgg ctg aag act tct cgc gcc Arg Arg Ile Leu Ser Arg Thr Asp Thr Trp Leu Lys Thr Ser Arg Ala 840 845 850	2659
gat ttt acg gaa gtg gga acg gag atg gac gta tcg gtg acc atc gat Asp Phe Thr Glu Val Gly Thr Glu Met Asp Val Ser Val Thr Ile Asp	2707

855	860	865	
gac tcc gta tcg atc cgt ggt cgc atg gac cgt ttg gag cga aac aaa			2755
Asp Ser Val Ser Ile Arg Gly Arg Met Asp Arg Leu Glu Arg Asn Lys			
870	875	880	885
tcc ggc gag ttg gtg gtt gtt gat ttc aaa acg ggc aaa act caa atc			2803
Ser Gly Glu Leu Val Val Val Asp Phe Lys Thr Gly Lys Thr Gln Ile			
	890	895	900
gct gca aaa gac atg ggc gat cac cca cag ttg ttt gcg tat caa ttg			2851
Ala Ala Lys Asp Met Gly Asp His Pro Gln Leu Phe Ala Tyr Gln Leu			
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gcg ttg tcg aaa ggc gtg ctg cat ggt gac aaa			2884
Ala Leu Ser Lys Gly Val Leu His Gly Asp Lys			
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<212> PRT

<213> Corynebacterium glutamicum

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Ile	Lys	Pro	Thr	Ser	Lys	Leu	Arg	Pro	Arg	Ser	Trp	Glu	Gly	Glu	Val
			20					25					30		

Ser	His	Leu	Val	Lys	Gln	Gly	Thr	Gly	Leu	Trp	Arg	Val	Thr	Gly	Glu
		35					40					45			

Ala	Gly	Ser	Gly	Val	Ser	Ser	Ala	Val	Val	Asp	Thr	Val	Leu	Glu	Arg
	50					55					60				

Ile	Arg	Gln	Gly	Trp	Glu	Pro	Ser	Ser	Met	Leu	Val	Val	Ala	Thr	Ser
65					70					75					80

Lys	Glu	Ala	Ala	Ser	Arg	Leu	Arg	Gln	Glu	Ile	Ser	Glu	Ser	Val	Ala
				85					90					95	

Gln	Met	Asp	Tyr	Val	Ser	Glu	Gly	Pro	Leu	Val	Arg	Ser	Val	His	Ser
			100					105					110		

Val	Ala	Phe	Ala	Leu	Ile	Arg	Asp	Ala	Ser	Asp	Asp	Asp	Val	Arg	Leu
		115					120					125			

Ile	Thr	Gly	Ala	Glu	Gln	Asp	Ala	Val	Ile	Arg	Glu	Leu	Leu	Arg	Gly
	130					135					140				

His	Ala	Asp	Asp	Gly	Arg	Gly	Gly	Trp	Pro	Gln	Glu	Gln	Arg	Glu	Gly
145					150					155					160

Leu	Arg	Met	Val	Gly	Phe	Ala	Arg	Gln	Leu	Arg	Asp	Phe	Leu	Leu	Arg
				165					170					175	

Ala	Val	Glu	Arg	Gly	Val	Gly	Pro	Asp	Glu	Leu	Val	Glu	Leu	Gly	Glu
			180					185					190		

Arg Phe Glu Arg Ala Asn Trp Val Ala Ala Gly Glu Phe Leu Arg Glu
 195 200 205
 Tyr Lys Gln Val Met Lys Leu Ser Gly Ala His Ser Phe Ser Ala Ser
 210 215 220
 Glu Leu Val Thr Glu Ala Leu Arg Gly Pro Glu Pro Ser Val Lys Tyr
 225 230 235 240
 Arg Gly Val Phe Ile Asp Asp Ala Gln His Leu Asp Pro Lys Ser Ala
 245 250 255
 Glu Leu Val Ser Arg Phe Phe Pro Glu Ala Glu Leu Ala Val Val Ala
 260 265 270
 Gly Asp Pro Gln Gln Ser Val Phe Arg Phe Arg Gly Ala Asn Pro Asp
 275 280 285
 Phe Leu Thr Lys Leu Ser Val Asp His Glu Val Val Leu Lys Gly Arg
 290 295 300
 Arg Lys Ala Ser Thr Ser Ile Val Val Ala Glu Thr Glu Ser Ala His
 305 310 315 320
 Ala Asp Leu Leu Ala Asp Thr Val Arg Arg Ala His Leu Ile Asp Gly
 325 330 335
 Arg Ser Trp Ser Glu Ile Ala Val Ile Val Arg Ser Ala Gly Met Ile
 340 345 350
 Ala Pro Ile Trp Arg Thr Leu Leu Ala Ala Gly Val Pro Val His Ile
 355 360 365
 Ser Pro Thr Asp Val Val Leu Ala Glu Gln Arg Ile Val Ala Ala Met
 370 375 380
 Ile Leu Gly Leu Arg Ala Leu Thr Glu Ser Leu Asn Ala Ile Glu Leu
 385 390 395 400
 Glu Asp Leu Leu Leu Gly Pro Ile Gly Gly Ala Asp Pro Val Thr Leu
 405 410 415
 Arg Arg Leu Leu Arg Gly Leu Arg Gln Ala Glu Met Lys Met Gly Gly
 420 425 430
 Gln Arg Arg Ala Ile Glu Val Leu Arg Ser Leu Leu Ala Glu Ser Asp
 435 440 445
 Ala Glu Met Leu Gly Phe Leu Thr Asp Arg Glu Leu Asn Leu Leu Glu
 450 455 460
 Arg Val Arg Ser Val Leu Glu Ala Gly Arg Glu Ala Leu Ala Glu His
 465 470 475 480
 Gly Ser Ile Glu Glu Val Leu Trp Ala Leu Trp Ser Ala Thr Asp Leu
 485 490 495
 Ser Asn Ser Leu Ser Ala Ile Ser Leu Arg Gly Gly Ala Ser Gly Ser
 500 505 510
 Gln Ala Asp Arg Asp Leu Asp Ala Met Met Ala Leu Phe Asp Ala Ala

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Gly	Asp	Tyr	Val	Glu	Arg	Tyr	Pro	Ser	Ala	Gly	Val	Arg	Ser	Phe	Ile
530						535					540				
Leu	His	Ile	Ser	Glu	Gln	Glu	Leu	Pro	Thr	Gly	Met	Arg	Glu	Arg	Arg
545					550					555					560
Gly	Ala	Ile	Pro	Glu	Ala	Val	Glu	Val	Leu	Thr	Ala	His	Ala	Thr	Thr
				565					570					575	
Gly	Arg	Glu	Trp	Lys	Arg	Val	Ile	Val	Ala	Glu	Val	Gln	Glu	Gly	Ser
			580					585					590		
Trp	Pro	Ser	Leu	Gly	Glu	Thr	Gly	Thr	Leu	Leu	Gly	Gln	Glu	Glu	Phe
		595					600					605			
Val	Asp	Leu	Val	Asp	Glu	Gly	Ile	Asp	Pro	Asp	Ile	Ile	Ile	Ser	Arg
610						615					620				
Ser	Ala	Glu	Arg	Leu	Ala	Glu	Glu	Arg	Arg	Leu	Phe	Tyr	Leu	Ala	Thr
625					630					635					640
Thr	Arg	Ser	Thr	Glu	Ser	Leu	Leu	Val	Thr	Ala	Val	Asn	Ser	Pro	Asp
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Ser	Asp	Glu	Val	Arg	Glu	Pro	Ser	Arg	Phe	Leu	Glu	Leu	Leu	Ser	Gln
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Pro	Ile	Val	Val	Leu	Glu	Gly	Glu	Glu	Ala	Ser	Ala	Ile	Ala	Glu	Pro
			675				680					685			
Glu	Glu	Ile	Gly	His	Arg	Leu	Leu	Ser	Ile	Pro	Ala	Met	Val	Ala	Glu
						695					700				
Leu	Arg	Arg	Val	Val	Asn	Asp	Pro	Arg	Asp	Pro	Arg	Arg	Lys	Gln	Ala
705					710					715					720
Ala	Arg	Gln	Leu	Ser	Arg	Leu	Ala	Glu	Ala	Gly	Ile	Pro	Gly	Ala	Asn
				725					730					735	
Pro	Ala	Glu	Trp	Thr	Asn	Leu	Arg	Thr	Pro	Ser	Thr	Asp	Glu	Glu	Leu
			740					745					750		
Ile	Lys	Gly	Ala	Val	Ser	Leu	Ser	Pro	Ser	Arg	Ile	Glu	Gln	Leu	Leu
		755					760					765			
Asn	Cys	Pro	Leu	Arg	Ala	Val	Leu	Asp	Arg	Leu	Asp	Ser	Glu	Glu	Glu
	770					775					780				
Thr	Pro	Ile	Ala	Met	Leu	Lys	Gly	Thr	Leu	Val	His	Ala	Phe	Ala	Glu
785					790					795					800
Ala	Val	Ala	Gly	Gly	Val	Asp	Ala	Ala	Leu	Ala	Glu	Glu	Lys	Val	Thr
				805					810					815	
Ser	Ala	Tyr	Met	Gln	Leu	Ala	Asn	Val	Pro	Ser	Trp	Ser	Arg	Glu	Ser
			820					825					830		
Thr	Glu	Ile	Ala	Phe	Arg	Arg	Ile	Leu	Ser	Arg	Thr	Asp	Thr	Trp	Leu
		835					840					845			

Lys Thr Ser Arg Ala Asp Phe Thr Glu Val Gly Thr Glu Met Asp Val
 850 855 860
 Ser Val Thr Ile Asp Asp Ser Val Ser Ile Arg Gly Arg Met Asp Arg
 865 870 875 880
 Leu Glu Arg Asn Lys Ser Gly Glu Leu Val Val Val Asp Phe Lys Thr
 885 890 895
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 Met Ser Glu Tyr Lys
 1 5
 cca ccc att cca tcg gat cca caa gtt cgg ctg att aag cca aca tcc 163
 Pro Pro Ile Pro Ser Asp Pro Gln Val Arg Leu Ile Lys Pro Thr Ser
 10 15 20
 aag ctt cgt cct cgt tcg tgg gag ggc gaa gtt tcg cat tta gtt aaa 211
 Lys Leu Arg Pro Arg Ser Trp Glu Gly Glu Val Ser His Leu Val Lys
 25 30 35
 caa ggc acc ggt ttg tgg cgg gtg act ggt gag gcg ggc tcg ggg gtg 259
 Gln Gly Thr Gly Leu Trp Arg Val Thr Gly Glu Ala Gly Ser Gly Val
 40 45 50
 agc tcc gct gtt gtc gat act gtc ctt gaa cgc att cgc caa ggg tgg 307
 Ser Ser Ala Val Val Asp Thr Val Leu Glu Arg Ile Arg Gln Gly Trp
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 Glu Pro Ser Ser Met Leu Val Val Ala Thr Ser Lys Glu Ala Ala Ser
 70 75 80 85
 cgc ttg agg caa gag atc tcg gaa tcc gta gcc cag atg gat tat gtg 403
 Arg Leu Arg Gln Glu Ile Ser Glu Ser Val Ala Gln Met Asp Tyr Val
 90 95 100

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Ser Glu Gly Pro Leu Val Arg Ser Val His Ser Val Ala Phe Ala Leu	
105 110 115	
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Ile Arg Asp Ala Ser Asp Asp Asp Val Arg Leu Ile Thr Gly Ala Glu	
120 125 130	
caa gat gcg gtg att cgg gag ttg ctg cgt ggt cat gct gat gat ggt	547
Gln Asp Ala Val Ile Arg Glu Leu Leu Arg Gly His Ala Asp Asp Gly	
135 140 145	
cgt ggg ggg tgg ccg cag gag cag cgt gag ggt ttg cgg atg gtg ggg	595
Arg Gly Gly Trp Pro Gln Glu Gln Arg Glu Gly Leu Arg Met Val Gly	
150 155 160 165	
ttc gct agg cag ttg cgt gac ttt ttg ctt cgt gcg gtg gag cgt ggt	643
Phe Ala Arg Gln Leu Arg Asp Phe Leu Leu Arg Ala Val Glu Arg Gly	
170 175 180	
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Val Gly Pro Asp Glu Leu Val Glu Leu Gly Glu Arg Phe Glu Arg Ala	
185 190 195	
aat tgg gtt gct gcg ggt gag ttc ctt cgt gag tac aag cag gtg atg	739
Asn Trp Val Ala Ala Gly Glu Phe Leu Arg Glu Tyr Lys Gln Val Met	
200 205 210	
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Lys Leu Ser Gly Ala His Ser Phe Ser Ala Ser Glu Leu Val Thr Glu	
215 220 225	
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Ala Leu Arg Gly Pro Glu Pro Ser Val Lys Tyr Arg Gly Val Phe Ile	
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Asp Asp Ala Gln His Leu Asp Pro Lys Ser Ala Glu Leu Val Ser Arg	
250 255 260	
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Phe Phe Pro Glu Ala Glu Leu Ala Val Val Ala Gly Asp Pro Gln Gln	
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Ser Val Phe Arg Phe Arg Gly Ala Asn Pro Asp Phe Leu Thr Lys Leu	
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agt gtg gat cac gag gtg gtg ttg aag ggg agg agg aaa gcg tcg aca	1027
Ser Val Asp His Glu Val Val Leu Lys Gly Arg Arg Lys Ala Ser Thr	
295 300 305	
agc att gtc gtg gca gag acc gag tcg gcg cat gcg gac ctg ctt gct	1075
Ser Ile Val Val Ala Glu Thr Glu Ser Ala His Ala Asp Leu Leu Ala	
310 315 320 325	
gac acg gtg cgg cgc gcg cat ctc att gat ggg cgc agc tgg tcg gag	1123
Asp Thr Val Arg Arg Ala His Leu Ile Asp Gly Arg Ser Trp Ser Glu	
330 335 340	
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Thr Leu Leu Ala Ala Gly Val Pro Val His Ile Ser Pro Thr Asp Val			
360	365	370	
gtg ctc gcc gaa caa cgt atc gtt gcc gca atg att ctc ggg ctg cgc			1267
Val Leu Ala Glu Gln Arg Ile Val Ala Ala Met Ile Leu Gly Leu Arg			
375	380	385	
gcg ctg acg gaa tcg ctc aac gcc atc gag ttg gag gat ctt ctc cta			1315
Ala Leu Thr Glu Ser Leu Asn Ala Ile Glu Leu Glu Asp Leu Leu Leu			
390	395	400	405
gga ccg atc ggt ggc gcc gat ccg gtg act ctg cgt cgt ttg ctg cgc			1363
Gly Pro Ile Gly Gly Ala Asp Pro Val Thr Leu Arg Arg Leu Leu Arg			
410	415	420	
ggg ttg cgg cag gcg gag atg aag atg ggt ggg cag agg cga gcg atc			1411
Gly Leu Arg Gln Ala Glu Met Lys Met Gly Gly Gln Arg Arg Ala Ile			
425	430	435	
gag gtg ctc aga agc ctg ctc gca gag tcg gat gcg gag atg ttg ggc			1459
Glu Val Leu Arg Ser Leu Leu Ala Glu Ser Asp Ala Glu Met Leu Gly			
440	445	450	
ttt ttg acc gat cgt gag ctg aat ttg ctc gag cgg gtg cga tct gtg			1507
Phe Leu Thr Asp Arg Glu Leu Asn Leu Leu Glu Arg Val Arg Ser Val			
455	460	465	
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Leu Glu Ala Gly Arg Glu Ala Leu Ala Glu His Gly Ser Ile Glu Glu			
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Val Leu Trp Ala Leu Trp Ser Ala Thr Asp Leu Ser Asn Ser Leu Ser			
490	495	500	
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Ala Ile Ser Leu Arg Gly Gly Ala Ser Gly Ser Gln Ala Asp Arg Asp			
505	510	515	
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Leu Asp Ala Met Met Ala Leu Phe Asp Ala Ala Gly Asp Tyr Val Glu			
520	525	530	
cgc tac ccg tca gcg ggc gtg cgg agt ttc att ctg cat att tct gag			1747
Arg Tyr Pro Ser Ala Gly Val Arg Ser Phe Ile Leu His Ile Ser Glu			
535	540	545	
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gcc gtc gag gtg ctg acg gcg cac gcg acg acg ggt cgt gag tgg aag			1843
Ala Val Glu Val Leu Thr Ala His Ala Thr Thr Gly Arg Glu Trp Lys			
570	575	580	
cgc gtg atc gtt gct gag gtg cag gag ggc agt tgg ccg tcg ctc ggt			1891
Arg Val Ile Val Ala Glu Val Gln Glu Gly Ser Trp Pro Ser Leu Gly			

585	590	595	
gaa act ggc acg ctg ctt ggt cag gaa gag ttc gtc gat ttg gtg gat Glu Thr Gly Thr Leu Leu Gly Gln Glu Glu Phe Val Asp Leu Val Asp 600 605 610			1939
gag ggt att gat ccc gat atc atc att tcc cga tcc gcc gaa cga ctg Glu Gly Ile Asp Pro Asp Ile Ile Ile Ser Arg Ser Ala Glu Arg Leu 615 620 625			1987
gcg gag gaa cgc cga ctg ttc tac ctc gcc acc acc aga tcc acc gaa Ala Glu Glu Arg Arg Leu Phe Tyr Leu Ala Thr Thr Arg Ser Thr Glu 630 635 640 645			2035
tcg ctc ctg gtt acc gct gtg aat tcc ccc gac tcc gac gaa gtc cgc Ser Leu Leu Val Thr Ala Val Asn Ser Pro Asp Ser Asp Glu Val Arg 650 655 660			2083
gaa ccc tcc cgg ttt ttg gaa ttg ctg agt caa ccg atc gtt gtt ctc Glu Pro Ser Arg Phe Leu Glu Leu Leu Ser Gln Pro Ile Val Val Leu 665 670 675			2131
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aat ctg cgc act ccg tcg act gat gag gag ttg atc aag ggg gcg gtg Asn Leu Arg Thr Pro Ser Thr Asp Glu Glu Leu Ile Lys Gly Ala Val 745 750 755			2371
tcg ttg tcg ccg tcg cgg att gag cag ttg ttg aat tgt ccg ctg cgc Ser Leu Ser Pro Ser Arg Ile Glu Gln Leu Leu Asn Cys Pro Leu Arg 760 765 770			2419
gct gtg ttg gat cgt ttg gac agt gag gag gaa acg ccg atc gcg atg Ala Val Leu Asp Arg Leu Asp Ser Glu Glu Glu Thr Pro Ile Ala Met 775 780 785			2467
ctc aag ggc acc ttg gtg cac gcg ttt gcg gag gcg gtc gcc ggt ggc Leu Lys Gly Thr Leu Val His Ala Phe Ala Glu Ala Val Ala Gly Gly 790 795 800 805			2515
gtc gat gcg gcg ctc gcc gaa gag aag gtg acc agc gcc tac atg cag Val Asp Ala Ala Leu Ala Glu Glu Lys Val Thr Ser Ala Tyr Met Gln 810 815 820			2563
ctg gcg aac gtg ccg agc tgg tcg cgc gaa agc acc gaa att gct ttt Leu Ala Asn Val Pro Ser Trp Ser Arg Glu Ser Thr Glu Ile Ala Phe 825 830 835			2611

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 Arg Arg Ile Leu Ser Arg Thr Asp Thr Trp Leu Lys Thr Ser Arg Ala
 840 845 850

 gat ttt acg gaa gtg gga acg gag atg gac gta tcg gtg acc atc gat 2707
 Asp Phe Thr Glu Val Gly Thr Glu Met Asp Val Ser Val Thr Ile Asp
 855 860 865

 gac tcc gta tcg atc cgt ggt cgc atg gac cgt ttg gag cga aac aaa 2755
 Asp Ser Val Ser Ile Arg Gly Arg Met Asp Arg Leu Glu Arg Asn Lys
 870 875 880 885

 tcc ggc gag ttg gtg gtt gtt gat ttc aaa acg ggc aaa act caa atc 2803
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 890 895 900

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 Ala Ala Lys Asp Met Gly Asp His Pro Gln Leu Phe Ala Tyr Gln Leu
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 Met Ser Glu Tyr Lys Pro Pro Ile Pro Ser Asp Pro Gln Val Arg Leu
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 Ile Lys Pro Thr Ser Lys Leu Arg Pro Arg Ser Trp Glu Gly Glu Val
 20 25 30

 Ser His Leu Val Lys Gln Gly Thr Gly Leu Trp Arg Val Thr Gly Glu
 35 40 45

 Ala Gly Ser Gly Val Ser Ser Ala Val Val Asp Thr Val Leu Glu Arg
 50 55 60

 Ile Arg Gln Gly Trp Glu Pro Ser Ser Met Leu Val Val Ala Thr Ser
 65 70 75 80

 Lys Glu Ala Ala Ser Arg Leu Arg Gln Glu Ile Ser Glu Ser Val Ala
 85 90 95

 Gln Met Asp Tyr Val Ser Glu Gly Pro Leu Val Arg Ser Val His Ser
 100 105 110

 Val Ala Phe Ala Leu Ile Arg Asp Ala Ser Asp Asp Val Arg Leu
 115 120 125

 Ile Thr Gly Ala Glu Gln Asp Ala Val Ile Arg Glu Leu Leu Arg Gly
 130 135 140

 His Ala Asp Asp Gly Arg Gly Gly Trp Pro Gln Glu Gln Arg Glu Gly
 145 150 155 160

Leu Arg Met Val Gly Phe Ala Arg Gln Leu Arg Asp Phe Leu Leu Arg
165 170 175

Ala Val Glu Arg Gly Val Gly Pro Asp Glu Leu Val Glu Leu Gly Glu
180 185 190

Arg Phe Glu Arg Ala Asn Trp Val Ala Ala Gly Glu Phe Leu Arg Glu
195 200 205

Tyr Lys Gln Val Met Lys Leu Ser Gly Ala His Ser Phe Ser Ala Ser
210 215 220

Glu Leu Val Thr Glu Ala Leu Arg Gly Pro Glu Pro Ser Val Lys Tyr
225 230 235 240

Arg Gly Val Phe Ile Asp Asp Ala Gln His Leu Asp Pro Lys Ser Ala
245 250 255

Glu Leu Val Ser Arg Phe Phe Pro Glu Ala Glu Leu Ala Val Val Ala
260 265 270

Gly Asp Pro Gln Gln Ser Val Phe Arg Phe Arg Gly Ala Asn Pro Asp
275 280 285

Phe Leu Thr Lys Leu Ser Val Asp His Glu Val Val Leu Lys Gly Arg
290 295 300

Arg Lys Ala Ser Thr Ser Ile Val Val Ala Glu Thr Glu Ser Ala His
305 310 315 320

Ala Asp Leu Leu Ala Asp Thr Val Arg Arg Ala His Leu Ile Asp Gly
325 330 335

Arg Ser Trp Ser Glu Ile Ala Val Ile Val Arg Ser Ala Gly Met Ile
340 345 350

Ala Pro Ile Trp Arg Thr Leu Leu Ala Ala Gly Val Pro Val His Ile
355 360 365

Ser Pro Thr Asp Val Val Leu Ala Glu Gln Arg Ile Val Ala Ala Met
370 375 380

Ile Leu Gly Leu Arg Ala Leu Thr Glu Ser Leu Asn Ala Ile Glu Leu
385 390 395 400

Glu Asp Leu Leu Leu Gly Pro Ile Gly Gly Ala Asp Pro Val Thr Leu
405 410 415

Arg Arg Leu Leu Arg Gly Leu Arg Gln Ala Glu Met Lys Met Gly Gly
420 425 430

Gln Arg Arg Ala Ile Glu Val Leu Arg Ser Leu Leu Ala Glu Ser Asp
435 440 445

Ala Glu Met Leu Gly Phe Leu Thr Asp Arg Glu Leu Asn Leu Leu Glu
450 455 460

Arg Val Arg Ser Val Leu Glu Ala Gly Arg Glu Ala Leu Ala Glu His
465 470 475 480

Gly Ser Ile Glu Glu Val Leu Trp Ala Leu Trp Ser Ala Thr Asp Leu
485 490 495

Ser Asn Ser Leu Ser Ala Ile Ser Leu Arg Gly Gly Ala Ser Gly Ser
500 505 510

Gln Ala Asp Arg Asp Leu Asp Ala Met Met Ala Leu Phe Asp Ala Ala
515 520 525

Gly Asp Tyr Val Glu Arg Tyr Pro Ser Ala Gly Val Arg Ser Phe Ile
530 535 540

Leu His Ile Ser Glu Gln Glu Leu Pro Thr Gly Met Arg Glu Arg Arg
545 550 555 560

Gly Ala Ile Pro Glu Ala Val Glu Val Leu Thr Ala His Ala Thr Thr
565 570 575

Gly Arg Glu Trp Lys Arg Val Ile Val Ala Glu Val Gln Glu Gly Ser
580 585 590

Trp Pro Ser Leu Gly Glu Thr Gly Thr Leu Leu Gly Gln Glu Glu Phe
595 600 605

Val Asp Leu Val Asp Glu Gly Ile Asp Pro Asp Ile Ile Ile Ser Arg
610 615 620

Ser Ala Glu Arg Leu Ala Glu Glu Arg Arg Leu Phe Tyr Leu Ala Thr
625 630 635 640

Thr Arg Ser Thr Glu Ser Leu Leu Val Thr Ala Val Asn Ser Pro Asp
645 650 655

Ser Asp Glu Val Arg Glu Pro Ser Arg Phe Leu Glu Leu Leu Ser Gln
660 665 670

Pro Ile Val Val Leu Glu Gly Glu Glu Ala Ser Ala Ile Ala Glu Pro
675 680 685

Glu Glu Ile Gly His Arg Leu Leu Ser Ile Pro Ala Met Val Ala Glu
690 695 700

Leu Arg Arg Val Val Asn Asp Pro Arg Asp Pro Arg Arg Lys Gln Ala
705 710 715 720

Ala Arg Gln Leu Ser Arg Leu Ala Glu Ala Gly Ile Pro Gly Ala Asn
725 730 735

Pro Ala Glu Trp Thr Asn Leu Arg Thr Pro Ser Thr Asp Glu Glu Leu
740 745 750

Ile Lys Gly Ala Val Ser Leu Ser Pro Ser Arg Ile Glu Gln Leu Leu
755 760 765

Asn Cys Pro Leu Arg Ala Val Leu Asp Arg Leu Asp Ser Glu Glu Glu
770 775 780

Thr Pro Ile Ala Met Leu Lys Gly Thr Leu Val His Ala Phe Ala Glu
785 790 795 800

Ala Val Ala Gly Gly Val Asp Ala Ala Leu Ala Glu Glu Lys Val Thr

805										810					815				
Ser	Ala	Tyr	Met	Gln	Leu	Ala	Asn	Val	Pro	Ser	Trp	Ser	Arg	Glu	Ser				
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Thr	Glu	Ile	Ala	Phe	Arg	Arg	Ile	Leu	Ser	Arg	Thr	Asp	Thr	Trp	Leu				
		835					840					845							
Lys	Thr	Ser	Arg	Ala	Asp	Phe	Thr	Glu	Val	Gly	Thr	Glu	Met	Asp	Val				
		850				855					860								
Ser	Val	Thr	Ile	Asp	Asp	Ser	Val	Ser	Ile	Arg	Gly	Arg	Met	Asp	Arg				
865					870					875					880				
Leu	Glu	Arg	Asn	Lys	Ser	Gly	Glu	Leu	Val	Val	Val	Asp	Phe	Lys	Thr				
				885					890					895					
Gly	Lys	Thr	Gln	Ile	Ala	Ala	Lys	Asp	Met	Gly	Asp	His	Pro	Gln	Leu				
			900					905					910						
Phe	Ala	Tyr	Gln	Leu	Ala	Leu	Ser	Lys	Gly	Val	Leu	His	Gly	Asp	Lys				
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<211> 2891

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

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gga	ttg	ctg	ctt	cca	gta	gaa	cct	tcc	gca	agg	ttg	atc	aca	caa	acg	96
Gly	Leu	Leu	Leu	Pro	Val	Glu	Pro	Ser	Ala	Arg	Leu	Ile	Thr	Gln	Thr	
			20					25					30			

gag	ctt	tat	cac	atc	gct	cgc	aac	gtg	gtg	aac	aac	tac	gac	ggt	gag	144
Glu	Leu	Tyr	His	Ile	Ala	Arg	Asn	Val	Val	Asn	Asn	Tyr	Asp	Gly	Glu	
		35				40						45				

ctc	acc	gcc	acc	caa	acg	ccg	gcc	act	gtc	acg	gaa	tac	ctc	ctc	aag	192
Leu	Thr	Ala	Thr	Gln	Thr	Pro	Ala	Thr	Val	Thr	Glu	Tyr	Leu	Leu	Lys	
		50				55					60					

ctg	gta	tcc	gaa	atg	gac	aac	cac	atg	gtt	acc	gca	gag	gat	atc	cgt	240
Leu	Val	Ser	Glu	Met	Asp	Asn	His	Met	Val	Thr	Ala	Glu	Asp	Ile	Arg	
	65				70				75						80	

gag	gag	tcc	gat	ccg	ttc	att	aag	ctt	ttc	gac	gaa	ctc	ccc	aag	ggc	288
Glu	Glu	Ser	Asp	Pro	Phe	Ile	Lys	Leu	Phe	Asp	Glu	Leu	Pro	Lys	Gly	
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aag ggt cag cgc gac aac ctc aac gcc gaa atg acg aag tgg cgg gat	336
Lys Gly Gln Arg Asp Asn Leu Asn Ala Glu Met Thr Lys Trp Arg Asp	
100 105 110	
aca cag gtc gct cgc ctc cag tac ttg ccc ctc gtg aag gct ttg aaa	384
Thr Gln Val Ala Arg Leu Gln Tyr Leu Pro Leu Val Lys Ala Leu Lys	
115 120 125	
gag gaa ctg cac aat cag gct gtg gtg acg ttt ggt gag cag atg tct	432
Glu Glu Leu His Asn Gln Ala Val Val Thr Phe Gly Glu Gln Met Ser	
130 135 140	
aag gca gct cat ctc gca tcg acg cat cct cag gtg ggc tat tcg cag	480
Lys Ala Ala His Leu Ala Ser Thr His Pro Gln Val Gly Tyr Ser Gln	
145 150 155 160	
agg cga cgg ttc cgc gtt gtc atg ctt gat gag tat cag gac acc agc	528
Arg Arg Arg Phe Arg Val Val Met Leu Asp Glu Tyr Gln Asp Thr Ser	
165 170 175	
cac tcg cag cgt gtg ttg ttg agc agt ctt ttc ggt ggc acc gat cct	576
His Ser Gln Arg Val Leu Leu Ser Ser Leu Phe Gly Gly Thr Asp Pro	
180 185 190	
ggt ctc act gtt aat gct gtg ggc gat cca atg cag gcg att tat ggt	624
Gly Leu Thr Val Asn Ala Val Gly Asp Pro Met Gln Ala Ile Tyr Gly	
195 200 205	
tgg cga ggt gcg aca gcg gcg aac ttg gag aat ttc gtt gac gat ttc	672
Trp Arg Gly Ala Thr Ala Ala Asn Leu Glu Asn Phe Val Asp Asp Phe	
210 215 220	
ccc gtc atc cat ctc gat gga aaa acg aga gca ccg aaa aac gag ttg	720
Pro Val Ile His Leu Asp Gly Lys Thr Arg Ala Pro Lys Asn Glu Leu	
225 230 235 240	
acc aca agt tgg cga aac cca cca gaa gtc ctc acc ctt gcc aac gca	768
Thr Thr Ser Trp Arg Asn Pro Pro Glu Val Leu Thr Leu Ala Asn Ala	
245 250 255	
gtt tcg cgg gag gtg ctt ggg tcg ccc gat gcg ccg act cgg acg gtg	816
Val Ser Arg Glu Val Leu Gly Ser Pro Asp Ala Pro Thr Arg Thr Val	
260 265 270	
cag ccg ctg cag cct cgg gaa ggc gca ccg acc ggt gaa gtg tcg ctc	864
Gln Pro Leu Gln Pro Arg Glu Gly Ala Pro Thr Gly Glu Val Ser Leu	
275 280 285	
gga tgg ttt ggt acg gcg gcg cag gaa cgt gag ttt gtg gct gat gag	912
Gly Trp Phe Gly Thr Ala Ala Gln Glu Arg Glu Phe Val Ala Asp Glu	
290 295 300	
atg gtg aag cat tgg aat gcg cgg gag gag aag ggc aca ttt act gct	960
Met Val Lys His Trp Asn Ala Arg Glu Glu Lys Gly Thr Phe Thr Ala	
305 310 315 320	
gcg gtg ttg gtg cgt aag aag cgt cat tcg gca ccg atg gcg gag gag	1008
Ala Val Leu Val Arg Lys Lys Arg His Ser Ala Pro Met Ala Glu Glu	
325 330 335	

ctg acc aag cgt ggc atc ccc gtg gag atc gtc gga ctg tct ggt ttg	1056
Leu Thr Lys Arg Gly Ile Pro Val Glu Ile Val Gly Leu Ser Gly Leu	
340 345 350	
ttg gat atc cct gag att gcc gat cta att tct cta gca act atg ctc	1104
Leu Asp Ile Pro Glu Ile Ala Asp Leu Ile Ser Leu Ala Thr Met Leu	
355 360 365	
gtg cgt cct cac gat aat cgg gct gcg ttg cgt att ttg gcg ggc ccg	1152
Val Arg Pro His Asp Asn Arg Ala Ala Leu Arg Ile Leu Ala Gly Pro	
370 375 380	
cat gtg ggt ttg ggt gtg gcg gat ttg cag cgg ttg cag ggt cgt gcg	1200
His Val Gly Leu Gly Val Ala Asp Leu Gln Arg Leu Gln Gly Arg Ala	
385 390 395 400	
cgc aat att gcg ggt cgt gtg tct cgt gag cgt cga gag aag aac cca	1248
Arg Asn Ile Ala Gly Arg Val Ser Arg Glu Arg Arg Glu Lys Asn Pro	
405 410 415	
gat cca tta gcg gag ctt gat gcg att att gag gaa gcg act gcg att	1296
Asp Pro Leu Ala Glu Leu Asp Ala Ile Ile Glu Glu Ala Thr Ala Ile	
420 425 430	
gaa ccg gaa gct gtg gtt ggt cta gct gat gcg gtt gcc gat ttg ggt	1344
Glu Pro Glu Ala Val Val Gly Leu Ala Asp Ala Val Ala Asp Leu Gly	
435 440 445	
gag ggc gat cgt ttc agc gag gag ggg ttg agt cgt ttg aag cga ctg	1392
Glu Gly Asp Arg Phe Ser Glu Glu Gly Leu Ser Arg Leu Lys Arg Leu	
450 455 460	
gcc act cag ttg cga tat ttg cgt aag tac agc ttg ggt cgt tcg gtg	1440
Ala Thr Gln Leu Arg Tyr Leu Arg Lys Tyr Ser Leu Gly Arg Ser Val	
465 470 475 480	
gcg gac att ttt gct gat att gaa act gtg ttc aat att cgc acg gag	1488
Ala Asp Ile Phe Ala Asp Ile Glu Thr Val Phe Asn Ile Arg Thr Glu	
485 490 495	
gtg ttg tcg agg cag gat cct cac gcc gat ggt gct gct gga acg gtg	1536
Val Leu Ser Arg Gln Asp Pro His Ala Asp Gly Ala Ala Gly Thr Val	
500 505 510	
cat ttg gat aag ttc gca gaa gag gtc gca agt cac ggt ggc att ggg	1584
His Leu Asp Lys Phe Ala Glu Glu Val Ala Ser His Gly Gly Ile Gly	
515 520 525	
ctg cct gag ctg ttg gac tat ttt gag ctc gcg aag gat cag gaa gag	1632
Leu Pro Glu Leu Leu Asp Tyr Phe Glu Leu Ala Lys Asp Gln Glu Glu	
530 535 540	
ggc ctt gag ccg ggt gag gtg acg gtt cgc agc gat cgt gtg cag atc	1680
Gly Leu Glu Pro Gly Glu Val Thr Val Arg Ser Asp Arg Val Gln Ile	
545 550 555 560	
ctt act gtc cac aag gct aag ggt ttg gag tgg gat atc gtt tcg gtg	1728
Leu Thr Val His Lys Ala Lys Gly Leu Glu Trp Asp Ile Val Ser Val	
565 570 575	
ttg cat gcc gat gcg tcg acc tat gat gcg aag gct tcg acg tgg ttg	1776

Leu His Ala Asp Ala Ser Thr Tyr Asp Ala Lys Ala Ser Thr Trp Leu	
580 585 590	
aaa aat gtc acg atg atc ccg tcg tcg ctt cgt ggc gat gcc ggg acc	1824
Lys Asn Val Thr Met Ile Pro Ser Ser Leu Arg Gly Asp Ala Gly Thr	
595 600 605	
ggc gcc cca gag atg gat acc tct gag gcg gac gat cgc aaa gct ctg	1872
Gly Ala Pro Glu Met Asp Thr Ser Glu Ala Asp Asp Arg Lys Ala Leu	
610 615 620	
gaa gat tcc ggc aag gag tac acc agt gaa gtg cgt gag ggg tta cgg	1920
Glu Asp Ser Gly Lys Glu Tyr Thr Ser Glu Val Arg Glu Gly Leu Arg	
625 630 635 640	
gag gaa aat tcg cga ctg ttt tat gtc ggt atc acg cgc agc gaa cgg	1968
Glu Glu Asn Ser Arg Leu Phe Tyr Val Gly Ile Thr Arg Ser Glu Arg	
645 650 655	
gtg ttg ctc gtg acg ggt tcg gcg ctt gat gaa agt ggc aca aag gcg	2016
Val Leu Leu Val Thr Gly Ser Ala Leu Asp Glu Ser Gly Thr Lys Ala	
660 665 670	
aaa gtt ccc tac ggc cac ttg gag atc ctt cgg gat aaa gcg ccg gag	2064
Lys Val Pro Tyr Gly His Leu Glu Ile Leu Arg Asp Lys Ala Pro Glu	
675 680 685	
tgc gtg gtg tcg tgg tgg gaa ggg gaa gag ggg gac gtc gaa aag caa	2112
Cys Val Val Ser Trp Trp Glu Gly Glu Glu Gly Asp Val Glu Lys Gln	
690 695 700	
aaa cct gcg gaa ggc gtc ttc ccg caa ctg ctc gcc gct gac tcc tcc	2160
Lys Pro Ala Glu Gly Val Phe Pro Gln Leu Leu Ala Ala Asp Ser Ser	
705 710 715 720	
ggc gcg gat ttg gtg cgc ggc ccg cgc gcc gag cca aac aac gag ggc	2208
Gly Ala Asp Leu Val Arg Gly Pro Arg Ala Glu Pro Asn Asn Glu Gly	
725 730 735	
ggg ctg gaa agc ttg tgg gaa aaa gag gta agc gcg ctt atc gac gaa	2256
Gly Leu Glu Ser Leu Trp Glu Lys Glu Val Ser Ala Leu Ile Asp Glu	
740 745 750	
cac cgc cgc ctt tcc aac ccc atc gtc gaa gtc gaa acg ccc cgc gaa	2304
His Arg Arg Leu Ser Asn Pro Ile Val Glu Val Glu Thr Pro Arg Glu	
755 760 765	
ctc acg gcc acc gac ctc gtc tct atg aaa aac aat ccc gaa cag ttc	2352
Leu Thr Ala Thr Asp Leu Val Ser Met Lys Asn Asn Pro Glu Gln Phe	
770 775 780	
gcc cga cga atg cgt cgc cct gtc ccg ttc aaa cca aac acc tac gca	2400
Ala Arg Arg Met Arg Arg Pro Val Pro Phe Lys Pro Asn Thr Tyr Ala	
785 790 795 800	
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Lys Arg Gly Thr Leu Phe His Gln Trp Leu Glu Asp Arg Phe Gly Ser	
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acc gcg ctt ctc gac gaa acc gag ctc ccc ggc atc gac gag gac tac	2496
Thr Ala Leu Leu Asp Glu Thr Glu Leu Pro Gly Ile Asp Glu Asp Tyr	

820	825	830	
tcg gat gac gca ttc atc gaa ctc cgc gac gcg ttc cta gga tct act			2544
Ser Asp Asp Ala Phe Ile Glu Leu Arg Asp Ala Phe Leu Gly Ser Thr			
835	840	845	
tgg gaa aac cgc aca ccg gaa ttc gtc gaa cat ccc ttc gaa gta acg			2592
Trp Glu Asn Arg Thr Pro Glu Phe Val Glu His Pro Phe Glu Val Thr			
850	855	860	
atc ggc gaa cac gtc atc cgc ggc cgc atg gac gcc gtc ttc cac acc			2640
Ile Gly Glu His Val Ile Arg Gly Arg Met Asp Ala Val Phe His Thr			
865	870	875	880
gat ggc acc tgg atg gtg gtc gac tgg aaa acc gga cgc acc cca acc			2688
Asp Gly Thr Trp Met Val Val Asp Trp Lys Thr Gly Arg Thr Pro Thr			
885	890	895	
ggc ccc gaa atg gac gca gcg atc atc cag ctc gct gtc tat aga ctc			2736
Gly Pro Glu Met Asp Ala Ala Ile Ile Gln Leu Ala Val Tyr Arg Leu			
900	905	910	
gcc tgg gca cga ctc aaa ggc ctc gaa cct gaa gaa gtc cgc gca gca			2784
Ala Trp Ala Arg Leu Lys Gly Leu Glu Pro Glu Glu Val Arg Ala Ala			
915	920	925	
ttc cat tac gtc gcc cac gat cac acc ttt gag ccg aac gat ctg ccg			2832
Phe His Tyr Val Ala His Asp His Thr Phe Glu Pro Asn Asp Leu Pro			
930	935	940	
act caa gaa gaa cta gcc cgg ctg ctc agt cag gaa tgatgcgcct			2878
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<211> 956

<212> PRT

<213> Corynebacterium glutamicum

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Glu	Leu	Tyr	His	Ile	Ala	Arg	Asn	Val	Val	Asn	Asn	Tyr	Asp	Gly	Glu
		35					40					45			

Leu	Thr	Ala	Thr	Gln	Thr	Pro	Ala	Thr	Val	Thr	Glu	Tyr	Leu	Leu	Lys
	50					55					60				

Leu	Val	Ser	Glu	Met	Asp	Asn	His	Met	Val	Thr	Ala	Glu	Asp	Ile	Arg
	65				70					75					80

Glu	Glu	Ser	Asp	Pro	Phe	Ile	Lys	Leu	Phe	Asp	Glu	Leu	Pro	Lys	Gly
				85					90					95	

Lys Gly Gln Arg Asp Asn Leu Asn Ala Glu Met Thr Lys Trp Arg Asp
100 105 110

Thr Gln Val Ala Arg Leu Gln Tyr Leu Pro Leu Val Lys Ala Leu Lys
115 120 125

Glu Glu Leu His Asn Gln Ala Val Val Thr Phe Gly Glu Gln Met Ser
130 135 140

Lys Ala Ala His Leu Ala Ser Thr His Pro Gln Val Gly Tyr Ser Gln
145 150 155 160

Arg Arg Arg Phe Arg Val Val Met Leu Asp Glu Tyr Gln Asp Thr Ser
165 170 175

His Ser Gln Arg Val Leu Leu Ser Ser Leu Phe Gly Gly Thr Asp Pro
180 185 190

Gly Leu Thr Val Asn Ala Val Gly Asp Pro Met Gln Ala Ile Tyr Gly
195 200 205

Trp Arg Gly Ala Thr Ala Ala Asn Leu Glu Asn Phe Val Asp Asp Phe
210 215 220

Pro Val Ile His Leu Asp Gly Lys Thr Arg Ala Pro Lys Asn Glu Leu
225 230 235 240

Thr Thr Ser Trp Arg Asn Pro Pro Glu Val Leu Thr Leu Ala Asn Ala
245 250 255

Val Ser Arg Glu Val Leu Gly Ser Pro Asp Ala Pro Thr Arg Thr Val
260 265 270

Gln Pro Leu Gln Pro Arg Glu Gly Ala Pro Thr Gly Glu Val Ser Leu
275 280 285

Gly Trp Phe Gly Thr Ala Ala Gln Glu Arg Glu Phe Val Ala Asp Glu
290 295 300

Met Val Lys His Trp Asn Ala Arg Glu Glu Lys Gly Thr Phe Thr Ala
305 310 315 320

Ala Val Leu Val Arg Lys Lys Arg His Ser Ala Pro Met Ala Glu Glu
325 330 335

Leu Thr Lys Arg Gly Ile Pro Val Glu Ile Val Gly Leu Ser Gly Leu
340 345 350

Leu Asp Ile Pro Glu Ile Ala Asp Leu Ile Ser Leu Ala Thr Met Leu
355 360 365

Val Arg Pro His Asp Asn Arg Ala Ala Leu Arg Ile Leu Ala Gly Pro
370 375 380

His Val Gly Leu Gly Val Ala Asp Leu Gln Arg Leu Gln Gly Arg Ala
385 390 395 400

Arg Asn Ile Ala Gly Arg Val Ser Arg Glu Arg Arg Glu Lys Asn Pro
405 410 415

Asp Pro Leu Ala Glu Leu Asp Ala Ile Ile Glu Glu Ala Thr Ala Ile

420					425					430					
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Glu	Gly	Asp	Arg	Phe	Ser	Glu	Glu	Gly	Leu	Ser	Arg	Leu	Lys	Arg	Leu
	450					455					460				
Ala	Thr	Gln	Leu	Arg	Tyr	Leu	Arg	Lys	Tyr	Ser	Leu	Gly	Arg	Ser	Val
	465					470					475				480
Ala	Asp	Ile	Phe	Ala	Asp	Ile	Glu	Thr	Val	Phe	Asn	Ile	Arg	Thr	Glu
			485						490					495	
Val	Leu	Ser	Arg	Gln	Asp	Pro	His	Ala	Asp	Gly	Ala	Ala	Gly	Thr	Val
			500					505					510		
His	Leu	Asp	Lys	Phe	Ala	Glu	Glu	Val	Ala	Ser	His	Gly	Gly	Ile	Gly
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Leu	Pro	Glu	Leu	Leu	Asp	Tyr	Phe	Glu	Leu	Ala	Lys	Asp	Gln	Glu	Glu
	530					535					540				
Gly	Leu	Glu	Pro	Gly	Glu	Val	Thr	Val	Arg	Ser	Asp	Arg	Val	Gln	Ile
	545					550					555				560
Leu	Thr	Val	His	Lys	Ala	Lys	Gly	Leu	Glu	Trp	Asp	Ile	Val	Ser	Val
			565						570					575	
Leu	His	Ala	Asp	Ala	Ser	Thr	Tyr	Asp	Ala	Lys	Ala	Ser	Thr	Trp	Leu
			580					585					590		
Lys	Asn	Val	Thr	Met	Ile	Pro	Ser	Ser	Leu	Arg	Gly	Asp	Ala	Gly	Thr
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Gly	Ala	Pro	Glu	Met	Asp	Thr	Ser	Glu	Ala	Asp	Asp	Arg	Lys	Ala	Leu
	610					615					620				
Glu	Asp	Ser	Gly	Lys	Glu	Tyr	Thr	Ser	Glu	Val	Arg	Glu	Gly	Leu	Arg
	625					630					635				640
Glu	Glu	Asn	Ser	Arg	Leu	Phe	Tyr	Val	Gly	Ile	Thr	Arg	Ser	Glu	Arg
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Val	Leu	Leu	Val	Thr	Gly	Ser	Ala	Leu	Asp	Glu	Ser	Gly	Thr	Lys	Ala
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Lys	Val	Pro	Tyr	Gly	His	Leu	Glu	Ile	Leu	Arg	Asp	Lys	Ala	Pro	Glu
		675					680					685			
Cys	Val	Val	Ser	Trp	Trp	Glu	Gly	Glu	Glu	Gly	Asp	Val	Glu	Lys	Gln
	690					695					700				
Lys	Pro	Ala	Glu	Gly	Val	Phe	Pro	Gln	Leu	Leu	Ala	Ala	Asp	Ser	Ser
	705					710					715				720
Gly	Ala	Asp	Leu	Val	Arg	Gly	Pro	Arg	Ala	Glu	Pro	Asn	Asn	Glu	Gly
			725						730					735	
Gly	Leu	Glu	Ser	Leu	Trp	Glu	Lys	Glu	Val	Ser	Ala	Leu	Ile	Asp	Glu
			740					745					750		

His Arg Arg Leu Ser Asn Pro Ile Val Glu Val Glu Thr Pro Arg Glu
 755 760 765
 Leu Thr Ala Thr Asp Leu Val Ser Met Lys Asn Asn Pro Glu Gln Phe
 770 775 780
 Ala Arg Arg Met Arg Arg Pro Val Pro Phe Lys Pro Asn Thr Tyr Ala
 785 790 795 800
 Lys Arg Gly Thr Leu Phe His Gln Trp Leu Glu Asp Arg Phe Gly Ser
 805 810 815
 Thr Ala Leu Leu Asp Glu Thr Glu Leu Pro Gly Ile Asp Glu Asp Tyr
 820 825 830
 Ser Asp Asp Ala Phe Ile Glu Leu Arg Asp Ala Phe Leu Gly Ser Thr
 835 840 845
 Trp Glu Asn Arg Thr Pro Glu Phe Val Glu His Pro Phe Glu Val Thr
 850 855 860
 Ile Gly Glu His Val Ile Arg Gly Arg Met Asp Ala Val Phe His Thr
 865 870 875 880
 Asp Gly Thr Trp Met Val Val Asp Trp Lys Thr Gly Arg Thr Pro Thr
 885 890 895
 Gly Pro Glu Met Asp Ala Ala Ile Ile Gln Leu Ala Val Tyr Arg Leu
 900 905 910
 Ala Trp Ala Arg Leu Lys Gly Leu Glu Pro Glu Glu Val Arg Ala Ala
 915 920 925
 Phe His Tyr Val Ala His Asp His Thr Phe Glu Pro Asn Asp Leu Pro
 930 935 940
 Thr Gln Glu Glu Leu Ala Arg Leu Leu Ser Gln Glu
 945 950 955

<210> 55

<211> 2412

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2389)

<223> RXA00095

<400> 55

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 Met Asn Thr Ser Pro
 1 5

ttt acc cca ggt tcc ccc gat ctc atc gat ggc ttg aat gag caa cag 163
 Phe Thr Pro Gly Ser Pro Asp Leu Ile Asp Gly Leu Asn Glu Gln Gln
 10 15 20

cgt gct gct gtg gag cat atc ggt tct ccg ctg ctg att gtc gct ggt	211
Arg Ala Ala Val Glu His Ile Gly Ser Pro Leu Leu Ile Val Ala Gly	
25 30 35	
gct ggt tca ggc aag act gct gtg ttg acc agg cgt att gct tat tta	259
Ala Gly Ser Gly Lys Thr Ala Val Leu Thr Arg Arg Ile Ala Tyr Leu	
40 45 50	
atg cgt tac cgt ggt gtg cat ccg cag caa att ttg gcc att acc ttt	307
Met Arg Tyr Arg Gly Val His Pro Gln Gln Ile Leu Ala Ile Thr Phe	
55 60 65	
acc aat aag gct gcc gct gag atg cgt gag cgt gtc agt cag ctg gtg	355
Thr Asn Lys Ala Ala Ala Glu Met Arg Glu Arg Val Ser Gln Leu Val	
70 75 80 85	
ggc ccg gtt gcg gag cgc atg tgg gtg gct acg ttc cac tcg gtg tgt	403
Gly Pro Val Ala Glu Arg Met Trp Val Ala Thr Phe His Ser Val Cys	
90 95 100	
gtg cgt att ttg cgt cag cag gcg cag ttg gtg gag ggg ctg aac act	451
Val Arg Ile Leu Arg Gln Gln Ala Gln Leu Val Glu Gly Leu Asn Thr	
105 110 115	
aac ttc act att tat gat tcg gat gat tcg agg cgt ttg ctc acg atg	499
Asn Phe Thr Ile Tyr Asp Ser Asp Ser Arg Arg Leu Leu Thr Met	
120 125 130	
atc gcc aag gat ctg gag ttg gat att aag aag ttc tcg gcg cgt acg	547
Ile Ala Lys Asp Leu Glu Leu Asp Ile Lys Lys Phe Ser Ala Arg Thr	
135 140 145	
ttg ctg ggt gct att tct aat ttg aaa aat gag ttg gtt act ccg cag	595
Leu Leu Gly Ala Ile Ser Asn Leu Lys Asn Glu Leu Val Thr Pro Gln	
150 155 160 165	
gag gct ctt gcg gat gct gaa cgc acg cac aat cct tat gaa aca gtc	643
Glu Ala Leu Ala Asp Ala Glu Arg Thr His Asn Pro Tyr Glu Thr Val	
170 175 180	
gtg gcc agg gcg ttt tcg gag tat cag agc agg ctt cgc cgt gcc aac	691
Val Ala Arg Ala Phe Ser Glu Tyr Gln Ser Arg Leu Arg Arg Ala Asn	
185 190 195	
gct gtg gat ttt gat gat ttg att ggg gag act gtt cgg att ttc cgg	739
Ala Val Asp Phe Asp Asp Leu Ile Gly Glu Thr Val Arg Ile Phe Arg	
200 205 210	
gag cat cca cct gtt gcg gag tat tac cgc aga cgt ttc cgc cac gtg	787
Glu His Pro Pro Val Ala Glu Tyr Tyr Arg Arg Arg Phe Arg His Val	
215 220 225	
ctg atc gat gag tat cag gac acc aac cac gct cag tat gag ctg att	835
Leu Ile Asp Glu Tyr Gln Asp Thr Asn His Ala Gln Tyr Glu Leu Ile	
230 235 240 245	
tct acg ctc gtc ggc aag cct gac cag gat ccg tct gag ctg tgt gtt	883
Ser Thr Leu Val Gly Lys Pro Asp Gln Asp Pro Ser Glu Leu Cys Val	
250 255 260	

gtg ggt gat tcg gat cag tct att tat gct ttc cgt ggc gcc acg atc	931
Val Gly Asp Ser Asp Gln Ser Ile Tyr Ala Phe Arg Gly Ala Thr Ile	
265 270 275	
cgc aac att gaa gag ttt gag cgc gat ttc tcc aac gcc cgc acc att	979
Arg Asn Ile Glu Glu Phe Glu Arg Asp Phe Ser Asn Ala Arg Thr Ile	
280 285 290	
ttg ctg gag cag aat tac cgt tcc acc cag acg att ctt tct gct gcc	1027
Leu Leu Glu Gln Asn Tyr Arg Ser Thr Gln Thr Ile Leu Ser Ala Ala	
295 300 305	
aac gcg gtg att tct caa aat gag aac cgt cga cct aaa aac ctg tgg	1075
Asn Ala Val Ile Ser Gln Asn Glu Asn Arg Arg Pro Lys Asn Leu Trp	
310 315 320 325	
act gcg ctg ggg gag ggc gag cag atc att ggt tat gtt gcc gac aat	1123
Thr Ala Leu Gly Glu Gly Glu Gln Ile Ile Gly Tyr Val Ala Asp Asn	
330 335 340	
gag cac gat gaa gcc cgt ttt att gct agt gag atc gac aat tta gtt	1171
Glu His Asp Glu Ala Arg Phe Ile Ala Ser Glu Ile Asp Asn Leu Val	
345 350 355	
gac cac ggc atg agc tat tcc gac atc gcg atc atg tac cgc acg aac	1219
Asp His Gly Met Ser Tyr Ser Asp Ile Ala Ile Met Tyr Arg Thr Asn	
360 365 370	
aat tcc tcg cgc gca cta gag gat gtc ttc atg cgc acc ggc gtc ccc	1267
Asn Ser Ser Arg Ala Leu Glu Asp Val Phe Met Arg Thr Gly Val Pro	
375 380 385	
tac aaa gta gtc ggc ggc acg aag ttc tac gaa cgc aaa gaa atc cgt	1315
Tyr Lys Val Val Gly Gly Thr Lys Phe Tyr Glu Arg Lys Glu Ile Arg	
390 395 400 405	
gac atc atc gct tac ctg cgc gtt tta gaa aac ccc gat gac acc gtc	1363
Asp Ile Ile Ala Tyr Leu Arg Val Leu Glu Asn Pro Asp Asp Thr Val	
410 415 420	
aac ctc cgt cgc atc atc aac acc ccc aag cgc ggc atc ggc gat cgc	1411
Asn Leu Arg Arg Ile Ile Asn Thr Pro Lys Arg Gly Ile Gly Asp Arg	
425 430 435	
gcg cag gcg ttc atc gcg ctg cac agc gag aac aat cag atc agc ttc	1459
Ala Gln Ala Phe Ile Ala Leu His Ser Glu Asn Asn Gln Ile Ser Phe	
440 445 450	
ggg caa gcg ctt ctc gac gcc gcc ctc ggc aag gtc gac ctg ctt gga	1507
Gly Gln Ala Leu Leu Asp Ala Ala Leu Gly Lys Val Asp Leu Leu Gly	
455 460 465	
gcg cgc ggc aag aat gcg gcg att aag ttc aat gag ctt ttc gac gcc	1555
Ala Arg Gly Lys Asn Ala Ala Ile Lys Phe Asn Glu Leu Phe Asp Ala	
470 475 480 485	
ctc cgc tcc gaa ctc ccc acc atg gtc aat gag gtc acc ggc ctg cca	1603
Leu Arg Ser Glu Leu Pro Thr Met Val Asn Glu Val Thr Gly Leu Pro	
490 495 500	
gac atc ggc caa gtc atc agt cgc atc ctc gac atc act ggc tac aag	1651

Asp	Ile	Gly	Gln	Val	Ile	Ser	Arg	Ile	Leu	Asp	Ile	Thr	Gly	Tyr	Lys		
			505					510					515				
gca	gaa	ctt	gag	gca	tcc	aac	gac	cct	caa	gat	ggc	gca	cgc	cta	gac	1699	
Ala	Glu	Leu	Glu	Ala	Ser	Asn	Asp	Pro	Gln	Asp	Gly	Ala	Arg	Leu	Asp		
		520					525					530					
aac	ctg	aac	gag	ctt	gtc	tcc	gtg	gcc	cgc	gag	ttc	tcc	tcc	gac	gcc	1747	
Asn	Leu	Asn	Glu	Leu	Val	Ser	Val	Ala	Arg	Glu	Phe	Ser	Ser	Asp	Ala		
		535					540				545						
gca	aac	cgc	atg	gtt	aat	gaa	gtt	cca	gaa	ggc	gaa	gcc	caa	ccg	ggc	1795	
Ala	Asn	Arg	Met	Val	Asn	Glu	Val	Pro	Glu	Gly	Glu	Ala	Gln	Pro	Gly		
		550				555				560					565		
agc	tta	cag	gca	ttc	ttg	gag	cga	gtc	tcc	ctg	gtt	gcc	gac	gcc	gac	1843	
Ser	Leu	Gln	Ala	Phe	Leu	Glu	Arg	Val	Ser	Leu	Val	Ala	Asp	Ala	Asp		
				570					575						580		
caa	atc	ccc	gat	tcc	gac	aac	ggc	gta	gtc	acc	ctc	atg	acc	ctg	cat	1891	
Gln	Ile	Pro	Asp	Ser	Asp	Asn	Gly	Val	Val	Thr	Leu	Met	Thr	Leu	His		
			585					590						595			
acc	gcc	aag	ggc	ctt	gaa	ttc	ccc	atc	gtg	ttc	ctc	aca	ggc	tgg	gaa	1939	
Thr	Ala	Lys	Gly	Leu	Glu	Phe	Pro	Ile	Val	Phe	Leu	Thr	Gly	Trp	Glu		
		600					605					610					
gac	gga	cag	ttc	cca	cac	ctg	cgt	tcc	ctt	ggt	gat	gcc	aaa	gaa	ctt	1987	
Asp	Gly	Gln	Phe	Pro	His	Leu	Arg	Ser	Leu	Gly	Asp	Ala	Lys	Glu	Leu		
		615				620					625						
gcc	gag	gaa	cgc	cgc	ctc	gcc	tac	gtg	ggt	atc	acc	cgc	gcc	cgc	aag	2035	
Ala	Glu	Glu	Arg	Arg	Leu	Ala	Tyr	Val	Gly	Ile	Thr	Arg	Ala	Arg	Lys		
		630				635				640					645		
cgc	ctc	tac	atg	acc	aga	gcc	atg	ctg	cgt	agc	tcc	tgg	ggc	aac	ccg	2083	
Arg	Leu	Tyr	Met	Thr	Arg	Ala	Met	Leu	Arg	Ser	Ser	Trp	Gly	Asn	Pro		
				650					655					660			
gtg	acc	aac	cca	ccg	tca	cgt	ttc	ctc	caa	gaa	gtg	ccc	gca	gaa	ctc	2131	
Val	Thr	Asn	Pro	Pro	Ser	Arg	Phe	Leu	Gln	Glu	Val	Pro	Ala	Glu	Leu		
			665					670					675				
atc	gat	tgg	agg	cgc	gaa	gaa	ccc	cag	atg	tct	tcc	gcc	tgg	gct	cct	2179	
Ile	Asp	Trp	Arg	Arg	Glu	Glu	Pro	Gln	Met	Ser	Ser	Ala	Trp	Ala	Pro		
		680					685					690					
cga	ccc	acc	cga	agc	atc	ccc	acc	aaa	act	cgc	acc	aac	aat	aag	cag	2227	
Arg	Pro	Thr	Arg	Ser	Ile	Pro	Thr	Lys	Thr	Arg	Thr	Asn	Asn	Lys	Gln		
		695				700					705						
ttg	gat	ctg	tcg	gtg	ggg	gat	cgc	gtc	aat	cac	gac	aag	tac	ggc	ttg	2275	
Leu	Asp	Leu	Ser	Val	Gly	Asp	Arg	Val	Asn	His	Asp	Lys	Tyr	Gly	Leu		
		710				715				720					725		
gga	acc	gtg	ctc	tct	tca	gat	ggc	agc	ggc	ccc	cga	gcc	acc	gtc	acc	2323	
Gly	Thr	Val	Leu	Ser	Ser	Asp	Gly	Ser	Gly	Pro	Arg	Ala	Thr	Val	Thr		
				730					735					740			
atc	gat	ttc	ggt	tcc	tcc	ggc	aag	gtt	aga	ttg	atg	ctt	ctt	ggt	ggc	2371	
Ile	Asp	Phe	Gly	Ser	Ser	Gly	Lys	Val	Arg	Leu	Met	Leu	Leu	Gly	Gly		

745

750

755

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 Val Pro Met Glu Lys Leu
 760

2412

<210> 56

<211> 763

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

Met Asn Thr Ser Pro Phe Thr Pro Gly Ser Pro Asp Leu Ile Asp Gly
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Leu Asn Glu Gln Gln Arg Ala Ala Val Glu His Ile Gly Ser Pro Leu
 20 25 30

Leu Ile Val Ala Gly Ala Gly Ser Gly Lys Thr Ala Val Leu Thr Arg
 35 40 45

Arg Ile Ala Tyr Leu Met Arg Tyr Arg Gly Val His Pro Gln Gln Ile
 50 55 60

Leu Ala Ile Thr Phe Thr Asn Lys Ala Ala Ala Glu Met Arg Glu Arg
 65 70 75 80

Val Ser Gln Leu Val Gly Pro Val Ala Glu Arg Met Trp Val Ala Thr
 85 90 95

Phe His Ser Val Cys Val Arg Ile Leu Arg Gln Gln Ala Gln Leu Val
 100 105 110

Glu Gly Leu Asn Thr Asn Phe Thr Ile Tyr Asp Ser Asp Asp Ser Arg
 115 120 125

Arg Leu Leu Thr Met Ile Ala Lys Asp Leu Glu Leu Asp Ile Lys Lys
 130 135 140

Phe Ser Ala Arg Thr Leu Leu Gly Ala Ile Ser Asn Leu Lys Asn Glu
 145 150 155 160

Leu Val Thr Pro Gln Glu Ala Leu Ala Asp Ala Glu Arg Thr His Asn
 165 170 175

Pro Tyr Glu Thr Val Val Ala Arg Ala Phe Ser Glu Tyr Gln Ser Arg
 180 185 190

Leu Arg Arg Ala Asn Ala Val Asp Phe Asp Asp Leu Ile Gly Glu Thr
 195 200 205

Val Arg Ile Phe Arg Glu His Pro Pro Val Ala Glu Tyr Tyr Arg Arg
 210 215 220

Arg Phe Arg His Val Leu Ile Asp Glu Tyr Gln Asp Thr Asn His Ala
 225 230 235 240

Gln Tyr Glu Leu Ile Ser Thr Leu Val Gly Lys Pro Asp Gln Asp Pro
 245 250 255

Ser Glu Leu Cys Val Val Gly Asp Ser Asp Gln Ser Ile Tyr Ala Phe
260 265 270

Arg Gly Ala Thr Ile Arg Asn Ile Glu Glu Phe Glu Arg Asp Phe Ser
275 280 285

Asn Ala Arg Thr Ile Leu Leu Glu Gln Asn Tyr Arg Ser Thr Gln Thr
290 295 300

Ile Leu Ser Ala Ala Asn Ala Val Ile Ser Gln Asn Glu Asn Arg Arg
305 310 315 320

Pro Lys Asn Leu Trp Thr Ala Leu Gly Glu Gly Glu Gln Ile Ile Gly
325 330 335

Tyr Val Ala Asp Asn Glu His Asp Glu Ala Arg Phe Ile Ala Ser Glu
340 345 350

Ile Asp Asn Leu Val Asp His Gly Met Ser Tyr Ser Asp Ile Ala Ile
355 360 365

Met Tyr Arg Thr Asn Asn Ser Ser Arg Ala Leu Glu Asp Val Phe Met
370 375 380

Arg Thr Gly Val Pro Tyr Lys Val Val Gly Gly Thr Lys Phe Tyr Glu
385 390 395 400

Arg Lys Glu Ile Arg Asp Ile Ile Ala Tyr Leu Arg Val Leu Glu Asn
405 410 415

Pro Asp Asp Thr Val Asn Leu Arg Arg Ile Ile Asn Thr Pro Lys Arg
420 425 430

Gly Ile Gly Asp Arg Ala Gln Ala Phe Ile Ala Leu His Ser Glu Asn
435 440 445

Asn Gln Ile Ser Phe Gly Gln Ala Leu Leu Asp Ala Ala Leu Gly Lys
450 455 460

Val Asp Leu Leu Gly Ala Arg Gly Lys Asn Ala Ala Ile Lys Phe Asn
465 470 475 480

Glu Leu Phe Asp Ala Leu Arg Ser Glu Leu Pro Thr Met Val Asn Glu
485 490 495

Val Thr Gly Leu Pro Asp Ile Gly Gln Val Ile Ser Arg Ile Leu Asp
500 505 510

Ile Thr Gly Tyr Lys Ala Glu Leu Glu Ala Ser Asn Asp Pro Gln Asp
515 520 525

Gly Ala Arg Leu Asp Asn Leu Asn Glu Leu Val Ser Val Ala Arg Glu
530 535 540

Phe Ser Ser Asp Ala Ala Asn Arg Met Val Asn Glu Val Pro Glu Gly
545 550 555 560

Glu Ala Gln Pro Gly Ser Leu Gln Ala Phe Leu Glu Arg Val Ser Leu
565 570 575

Val Ala Asp Ala Asp Gln Ile Pro Asp Ser Asp Asn Gly Val Val Thr

580					585					590					
Leu	Met	Thr	Leu	His	Thr	Ala	Lys	Gly	Leu	Glu	Phe	Pro	Ile	Val	Phe
	595						600					605			
Leu	Thr	Gly	Trp	Glu	Asp	Gly	Gln	Phe	Pro	His	Leu	Arg	Ser	Leu	Gly
	610					615					620				
Asp	Ala	Lys	Glu	Leu	Ala	Glu	Glu	Arg	Arg	Leu	Ala	Tyr	Val	Gly	Ile
625					630					635					640
Thr	Arg	Ala	Arg	Lys	Arg	Leu	Tyr	Met	Thr	Arg	Ala	Met	Leu	Arg	Ser
				645					650					655	
Ser	Trp	Gly	Asn	Pro	Val	Thr	Asn	Pro	Pro	Ser	Arg	Phe	Leu	Gln	Glu
			660					665					670		
Val	Pro	Ala	Glu	Leu	Ile	Asp	Trp	Arg	Arg	Glu	Glu	Pro	Gln	Met	Ser
		675					680					685			
Ser	Ala	Trp	Ala	Pro	Arg	Pro	Thr	Arg	Ser	Ile	Pro	Thr	Lys	Thr	Arg
	690					695					700				
Thr	Asn	Asn	Lys	Gln	Leu	Asp	Leu	Ser	Val	Gly	Asp	Arg	Val	Asn	His
705					710					715					720
Asp	Lys	Tyr	Gly	Leu	Gly	Thr	Val	Leu	Ser	Ser	Asp	Gly	Ser	Gly	Pro
			725					730						735	
Arg	Ala	Thr	Val	Thr	Ile	Asp	Phe	Gly	Ser	Ser	Gly	Lys	Val	Arg	Leu
		740						745					750		
Met	Leu	Leu	Gly	Gly	Val	Pro	Met	Glu	Lys	Leu					
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<211> 1070

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1047)

<223> RXN02819

<400> 57

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1				5				10						15		

ggt	ctc	gca	gta	gtg	atg	acg	cct	gct	aat	cag	agc	aga	gat	ccc	cgc	96
Val	Leu	Ala	Val	Val	Met	Thr	Pro	Ala	Asn	Gln	Ser	Arg	Asp	Pro	Arg	
			20					25					30			

cca	tgg	gtg	acc	acc	gaa	tct	ggt	tgg	tca	ggt	cgt	gtg	gat	gcg	gaa	144
Pro	Trp	Val	Thr	Thr	Glu	Ser	Gly	Trp	Ser	Gly	Arg	Val	Asp	Ala	Glu	
			35				40					45				

tcc	ttt	act	aat	ccg	ccg	atc	acc	att	ggg	cat	atg	cgt	ctg	cct	cgc	192
Ser	Phe	Thr	Asn	Pro	Pro	Ile	Thr	Ile	Gly	His	Met	Arg	Leu	Pro	Arg	

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ttt agg cgt gag cac ttc aag cga ccc aac aag atg cgg gag ttt gct Phe Arg Arg Glu His Phe Lys Arg Pro Asn Lys Met Arg Glu Phe Ala 85 90 95			288
cgg gtt cgt ccc aat gag gca gtg acc aaa ctg cgt aat gct att cgg Arg Val Arg Pro Asn Glu Ala Val Thr Lys Leu Arg Asn Ala Ile Arg 100 105 110			336
gat cat gag gcg cat cat tgg cct gat cgg gag cac ttg gct cgc acc Asp His Glu Ala His His Trp Pro Asp Arg Glu His Leu Ala Arg Thr 115 120 125			384
gcg gag cgt atg atc cgt aaa gaa cgt gat ctg gct aag ttg acc ggc Ala Glu Arg Met Ile Arg Lys Glu Arg Asp Leu Ala Lys Leu Thr Gly 130 135 140			432
aat gtg gat aaa gcc agg gaa acc ctc ggt agg acg ttt gag cgc att Asn Val Asp Lys Ala Arg Glu Thr Leu Gly Arg Thr Phe Glu Arg Ile 145 150 155 160			480
ttg tcg ctg ctc agt gaa atg gac tat gtg gat tac tct aat cca gat Leu Ser Leu Leu Ser Glu Met Asp Tyr Val Asp Tyr Ser Asn Pro Asp 165 170 175			528
aat cca gtg atc act gat gaa ggt gag cgt ttg gcg aaa atc cac agt Asn Pro Val Ile Thr Asp Glu Gly Glu Arg Leu Ala Lys Ile His Ser 180 185 190			576
gag gca gac ctg ttg gtt gct cag tgc ctc aag cgt ggc att tgg gac Glu Ala Asp Leu Leu Val Ala Gln Cys Leu Lys Arg Gly Ile Trp Asp 195 200 205			624
aac ctt gat ccc gca gag ctc gcc ggt gtg gtg agt atg tgc acg ttt Asn Leu Asp Pro Ala Glu Leu Ala Gly Val Val Ser Met Cys Thr Phe 210 215 220			672
gaa aat cgt cgc gaa acc ggt ggt gag gct caa gct gtc aca gag gcc Glu Asn Arg Arg Glu Thr Gly Gly Glu Ala Gln Ala Val Thr Glu Ala 225 230 235 240			720
atg gct gat tcc atg aat agc gtg gaa cgt att tgg ggt gag ctg gtt Met Ala Asp Ser Met Asn Ser Val Glu Arg Ile Trp Gly Glu Leu Val 245 250 255			768
gaa gat gag cgc cgt cac cgt ctg cca att act cgc cag ccg gaa gca Glu Asp Glu Arg Arg His Arg Leu Pro Ile Thr Arg Gln Pro Glu Ala 260 265 270			816
ggt ttt gcc acc gcg atc cac cag tgg gct tca ggt gct ccg ctg gga Gly Phe Ala Thr Ala Ile His Gln Trp Ala Ser Gly Ala Pro Leu Gly 275 280 285			864
tat tgc atg gct gcg gca gcg gaa aac ggc gcg gag ttg acc cct ggt Tyr Cys Met Ala Ala Ala Ala Glu Asn Gly Ala Glu Leu Thr Pro Gly 290 295 300			912

gac ttc gtg cgc tgg tgc cgt caa gtc atc gat ctt cta gag cag gtt 960
 Asp Phe Val Arg Trp Cys Arg Gln Val Ile Asp Leu Leu Glu Gln Val
 305 310 315 320
 gct aag act gcc tac ttt gat gag acc aca cgg aat gct cgt cag gct 1008
 Ala Lys Thr Ala Tyr Phe Asp Glu Thr Thr Arg Asn Ala Arg Gln Ala
 325 330 335
 att gat gcg att agg cgt gga gtt gtg gcg atc ggt tcc tagcgagcta 1057
 Ile Asp Ala Ile Arg Arg Gly Val Val Ala Ile Gly Ser
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 gctatgttcg agc 1070

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 <211> 349
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 58
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 35 40 45
 Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly His Met Arg Leu Pro Arg
 50 55 60
 Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala Arg Arg Val Gln Glu Leu
 65 70 75 80
 Phe Arg Arg Glu His Phe Lys Arg Pro Asn Lys Met Arg Glu Phe Ala
 85 90 95
 Arg Val Arg Pro Asn Glu Ala Val Thr Lys Leu Arg Asn Ala Ile Arg
 100 105 110
 Asp His Glu Ala His His Trp Pro Asp Arg Glu His Leu Ala Arg Thr
 115 120 125
 Ala Glu Arg Met Ile Arg Lys Glu Arg Asp Leu Ala Lys Leu Thr Gly
 130 135 140
 Asn Val Asp Lys Ala Arg Glu Thr Leu Gly Arg Thr Phe Glu Arg Ile
 145 150 155 160
 Leu Ser Leu Leu Ser Glu Met Asp Tyr Val Asp Tyr Ser Asn Pro Asp
 165 170 175
 Asn Pro Val Ile Thr Asp Glu Gly Glu Arg Leu Ala Lys Ile His Ser
 180 185 190
 Glu Ala Asp Leu Leu Val Ala Gln Cys Leu Lys Arg Gly Ile Trp Asp
 195 200 205

Asn Leu Asp Pro Ala Glu Leu Ala Gly Val Val Ser Met Cys Thr Phe
 210 215 220
 Glu Asn Arg Arg Glu Thr Gly Gly Glu Ala Gln Ala Val Thr Glu Ala
 225 230 235 240
 Met Ala Asp Ser Met Asn Ser Val Glu Arg Ile Trp Gly Glu Leu Val
 245 250 255
 Glu Asp Glu Arg Arg His Arg Leu Pro Ile Thr Arg Gln Pro Glu Ala
 260 265 270
 Gly Phe Ala Thr Ala Ile His Gln Trp Ala Ser Gly Ala Pro Leu Gly
 275 280 285
 Tyr Cys Met Ala Ala Ala Ala Glu Asn Gly Ala Glu Leu Thr Pro Gly
 290 295 300
 Asp Phe Val Arg Trp Cys Arg Gln Val Ile Asp Leu Leu Glu Gln Val
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 325 330 335
 Ile Asp Ala Ile Arg Arg Gly Val Val Ala Ile Gly Ser
 340 345

<210> 59
 <211> 612
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(612)
 <223> FRXA02819

<400> 59
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 Val Leu Ala Val Val Met Thr Pro Ala Asn Gln Ser Arg Asp Pro Arg
 20 25 30
 cca tgg gtg acc acc gaa tct ggt tgg tca ggt cgt gtg gat gcg gaa 144
 Pro Trp Val Thr Thr Glu Ser Gly Trp Ser Gly Arg Val Asp Ala Glu
 35 40 45
 tcc ttt act aat ccg ccg atc acc att ggg cat atg cgt ctg cct cgc 192
 Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly His Met Arg Leu Pro Arg
 50 55 60
 caa gct att gaa gag cct cgc cgc aat gcc cgg cgc gtc cag gaa ctg 240
 Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala Arg Arg Val Gln Glu Leu
 65 70 75 80
 ttt agg cgt gag cac ttc aag cga ccc aac aag atg cgg gag ttt gct 288
 Phe Arg Arg Glu His Phe Lys Arg Pro Asn Lys Met Arg Glu Phe Ala

85										90					95					
cgg gtt cgt ccc aat gag gca gtg acc aaa ctg cgt aat gct att cgg	336																			
Arg Val Arg Pro Asn Glu Ala Val Thr Lys Leu Arg Asn Ala Ile Arg																				
100 105 110																				
gat cat gag gcg cat cat tgg cct gat cgg gag cac ttg gct cgc acc	384																			
Asp His Glu Ala His His Trp Pro Asp Arg Glu His Leu Ala Arg Thr																				
115 120 125																				
gcg gag cgt atg atc cgt aaa gaa cgt gat ctg gct aag ttg acc ggc	432																			
Ala Glu Arg Met Ile Arg Lys Glu Arg Asp Leu Ala Lys Leu Thr Gly																				
130 135 140																				
aat gtg gat aaa gcc agg gaa acc ctc ggt agg acg ttt gag cgc att	480																			
Asn Val Asp Lys Ala Arg Glu Thr Leu Gly Arg Thr Phe Glu Arg Ile																				
145 150 155 160																				
ttg tcg ctg ctc agt gaa atg gac tat gtg gat tac tct aat cca gat	528																			
Leu Ser Leu Leu Ser Glu Met Asp Tyr Val Asp Tyr Ser Asn Pro Asp																				
165 170 175																				
aat cca gtg atc act gat gaa ggt gag cgt ttg gcg aaa atc cac agt	576																			
Asn Pro Val Ile Thr Asp Glu Gly Glu Arg Leu Ala Lys Ile His Ser																				
180 185 190																				
gag gca gac ctg ttg gtt gct cag tgc ctc aag cgt	612																			
Glu Ala Asp Leu Leu Val Ala Gln Cys Leu Lys Arg																				
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<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

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Pro Trp Val Thr Thr Glu Ser Gly Trp Ser Gly Arg Val Asp Ala Glu	
35 40 45	
Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly His Met Arg Leu Pro Arg	
50 55 60	
Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala Arg Arg Val Gln Glu Leu	
65 70 75 80	
Phe Arg Arg Glu His Phe Lys Arg Pro Asn Lys Met Arg Glu Phe Ala	
85 90 95	
Arg Val Arg Pro Asn Glu Ala Val Thr Lys Leu Arg Asn Ala Ile Arg	
100 105 110	
Asp His Glu Ala His His Trp Pro Asp Arg Glu His Leu Ala Arg Thr	
115 120 125	

Ala Glu Arg Met Ile Arg Lys Glu Arg Asp Leu Ala Lys Leu Thr Gly
 130 135 140

Asn Val Asp Lys Ala Arg Glu Thr Leu Gly Arg Thr Phe Glu Arg Ile
 145 150 155 160

Leu Ser Leu Leu Ser Glu Met Asp Tyr Val Asp Tyr Ser Asn Pro Asp
 165 170 175

Asn Pro Val Ile Thr Asp Glu Gly Glu Arg Leu Ala Lys Ile His Ser
 180 185 190

Glu Ala Asp Leu Leu Val Ala Gln Cys Leu Lys Arg
 195 200

<210> 61

<211> 1705

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1705)

<223> RXA01157

<400> 61

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 Met Ser Phe Ser Ala
 1 5

gaa aag ggc acc cac ctt tca gag ttc ata gca gac ctg ggc ttt gat 163
 Glu Lys Gly Thr His Leu Ser Glu Phe Ile Ala Asp Leu Gly Phe Asp
 10 15 20

ctg gac gag ttc caa atc aaa ggc tgc cac gct gtg gaa gaa gac cac 211
 Leu Asp Glu Phe Gln Ile Lys Gly Cys His Ala Val Glu Glu Asp His
 25 30 35

ggt gtt tta gta tgt gcg ccc acc ggc gcg ggc aaa aca att gtt ggt 259
 Gly Val Leu Val Cys Ala Pro Thr Gly Ala Gly Lys Thr Ile Val Gly
 40 45 50

gaa ttc gca gtg tcc ctc gca tta tcg cgg ggg aca aag tgt ttc tac 307
 Glu Phe Ala Val Ser Leu Ala Leu Ser Arg Gly Thr Lys Cys Phe Tyr
 55 60 65

acc acc ccc atc aaa gcg ctg agc aac cag aag tac cac gat ttg gtg 355
 Thr Thr Pro Ile Lys Ala Leu Ser Asn Gln Lys Tyr His Asp Leu Val
 70 75 80 85

gct aaa cac ggc tcc gat gcc gtt ggt ctg ctc acc ggt gat gtt tcc 403
 Ala Lys His Gly Ser Asp Ala Val Gly Leu Leu Thr Gly Asp Val Ser
 90 95 100

att aac cat gat gct gac atc gtg gtc atg acc acc gaa gtg ctg cgc 451
 Ile Asn His Asp Ala Asp Ile Val Val Met Thr Thr Glu Val Leu Arg
 105 110 115

aac atg att tac gcg ggc tct ttt gcg ctt gag cgc tta agc cac gtg Asn Met Ile Tyr Ala Gly Ser Phe Ala Leu Glu Arg Leu Ser His Val 120 125 130	499
gtc atg gat gag atc cac ttc ctt gct gat gcc tcc cgt ggc gcg gtg Val Met Asp Glu Ile His Phe Leu Ala Asp Ala Ser Arg Gly Ala Val 135 140 145	547
tgg gaa gaa gtg atc ctc aac ttg gat gat tcc gtc aac atc atc ggt Trp Glu Glu Val Ile Leu Asn Leu Asp Asp Ser Val Asn Ile Ile Gly 150 155 160 165	595
cta tct gcc acg gtg tcc aac tca gag gag ttt ggt gag tgg ctg acc Leu Ser Ala Thr Val Ser Asn Ser Glu Glu Phe Gly Glu Trp Leu Thr 170 175 180	643
act gtt cgc ggc gat acc cgt gtg att gtt act gat cac cgc ccc gtt Thr Val Arg Gly Asp Thr Arg Val Ile Val Thr Asp His Arg Pro Val 185 190 195	691
ccg ctt gat cag tac atg atg gtg cag cgc aaa gtg atg cca ctg ttt Pro Leu Asp Gln Tyr Met Met Val Gln Arg Lys Val Met Pro Leu Phe 200 205 210	739
gag cct ggc acc gat gga cgc gtg aac aag gag tta gag gca acg att Glu Pro Gly Thr Asp Gly Arg Val Asn Lys Glu Leu Glu Ala Thr Ile 215 220 225	787
gat cgc ctc aac agc aag caa agc gaa caa ggc cgt gcg gca tac cgc Asp Arg Leu Asn Ser Lys Gln Ser Glu Gln Gly Arg Ala Ala Tyr Arg 230 235 240 245	835
tct ggt gaa ggc ttc cgt gca cgc agc aaa ggc gat aag cag gat tct Ser Gly Glu Gly Phe Arg Ala Arg Ser Lys Gly Asp Lys Gln Asp Ser 250 255 260	883
cgc act ggt aag cca cgg gaa caa gac cgc cac agg cca ctg ggt cgg Arg Thr Gly Lys Pro Arg Glu Gln Asp Arg His Arg Pro Leu Gly Arg 265 270 275	931
cct gaa gtg ctc agc atc ctc aag ggc atc aac atg ctg cca gcg att Pro Glu Val Leu Ser Ile Leu Lys Gly Ile Asn Met Leu Pro Ala Ile 280 285 290	979
acg ttt atc ttc tcc cgc gcg ggc tgt gat ggt gcg ctg tac caa tgc Thr Phe Ile Phe Ser Arg Ala Gly Cys Asp Gly Ala Leu Tyr Gln Cys 295 300 305	1027
ttg cgt tct aag ttg gtc ttg acg gat caa gca gaa tca gaa gag att Leu Arg Ser Lys Leu Val Leu Thr Asp Gln Ala Glu Ser Glu Glu Ile 310 315 320 325	1075
gca cgc att gtc gac gcc ggc gtg gtg ggg atc ccc gag gaa gac ctt Ala Arg Ile Val Asp Ala Gly Val Val Gly Ile Pro Glu Glu Asp Leu 330 335 340	1123
caa gta ctg aac ttt aag cag tgg cgt gct gca ctg atg cgc ggt ttc Gln Val Leu Asn Phe Lys Gln Trp Arg Ala Ala Leu Met Arg Gly Phe 345 350 355	1171
gca gcc cac cac gcg ggt atg ctt cca gcg ttt agg cac atc gtg gaa	1219

Ala Ala His His Ala Gly Met Leu Pro Ala Phe Arg His Ile Val Glu
 360 365 370

gag ctc ttt gtt aaa ggt ctt gtc cgc gcg gtg ttt gcc acg gaa acc 1267
 Glu Leu Phe Val Lys Gly Leu Val Arg Ala Val Phe Ala Thr Glu Thr
 375 380 385

ctg gca ttg gga atc aac atg cca gcg cgc acc gtg gtg ttg gaa aag 1315
 Leu Ala Leu Gly Ile Asn Met Pro Ala Arg Thr Val Val Leu Glu Lys
 390 395 400 405

atg gtc aaa ttt gac ggc gaa ggc cac gtt gat ctc acc cct ggc caa 1363
 Met Val Lys Phe Asp Gly Glu Gly His Val Asp Leu Thr Pro Gly Gln
 410 415 420

tac acg cag ctg acc ggt cgt gct ggt cga cgt ggc atc gat gtg ttg 1411
 Tyr Thr Gln Leu Thr Gly Arg Ala Gly Arg Arg Gly Ile Asp Val Leu
 425 430 435

ggt aat gct gtg gtg cag tgg tca cca gca ctt gat cca cga tgg gtg 1459
 Gly Asn Ala Val Val Gln Trp Ser Pro Ala Leu Asp Pro Arg Trp Val
 440 445 450

gca ggt ctt gcc tct acg cgt acc tac ccg ctg atc tct acg ttc cag 1507
 Ala Gly Leu Ala Ser Thr Arg Thr Tyr Pro Leu Ile Ser Thr Phe Gln
 455 460 465

ccg ggc tac aac atg tcg gtt aac ctg ctg aaa acc att ggt tat gag 1555
 Pro Gly Tyr Asn Met Ser Val Asn Leu Leu Lys Thr Ile Gly Tyr Glu
 470 475 480 485

cct tcg ctg cgc ctt ttg gaa aaa tct ttt gca cag ttc caa gcc gat 1603
 Pro Ser Leu Arg Leu Leu Glu Lys Ser Phe Ala Gln Phe Gln Ala Asp
 490 495 500

ggt tcc gtc gtg ggc gat gtg cgt gaa att gaa cgt gca gaa gcc aag 1651
 Gly Ser Val Val Gly Asp Val Arg Glu Ile Glu Arg Ala Glu Ala Lys
 505 510 515

gtg gca gaa ttg cgt gcc cag ctg aac aaa gag att gct gcc acc aac 1699
 Val Ala Glu Leu Arg Ala Gln Leu Asn Lys Glu Ile Ala Ala Thr Asn
 520 525 530

cct gcg 1705
 Pro Ala
 535

<210> 62

<211> 535

<212> PRT

<213> Corynebacterium glutamicum

<400> 62

Met Ser Phe Ser Ala Glu Lys Gly Thr His Leu Ser Glu Phe Ile Ala
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Asp Leu Gly Phe Asp Leu Asp Glu Phe Gln Ile Lys Gly Cys His Ala
 20 25 30

Val Glu Glu Asp His Gly Val Leu Val Cys Ala Pro Thr Gly Ala Gly

35					40					45					
Lys	Thr	Ile	Val	Gly	Glu	Phe	Ala	Val	Ser	Leu	Ala	Leu	Ser	Arg	Gly
50						55					60				
Thr	Lys	Cys	Phe	Tyr	Thr	Thr	Pro	Ile	Lys	Ala	Leu	Ser	Asn	Gln	Lys
65					70					75					80
Tyr	His	Asp	Leu	Val	Ala	Lys	His	Gly	Ser	Asp	Ala	Val	Gly	Leu	Leu
				85					90					95	
Thr	Gly	Asp	Val	Ser	Ile	Asn	His	Asp	Ala	Asp	Ile	Val	Val	Met	Thr
			100					105					110		
Thr	Glu	Val	Leu	Arg	Asn	Met	Ile	Tyr	Ala	Gly	Ser	Phe	Ala	Leu	Glu
		115					120					125			
Arg	Leu	Ser	His	Val	Val	Met	Asp	Glu	Ile	His	Phe	Leu	Ala	Asp	Ala
						135					140				
Ser	Arg	Gly	Ala	Val	Trp	Glu	Glu	Val	Ile	Leu	Asn	Leu	Asp	Asp	Ser
145					150					155					160
Val	Asn	Ile	Ile	Gly	Leu	Ser	Ala	Thr	Val	Ser	Asn	Ser	Glu	Glu	Phe
				165					170					175	
Gly	Glu	Trp	Leu	Thr	Thr	Val	Arg	Gly	Asp	Thr	Arg	Val	Ile	Val	Thr
			180					185					190		
Asp	His	Arg	Pro	Val	Pro	Leu	Asp	Gln	Tyr	Met	Met	Val	Gln	Arg	Lys
		195					200					205			
Val	Met	Pro	Leu	Phe	Glu	Pro	Gly	Thr	Asp	Gly	Arg	Val	Asn	Lys	Glu
		210				215					220				
Leu	Glu	Ala	Thr	Ile	Asp	Arg	Leu	Asn	Ser	Lys	Gln	Ser	Glu	Gln	Gly
225					230					235					240
Arg	Ala	Ala	Tyr	Arg	Ser	Gly	Glu	Gly	Phe	Arg	Ala	Arg	Ser	Lys	Gly
				245					250					255	
Asp	Lys	Gln	Asp	Ser	Arg	Thr	Gly	Lys	Pro	Arg	Glu	Gln	Asp	Arg	His
			260					265					270		
Arg	Pro	Leu	Gly	Arg	Pro	Glu	Val	Leu	Ser	Ile	Leu	Lys	Gly	Ile	Asn
		275				280						285			
Met	Leu	Pro	Ala	Ile	Thr	Phe	Ile	Phe	Ser	Arg	Ala	Gly	Cys	Asp	Gly
		290				295					300				
Ala	Leu	Tyr	Gln	Cys	Leu	Arg	Ser	Lys	Leu	Val	Leu	Thr	Asp	Gln	Ala
305					310					315					320
Glu	Ser	Glu	Glu	Ile	Ala	Arg	Ile	Val	Asp	Ala	Gly	Val	Val	Gly	Ile
				325					330					335	
Pro	Glu	Glu	Asp	Leu	Gln	Val	Leu	Asn	Phe	Lys	Gln	Trp	Arg	Ala	Ala
			340					345					350		
Leu	Met	Arg	Gly	Phe	Ala	Ala	His	His	Ala	Gly	Met	Leu	Pro	Ala	Phe
		355					360					365			

Arg His Ile Val Glu Glu Leu Phe Val Lys Gly Leu Val Arg Ala Val
 370 375 380
 Phe Ala Thr Glu Thr Leu Ala Leu Gly Ile Asn Met Pro Ala Arg Thr
 385 390 395 400
 Val Val Leu Glu Lys Met Val Lys Phe Asp Gly Glu Gly His Val Asp
 405 410 415
 Leu Thr Pro Gly Gln Tyr Thr Gln Leu Thr Gly Arg Ala Gly Arg Arg
 420 425 430
 Gly Ile Asp Val Leu Gly Asn Ala Val Val Gln Trp Ser Pro Ala Leu
 435 440 445
 Asp Pro Arg Trp Val Ala Gly Leu Ala Ser Thr Arg Thr Tyr Pro Leu
 450 455 460
 Ile Ser Thr Phe Gln Pro Gly Tyr Asn Met Ser Val Asn Leu Leu Lys
 465 470 475 480
 Thr Ile Gly Tyr Glu Pro Ser Leu Arg Leu Leu Glu Lys Ser Phe Ala
 485 490 495
 Gln Phe Gln Ala Asp Gly Ser Val Val Gly Asp Val Arg Glu Ile Glu
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 Arg Ala Glu Ala Lys Val Ala Glu Leu Arg Ala Gln Leu Asn Lys Glu
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 <211> 1974
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1951)
 <223> RXN01876

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 Met Ala Arg Pro Phe
 1 5
 tat ctg gcc acc acc gtt tca ccg gag ggc gtg cat atc cgc cgg cac 163
 Tyr Leu Ala Thr Thr Val Ser Pro Glu Gly Val His Ile Arg Arg His
 10 15 20
 att cgc acc cgt ggg cgc gtt gtc acg ggt gtt gat gat gag gta ttg 211
 Ile Arg Thr Arg Gly Arg Val Val Thr Gly Val Asp Asp Glu Val Leu
 25 30 35
 acc ggt gag atg gcc gat gtt atc gag cag ggt ggt gtc ggc tct gaa 259

Thr	Gly	Glu	Met	Ala	Asp	Val	Ile	Glu	Gln	Gly	Gly	Val	Gly	Ser	Glu		
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tct	gtg	ctg	cac	cag	gcg	ttg	gaa	cag	gcc	cgc	agc	ggc	cac	atg	cgc	307	
Ser	Val	Leu	His	Gln	Ala	Leu	Glu	Gln	Ala	Arg	Ser	Gly	His	Met	Arg		
	55					60					65						
aac	atc	gtt	gaa	aca	att	cag	cgc	gag	cag	gat	gag	atc	atc	cgc	gat	355	
Asn	Ile	Val	Glu	Thr	Ile	Gln	Arg	Glu	Gln	Asp	Glu	Ile	Ile	Arg	Asp		
70					75					80					85		
acc	acc	cgc	ggt	gtc	atg	gtt	gtt	caa	ggt	ggc	cct	gga	aca	ggt	aaa	403	
Thr	Thr	Arg	Gly	Val	Met	Val	Val	Gln	Gly	Gly	Pro	Gly	Thr	Gly	Lys		
				90					95					100			
act	gcg	gtc	gcg	ttg	cac	cgt	gtg	gct	tat	ctg	ctt	tat	acc	tgg	cgc	451	
Thr	Ala	Val	Ala	Leu	His	Arg	Val	Ala	Tyr	Leu	Leu	Tyr	Thr	Trp	Arg		
			105					110					115				
gat	cag	ctg	gct	aag	tct	ggc	gtg	ttg	atc	att	ggc	ccg	aac	aag	aca	499	
Asp	Gln	Leu	Ala	Lys	Ser	Gly	Val	Leu	Ile	Ile	Gly	Pro	Asn	Lys	Thr		
		120					125					130					
ttt	ttg	gag	tat	att	tct	cac	gtt	ttg	cct	gaa	ctc	ggc	gag	act	ggc	547	
Phe	Leu	Glu	Tyr	Ile	Ser	His	Val	Leu	Pro	Glu	Leu	Gly	Glu	Thr	Gly		
	135					140					145						
gtg	gtg	ttg	tcc	acc	gtc	ggt	gag	ctg	ttc	ccc	ggt	atc	gtc	cca	acg	595	
Val	Val	Leu	Ser	Thr	Val	Gly	Glu	Leu	Phe	Pro	Gly	Ile	Val	Pro	Thr		
150					155					160					165		
ggt	tcc	gag	gac	act	ttg	acc	agg	gaa	att	aag	ggc	agc	gag	gaa	atg	643	
Gly	Ser	Glu	Asp	Thr	Leu	Thr	Arg	Glu	Ile	Lys	Gly	Ser	Glu	Glu	Met		
				170					175					180			
gcc	agc	att	ttg	gcc	gag	gca	gtc	aag	gcg	tat	caa	gtg	ctg	cca	gag	691	
Ala	Ser	Ile	Leu	Ala	Glu	Ala	Val	Lys	Ala	Tyr	Gln	Val	Leu	Pro	Glu		
			185					190					195				
aag	acc	atc	gtg	gtc	tct	gtt	gat	ggc	atc	gag	att	tcc	att	gat	gag	739	
Lys	Thr	Ile	Val	Val	Ser	Val	Asp	Gly	Ile	Glu	Ile	Ser	Ile	Asp	Glu		
		200					205					210					
aaa	acg	gtg	gca	aaa	tcc	cgc	acc	cga	gct	cgt	cgt	gcc	agg	cag	tcg	787	
Lys	Thr	Val	Ala	Lys	Ser	Arg	Thr	Arg	Ala	Arg	Arg	Ala	Arg	Gln	Ser		
		215				220					225						
cac	aat	tcc	gca	cgc	cca	att	ttc	cgc	gag	cat	tta	gtc	gaa	caa	ctc	835	
His	Asn	Ser	Ala	Arg	Pro	Ile	Phe	Arg	Glu	His	Leu	Val	Glu	Gln	Leu		
230					235					240					245		
gcg	cac	caa	atg	gct	caa	acg	atc	ggc	gcg	gat	ccg	ctg	ggc	ggc	aaa	883	
Ala	His	Gln	Met	Ala	Gln	Thr	Ile	Gly	Ala	Asp	Pro	Leu	Gly	Gly	Lys		
				250				255						260			
aac	ctg	ctg	tca	gcc	gcc	gac	atc	gat	cag	ctg	cac	gat	gat	ttg	ctt	931	
Asn	Leu	Leu	Ser	Ala	Ala	Asp	Ile	Asp	Gln	Leu	His	Asp	Asp	Leu	Leu		
			265					270					275				
gac	gac	gcg	gcc	ctc	cag	tcc	gtc	atc	gac	gat	ttc	tgg	ccg	gag	ctc	979	
Asp	Asp	Ala	Ala	Leu	Gln	Ser	Val	Ile	Asp	Asp	Phe	Trp	Pro	Glu	Leu		

280	285	290	
cgg cct cag gac gtc ctg cat gat ctg ttg att tcc gaa gag cgc att Arg Pro Gln Asp Val Leu His Asp Leu Leu Ile Ser Glu Glu Arg Ile 295 300 305			1027
aat gtt gct gcc gcg ggg tat gac gag gaa act aag tct gct ttg ctg Asn Val Ala Ala Ala Gly Tyr Asp Glu Glu Thr Lys Ser Ala Leu Leu 310 315 320 325			1075
cgt ggt gaa ctc gat ccg tgg gca cca tcg gac gct gca ttg ctt gat Arg Gly Glu Leu Asp Pro Trp Ala Pro Ser Asp Ala Ala Leu Leu Asp 330 335 340			1123
gag tta gcc ctg ctc atc ggt ctt ccc gat cca gag gag gca cgg gag Glu Leu Ala Leu Leu Ile Gly Leu Pro Asp Pro Glu Glu Ala Arg Glu 345 350 355			1171
aag gct gag gcc aaa tgg cgc gag cag atc gat gac gct cag gaa gtc Lys Ala Glu Ala Lys Trp Arg Glu Gln Ile Asp Asp Ala Gln Glu Val 360 365 370			1219
ctg gac gtt ctt agt tca tca cag tca tcg gat att gat gat gtc acg Leu Asp Val Leu Ser Ser Ser Gln Ser Ser Asp Ile Asp Asp Val Thr 375 380 385			1267
gaa gct gaa gtt ctc tcc gct ttc gac gtc atc gat gcg gaa act ttg Glu Ala Glu Val Leu Ser Ala Phe Asp Val Ile Asp Ala Glu Thr Leu 390 395 400 405			1315
gca caa cgc caa act gtc acg gat aat cgc acc act gcg gaa cgt gca Ala Gln Arg Gln Thr Val Thr Asp Asn Arg Thr Thr Ala Glu Arg Ala 410 415 420			1363
cag gcg gat cat aag tgg gca tat ggt cac gtg att gta gat gaa gct Gln Ala Asp His Lys Trp Ala Tyr Gly His Val Ile Val Asp Glu Ala 425 430 435			1411
cag gag ctc agt ccg atg gaa tgg cgc atg gtg ttt cgc cgt agc cct Gln Glu Leu Ser Pro Met Glu Trp Arg Met Val Phe Arg Arg Ser Pro 440 445 450			1459
tcg cga tgg atg acc ctt gtg ggc gat att gca caa act ggt tgg cct Ser Arg Trp Met Thr Leu Val Gly Asp Ile Ala Gln Thr Gly Trp Pro 455 460 465			1507
gcc ggc gtt gac gat tgg gca gaa tca ctg tgg ccc ttc gtc gaa aag Ala Gly Val Asp Asp Trp Ala Glu Ser Leu Trp Pro Phe Val Glu Lys 470 475 480 485			1555
cgt ttc agg cac cac gag ctc acc gtt aac tac cgc acc ccg gcc gag Arg Phe Arg His His Glu Leu Thr Val Asn Tyr Arg Thr Pro Ala Glu 490 495 500			1603
atc atg tcg gtg gcc aat gag ctt ttg acg cag atc aat cct gat att Ile Met Ser Val Ala Asn Glu Leu Leu Thr Gln Ile Asn Pro Asp Ile 505 510 515			1651
gcg ccg gca atg gcg atc cgc gaa tct ggt cga gag gta gtg aac ttg Ala Pro Ala Met Ala Ile Arg Glu Ser Gly Arg Glu Val Val Asn Leu 520 525 530			1699

ccg ctt gat gcc gat ttg tcg gca gtg atg gat agt ttg cgt gag gag 1747
 Pro Leu Asp Ala Asp Leu Ser Ala Val Met Asp Ser Leu Arg Glu Glu
 535 540 545
 gat tca cag cgc acc atc gcg gtg att tct tcg cgc cgc cac cac gaa 1795
 Asp Ser Gln Arg Thr Ile Ala Val Ile Ser Ser Arg Arg His His Glu
 550 555 560 565
 agc gat ttc tac ctg gtc gat gac atc aag ggc tta gag ttt gac cac 1843
 Ser Asp Phe Tyr Leu Val Asp Asp Ile Lys Gly Leu Glu Phe Asp His
 570 575 580
 gtc atc gtg gtg gat cct gcg gga atc gtt gaa gaa tcc ccc cag gga 1891
 Val Ile Val Val Asp Pro Ala Gly Ile Val Glu Glu Ser Pro Gln Gly
 585 590 595
 ttg caa gac ctc tac gtt gcg gtc act cgt gca acg cag agc ctc acc 1939
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 Ile Leu Gly Glu
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<210> 64

<211> 617

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

Met Ala Arg Pro Phe Tyr Leu Ala Thr Thr Val Ser Pro Glu Gly Val
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 His Ile Arg Arg His Ile Arg Thr Arg Gly Arg Val Val Thr Gly Val
 20 25 30
 Asp Asp Glu Val Leu Thr Gly Glu Met Ala Asp Val Ile Glu Gln Gly
 35 40 45
 Gly Val Gly Ser Glu Ser Val Leu His Gln Ala Leu Glu Gln Ala Arg
 50 55 60
 Ser Gly His Met Arg Asn Ile Val Glu Thr Ile Gln Arg Glu Gln Asp
 65 70 75 80
 Glu Ile Ile Arg Asp Thr Thr Arg Gly Val Met Val Val Gln Gly Gly
 85 90 95
 Pro Gly Thr Gly Lys Thr Ala Val Ala Leu His Arg Val Ala Tyr Leu
 100 105 110
 Leu Tyr Thr Trp Arg Asp Gln Leu Ala Lys Ser Gly Val Leu Ile Ile
 115 120 125
 Gly Pro Asn Lys Thr Phe Leu Glu Tyr Ile Ser His Val Leu Pro Glu
 130 135 140
 Leu Gly Glu Thr Gly Val Val Leu Ser Thr Val Gly Glu Leu Phe Pro
 145 150 155 160

Gly Ile Val Pro Thr Gly Ser Glu Asp Thr Leu Thr Arg Glu Ile Lys
165 170 175

Gly Ser Glu Glu Met Ala Ser Ile Leu Ala Glu Ala Val Lys Ala Tyr
180 185 190

Gln Val Leu Pro Glu Lys Thr Ile Val Val Ser Val Asp Gly Ile Glu
195 200 205

Ile Ser Ile Asp Glu Lys Thr Val Ala Lys Ser Arg Thr Arg Ala Arg
210 215 220

Arg Ala Arg Gln Ser His Asn Ser Ala Arg Pro Ile Phe Arg Glu His
225 230 235 240

Leu Val Glu Gln Leu Ala His Gln Met Ala Gln Thr Ile Gly Ala Asp
245 250 255

Pro Leu Gly Gly Lys Asn Leu Leu Ser Ala Ala Asp Ile Asp Gln Leu
260 265 270

His Asp Asp Leu Leu Asp Asp Ala Ala Leu Gln Ser Val Ile Asp Asp
275 280 285

Phe Trp Pro Glu Leu Arg Pro Gln Asp Val Leu His Asp Leu Leu Ile
290 295 300

Ser Glu Glu Arg Ile Asn Val Ala Ala Ala Gly Tyr Asp Glu Glu Thr
305 310 315 320

Lys Ser Ala Leu Leu Arg Gly Glu Leu Asp Pro Trp Ala Pro Ser Asp
325 330 335

Ala Ala Leu Leu Asp Glu Leu Ala Leu Leu Ile Gly Leu Pro Asp Pro
340 345 350

Glu Glu Ala Arg Glu Lys Ala Glu Ala Lys Trp Arg Glu Gln Ile Asp
355 360 365

Asp Ala Gln Glu Val Leu Asp Val Leu Ser Ser Ser Gln Ser Ser Asp
370 375 380

Ile Asp Asp Val Thr Glu Ala Glu Val Leu Ser Ala Phe Asp Val Ile
385 390 395 400

Asp Ala Glu Thr Leu Ala Gln Arg Gln Thr Val Thr Asp Asn Arg Thr
405 410 415

Thr Ala Glu Arg Ala Gln Ala Asp His Lys Trp Ala Tyr Gly His Val
420 425 430

Ile Val Asp Glu Ala Gln Glu Leu Ser Pro Met Glu Trp Arg Met Val
435 440 445

Phe Arg Arg Ser Pro Ser Arg Trp Met Thr Leu Val Gly Asp Ile Ala
450 455 460

Gln Thr Gly Trp Pro Ala Gly Val Asp Asp Trp Ala Glu Ser Leu Trp
465 470 475 480

Pro Phe Val Glu Lys Arg Phe Arg His His Glu Leu Thr Val Asn Tyr
485 490 495

Arg Thr Pro Ala Glu Ile Met Ser Val Ala Asn Glu Leu Leu Thr Gln
500 505 510

Ile Asn Pro Asp Ile Ala Pro Ala Met Ala Ile Arg Glu Ser Gly Arg
515 520 525

Glu Val Val Asn Leu Pro Leu Asp Ala Asp Leu Ser Ala Val Met Asp
530 535 540

Ser Leu Arg Glu Glu Asp Ser Gln Arg Thr Ile Ala Val Ile Ser Ser
545 550 555 560

Arg Arg His His Glu Ser Asp Phe Tyr Leu Val Asp Asp Ile Lys Gly
565 570 575

Leu Glu Phe Asp His Val Ile Val Val Asp Pro Ala Gly Ile Val Glu
580 585 590

Glu Ser Pro Gln Gly Leu Gln Asp Leu Tyr Val Ala Val Thr Arg Ala
595 600 605

Thr Gln Ser Leu Thr Ile Leu Gly Glu
610 615

<210> 65

<211> 1496

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1473)

<223> FRXA01876

<400> 65

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Ile Ile Gly Pro Asn Lys Thr Phe Leu Glu Tyr Ile Ser His Val Leu
1 5 10 15

cct gaa ctc ggc gag act ggc gtg gtg ttg tcc acc gtc ggt gag ctg 96
Pro Glu Leu Gly Glu Thr Gly Val Val Leu Ser Thr Val Gly Glu Leu
20 25 30

ttc ccc ggt atc gtc cca acg ggt tcc gag gac act ttg acc agg gaa 144
Phe Pro Gly Ile Val Pro Thr Gly Ser Glu Asp Thr Leu Thr Arg Glu
35 40 45

att aag ggc agc gag gaa atg gcc agc att ttg gcc gag gca gtc aag 192
Ile Lys Gly Ser Glu Glu Met Ala Ser Ile Leu Ala Glu Ala Val Lys
50 55 60

gcg tat caa gtg ctg cca gag aag acc atc gtg gtc tct gtt gat ggc 240
Ala Tyr Gln Val Leu Pro Glu Lys Thr Ile Val Val Ser Val Asp Gly
65 70 75 80

atc gag att tcc att gat gag aaa acg gtg gca aaa tcc cgc acc cga 288
Ile Glu Ile Ser Ile Asp Glu Lys Thr Val Ala Lys Ser Arg Thr Arg

85										90					95					
gct	cgt	cgt	gcc	agg	cag	tcg	cac	aat	tcc	gca	cgc	cca	att	ttc	cgc	336				
Ala	Arg	Arg	Ala	Arg	Gln	Ser	His	Asn	Ser	Ala	Arg	Pro	Ile	Phe	Arg					
			100					105					110							
gag	cat	tta	gtc	gaa	caa	ctc	gcg	cac	caa	atg	gct	caa	acg	atc	ggc	384				
Glu	His	Leu	Val	Glu	Gln	Leu	Ala	His	Gln	Met	Ala	Gln	Thr	Ile	Gly					
		115					120					125								
gcg	gat	ccg	ctg	ggc	ggc	aaa	aac	ctg	ctg	tca	gcc	gcc	gac	atc	gat	432				
Ala	Asp	Pro	Leu	Gly	Gly	Lys	Asn	Leu	Leu	Ser	Ala	Ala	Asp	Ile	Asp					
	130					135					140									
cag	ctg	cac	gat	gat	ttg	ctt	gac	gac	gcg	gcc	ctc	cag	tcc	gtc	atc	480				
Gln	Leu	His	Asp	Asp	Leu	Leu	Asp	Asp	Ala	Ala	Leu	Gln	Ser	Val	Ile					
145					150					155					160					
gac	gat	ttc	tgg	ccg	gag	ctc	cgg	cct	cag	gac	gtc	ctg	cat	gat	ctg	528				
Asp	Asp	Phe	Trp	Pro	Glu	Leu	Arg	Pro	Gln	Asp	Val	Leu	His	Asp	Leu					
				165				170						175						
ttg	att	tcc	gaa	gag	cgc	att	aat	gtt	gct	gcc	gcg	ggg	tat	gac	gag	576				
Leu	Ile	Ser	Glu	Glu	Arg	Ile	Asn	Val	Ala	Ala	Ala	Gly	Tyr	Asp	Glu					
			180				185						190							
gaa	act	aag	tct	gct	ttg	ctg	cgt	ggg	gaa	ctc	gat	ccg	tgg	gca	cca	624				
Glu	Thr	Lys	Ser	Ala	Leu	Leu	Arg	Gly	Glu	Leu	Asp	Pro	Trp	Ala	Pro					
		195					200					205								
tcg	gac	gct	gca	ttg	ctt	gat	gag	tta	gcc	ctg	ctc	atc	ggg	ctt	ccc	672				
Ser	Asp	Ala	Ala	Leu	Leu	Asp	Glu	Leu	Ala	Leu	Leu	Ile	Gly	Leu	Pro					
	210					215					220									
gat	cca	gag	gag	gca	cgg	gag	aag	gct	gag	gcc	aaa	tgg	cgc	gag	cag	720				
Asp	Pro	Glu	Glu	Ala	Arg	Glu	Lys	Ala	Glu	Ala	Lys	Trp	Arg	Glu	Gln					
225					230					235					240					
atc	gat	gac	gct	cag	gaa	gtc	ctg	gac	gtt	ctt	agt	tca	tca	cag	tca	768				
Ile	Asp	Asp	Ala	Gln	Glu	Val	Leu	Asp	Val	Leu	Ser	Ser	Ser	Gln	Ser					
				245				250						255						
tcg	gat	att	gat	gat	gtc	acg	gaa	gct	gaa	gtt	ctc	tcc	gct	ttc	gac	816				
Ser	Asp	Ile	Asp	Asp	Val	Thr	Glu	Ala	Glu	Val	Leu	Ser	Ala	Phe	Asp					
			260				265						270							
gtc	atc	gat	gcg	gaa	act	ttg	gca	caa	cgc	caa	act	gtc	acg	gat	aat	864				
Val	Ile	Asp	Ala	Glu	Thr	Leu	Ala	Gln	Arg	Gln	Thr	Val	Thr	Asp	Asn					
		275					280					285								
cgc	acc	act	gcg	gaa	cgt	gca	cag	gcg	gat	cat	aag	tgg	gca	tat	ggg	912				
Arg	Thr	Thr	Ala	Glu	Arg	Ala	Gln	Ala	Asp	His	Lys	Trp	Ala	Tyr	Gly					
	290					295					300									
cac	gtg	att	gta	gat	gaa	gct	cag	gag	ctc	agt	ccg	atg	gaa	tgg	cgc	960				
His	Val	Ile	Val	Asp	Glu	Ala	Gln	Glu	Leu	Ser	Pro	Met	Glu	Trp	Arg					
305					310				315						320					
atg	gtg	ttt	cgc	cgt	agc	cct	tcg	cga	tgg	atg	acc	ctt	gtg	ggc	gat	1008				
Met	Val	Phe	Arg	Arg	Ser	Pro	Ser	Arg	Trp	Met	Thr	Leu	Val	Gly	Asp					
				325					330					335						

att gca caa act ggt tgg cct gcc ggc gtt gac gat tgg gca gaa tca 1056
 Ile Ala Gln Thr Gly Trp Pro Ala Gly Val Asp Asp Trp Ala Glu Ser
 340 345 350

ctg tgg ccc ttc gtc gaa aag cgt ttc agg cac cac gag ctc acc gtt 1104
 Leu Trp Pro Phe Val Glu Lys Arg Phe Arg His His Glu Leu Thr Val
 355 360 365

aac tac cgc acc ccg gcc gag atc atg tcg gtg gcc aat gag ctt ttg 1152
 Asn Tyr Arg Thr Pro Ala Glu Ile Met Ser Val Ala Asn Glu Leu Leu
 370 375 380

acg cag atc aat cct gat att gcg ccg gca atg gcg atc cgc gaa tct 1200
 Thr Gln Ile Asn Pro Asp Ile Ala Pro Ala Met Ala Ile Arg Glu Ser
 385 390 395 400

ggt cga gag gta gtg aac ttg ccg ctt gat gcc gat ttg tcg gca gtg 1248
 Gly Arg Glu Val Val Asn Leu Pro Leu Asp Ala Asp Leu Ser Ala Val
 405 410 415

atg gat agt ttg cgt gag gag gat tca cag cgc acc atc gcg gtg att 1296
 Met Asp Ser Leu Arg Glu Glu Asp Ser Gln Arg Thr Ile Ala Val Ile
 420 425 430

tct tcg cgc cgc cac cac gaa agc gat ttc tac ctg gtc gat gac atc 1344
 Ser Ser Arg Arg His His Glu Ser Asp Phe Tyr Leu Val Asp Asp Ile
 435 440 445

aag ggc tta gag ttt gac cac gtc atc gtg gtg gat cct gcg gga atc 1392
 Lys Gly Leu Glu Phe Asp His Val Ile Val Val Asp Pro Ala Gly Ile
 450 455 460

gtt gaa gaa tcc ccc cag gga ttg caa gac ctc tac gtt gcg gtc act 1440
 Val Glu Glu Ser Pro Gln Gly Leu Gln Asp Leu Tyr Val Ala Val Thr
 465 470 475 480

cgt gca acg cag agc ctc acc att tta ggt gag tagcagggtta tgagctcagg 1493
 Arg Ala Thr Gln Ser Leu Thr Ile Leu Gly Glu
 485 490

gcc 1496

<210> 66

<211> 491

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

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Pro Glu Leu Gly Glu Thr Gly Val Val Leu Ser Thr Val Gly Glu Leu
 20 25 30

Phe Pro Gly Ile Val Pro Thr Gly Ser Glu Asp Thr Leu Thr Arg Glu
 35 40 45

Ile Lys Gly Ser Glu Glu Met Ala Ser Ile Leu Ala Glu Ala Val Lys
 50 55 60

Ala Tyr Gln Val Leu Pro Glu Lys Thr Ile Val Val Ser Val Asp Gly
 65 70 75 80
 Ile Glu Ile Ser Ile Asp Glu Lys Thr Val Ala Lys Ser Arg Thr Arg
 85 90 95
 Ala Arg Arg Ala Arg Gln Ser His Asn Ser Ala Arg Pro Ile Phe Arg
 100 105 110
 Glu His Leu Val Glu Gln Leu Ala His Gln Met Ala Gln Thr Ile Gly
 115 120 125
 Ala Asp Pro Leu Gly Gly Lys Asn Leu Leu Ser Ala Ala Asp Ile Asp
 130 135 140
 Gln Leu His Asp Asp Leu Leu Asp Asp Ala Ala Leu Gln Ser Val Ile
 145 150 155 160
 Asp Asp Phe Trp Pro Glu Leu Arg Pro Gln Asp Val Leu His Asp Leu
 165 170 175
 Leu Ile Ser Glu Glu Arg Ile Asn Val Ala Ala Ala Gly Tyr Asp Glu
 180 185 190
 Glu Thr Lys Ser Ala Leu Leu Arg Gly Glu Leu Asp Pro Trp Ala Pro
 195 200 205
 Ser Asp Ala Ala Leu Leu Asp Glu Leu Ala Leu Leu Ile Gly Leu Pro
 210 215 220
 Asp Pro Glu Glu Ala Arg Glu Lys Ala Glu Ala Lys Trp Arg Glu Gln
 225 230 235 240
 Ile Asp Asp Ala Gln Glu Val Leu Asp Val Leu Ser Ser Ser Gln Ser
 245 250 255
 Ser Asp Ile Asp Asp Val Thr Glu Ala Glu Val Leu Ser Ala Phe Asp
 260 265 270
 Val Ile Asp Ala Glu Thr Leu Ala Gln Arg Gln Thr Val Thr Asp Asn
 275 280 285
 Arg Thr Thr Ala Glu Arg Ala Gln Ala Asp His Lys Trp Ala Tyr Gly
 290 295 300
 His Val Ile Val Asp Glu Ala Gln Glu Leu Ser Pro Met Glu Trp Arg
 305 310 315 320
 Met Val Phe Arg Arg Ser Pro Ser Arg Trp Met Thr Leu Val Gly Asp
 325 330 335
 Ile Ala Gln Thr Gly Trp Pro Ala Gly Val Asp Asp Trp Ala Glu Ser
 340 345 350
 Leu Trp Pro Phe Val Glu Lys Arg Phe Arg His His Glu Leu Thr Val
 355 360 365
 Asn Tyr Arg Thr Pro Ala Glu Ile Met Ser Val Ala Asn Glu Leu Leu
 370 375 380

Thr Gln Ile Asn Pro Asp Ile Ala Pro Ala Met Ala Ile Arg Glu Ser
385 390 395 400

Gly Arg Glu Val Val Asn Leu Pro Leu Asp Ala Asp Leu Ser Ala Val
405 410 415

Met Asp Ser Leu Arg Glu Glu Asp Ser Gln Arg Thr Ile Ala Val Ile
420 425 430

Ser Ser Arg Arg His His Glu Ser Asp Phe Tyr Leu Val Asp Asp Ile
435 440 445

Lys Gly Leu Glu Phe Asp His Val Ile Val Val Asp Pro Ala Gly Ile
450 455 460

Val Glu Glu Ser Pro Gln Gly Leu Gln Asp Leu Tyr Val Ala Val Thr
465 470 475 480

Arg Ala Thr Gln Ser Leu Thr Ile Leu Gly Glu
485 490

<210> 67

<211> 1653

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1630)

<223> RXA00544

<400> 67

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ggggctagag tgaacttaga atcagattgg ggaaaagaaa atg gct aca gat aca 115
Met Ala Thr Asp Thr
1 5

cac gcc gca agt ttt gat gat gac tac gta cct cca cag gag cca agc 163
His Ala Ala Ser Phe Asp Asp Asp Tyr Val Pro Pro Gln Glu Pro Ser
10 15 20

gat tcc ttc gcg gat gac gca cac gta gat gtc cct gct ccg gcg ttt 211
Asp Ser Phe Ala Asp Asp Ala His Val Asp Val Pro Ala Pro Ala Phe
25 30 35

gaa gat ttc tcc ccg gcc cag gcc ttt ggt cag gga act agg gga gga 259
Glu Asp Phe Ser Pro Ala Gln Ala Phe Gly Gln Gly Thr Arg Gly Gly
40 45 50

gac tct cag ggc ttc aag aag agg ggt cgc aag gac gag tcc cgt gaa 307
Asp Ser Gln Gly Phe Lys Lys Arg Gly Arg Lys Asp Glu Ser Arg Glu
55 60 65

tac cga gac ttc cgc caa cct ccc tat gac aat gac gct gag atg ggc 355
Tyr Arg Asp Phe Arg Gln Pro Pro Tyr Asp Asn Asp Ala Glu Met Gly
70 75 80 85

gtg ctg ggc gcg atg ctg ctc agt ccg acc acg gtc atc gac att ctg 403
Val Leu Gly Ala Met Leu Leu Ser Pro Thr Thr Val Ile Asp Ile Leu

90										95					100					
gat	atc	ctc	acc	cca	gaa	gac	ttc	tac	agg	cgc	tcc	cac	cag	ctg	att	451				
Asp	Ile	Leu	Thr	Pro	Glu	Asp	Phe	Tyr	Arg	Pro	Ser	His	Gln	Leu	Ile					
			105					110					115							
ttc	cag	gcg	atc	att	gac	ctg	ttc	agt	gac	aac	cgt	gat	att	gac	ccc	499				
Phe	Gln	Ala	Ile	Ile	Asp	Leu	Phe	Ser	Asp	Asn	Arg	Asp	Ile	Asp	Pro					
		120					125					130								
gtg	att	gtc	tcc	ggt	cgc	ctc	gat	cga	acc	aac	gat	ctg	gac	cgc	gtc	547				
Val	Ile	Val	Ser	Gly	Arg	Leu	Asp	Arg	Thr	Asn	Asp	Leu	Asp	Arg	Val					
	135					140					145									
ggc	ggt	ggc	gcg	tac	ctc	cac	gac	ctc	atc	cag	tcc	gtt	ccc	acc	gca	595				
Gly	Gly	Gly	Ala	Tyr	Leu	His	Asp	Leu	Ile	Gln	Ser	Val	Pro	Thr	Ala					
150					155					160					165					
gcc	aac	gcg	cgc	tac	tat	gcg	gaa	atc	gtt	tcg	gaa	aag	gca	gtg	ctt	643				
Ala	Asn	Ala	Arg	Tyr	Tyr	Ala	Glu	Ile	Val	Ser	Glu	Lys	Ala	Val	Leu					
				170					175					180						
cgc	agg	ctt	gtc	gac	gcc	ggc	acc	cgc	gtc	gtc	cag	ctc	ggc	tac	gag	691				
Arg	Arg	Leu	Val	Asp	Ala	Gly	Thr	Arg	Val	Val	Gln	Leu	Gly	Tyr	Glu					
			185					190					195							
ggc	gat	gaa	ggc	gcc	gaa	att	gac	gcg	gtg	att	gac	cgc	gcg	cag	caa	739				
Gly	Asp	Glu	Gly	Ala	Glu	Ile	Asp	Ala	Val	Ile	Asp	Arg	Ala	Gln	Gln					
		200					205					210								
gaa	gtc	ttc	gcc	gtt	tcc	caa	aag	aat	cag	agc	gaa	gac	tat	gca	gtc	787				
Glu	Val	Phe	Ala	Val	Ser	Gln	Lys	Asn	Gln	Ser	Glu	Asp	Tyr	Ala	Val					
	215					220					225									
cta	gcc	gat	att	ctg	gat	gaa	acc	atg	gct	gag	ctg	gaa	atg	ctc	aac	835				
Leu	Ala	Asp	Ile	Leu	Asp	Glu	Thr	Met	Ala	Glu	Leu	Glu	Met	Leu	Asn					
230					235					240					245					
gac	ggc	ggc	atc	gcc	acc	ggt	att	cca	acc	ggc	ttc	aaa	gat	ctc	gat	883				
Asp	Gly	Gly	Ile	Ala	Thr	Gly	Ile	Pro	Thr	Gly	Phe	Lys	Asp	Leu	Asp					
				250					255					260						
gac	ctc	acc	aac	ggt	ctg	cgc	ggt	ggc	cag	atg	atc	atc	gtt	gca	gct	931				
Asp	Leu	Thr	Asn	Gly	Leu	Arg	Gly	Gly	Gln	Met	Ile	Ile	Val	Ala	Ala					
			265				270						275							
cgt	cct	ggt	gtg	ggt	aaa	tcc	acc	atc	gcc	ttg	gac	ttc	atg	cgt	tcg	979				
Arg	Pro	Gly	Val	Gly	Lys	Ser	Thr	Ile	Ala	Leu	Asp	Phe	Met	Arg	Ser					
		280					285					290								
gca	tcc	atc	aag	aac	aac	atg	gcg	tct	gtc	att	ttc	tcc	ttg	gaa	atg	1027				
Ala	Ser	Ile	Lys	Asn	Asn	Met	Ala	Ser	Val	Ile	Phe	Ser	Leu	Glu	Met					
	295					300					305									
tcc	aag	tca	gag	atc	gtg	atg	cgt	ttg	ctc	tct	gca	gaa	aca	gaa	atc	1075				
Ser	Lys	Ser	Glu	Ile	Val	Met	Arg	Leu	Leu	Ser	Ala	Glu	Thr	Glu	Ile					
310					315					320					325					
cgc	ctg	gct	gat	atg	cgt	ggt	gga	aag	atg	gat	gaa	acc	gca	tgg	gaa	1123				
Arg	Leu	Ala	Asp	Met	Arg	Gly	Gly	Lys	Met	Asp	Glu	Thr	Ala	Trp	Glu					
				330					335					340						

aag atg gtg cag aag tta gac aag gta gcc cag gca cct ttg ttc atc 1171
 Lys Met Val Gln Lys Leu Asp Lys Val Ala Gln Ala Pro Leu Phe Ile
 345 350 355

gat gac tcc gcg aac ctc acc atg atg gaa atc cgc tcc aag gcc aga 1219
 Asp Asp Ser Ala Asn Leu Thr Met Met Glu Ile Arg Ser Lys Ala Arg
 360 365 370

aag ctg aag cag aag cat gat ctg aaa atg atc gtg gtg gac tac ctc 1267
 Lys Leu Lys Gln Lys His Asp Leu Lys Met Ile Val Val Asp Tyr Leu
 375 380 385

cag ctg atg agc tcc ggt aaa cgc gtg gaa tcc cgt cag cag gaa gtc 1315
 Gln Leu Met Ser Ser Gly Lys Arg Val Glu Ser Arg Gln Gln Glu Val
 390 395 400 405

tcc gag ttc tcc cgt cag ctc aag ctg ctg gcc aaa gaa ctc gat gtg 1363
 Ser Glu Phe Ser Arg Gln Leu Lys Leu Leu Ala Lys Glu Leu Asp Val
 410 415 420

ccg ttg atc gcg att tcc cag ctg aac cgt gga cct gaa tcc cgt acc 1411
 Pro Leu Ile Ala Ile Ser Gln Leu Asn Arg Gly Pro Glu Ser Arg Thr
 425 430 435

gat aag cga cca cag ctt gct gac ctt cgt gaa tcc ggc tcg ctg gag 1459
 Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Ser Leu Glu
 440 445 450

cag gac gcc gat atc gtt atg ctg cta tac cgc cca gac tcc cag gat 1507
 Gln Asp Ala Asp Ile Val Met Leu Leu Tyr Arg Pro Asp Ser Gln Asp
 455 460 465

aag gac gac gag cgc gcg ggc gag gcc gac atc att ttg gct aag cac 1555
 Lys Asp Asp Glu Arg Ala Gly Glu Ala Asp Ile Ile Leu Ala Lys His
 470 475 480 485

cgt ggt ggc ccg atc gat acc gtc cag gtg gcg cac cag ctg cac tat 1603
 Arg Gly Gly Pro Ile Asp Thr Val Gln Val Ala His Gln Leu His Tyr
 490 495 500

tca cgt ttt gtg gac atg gcg cgc ggt taagaaaagt tcatttttct 1650
 Ser Arg Phe Val Asp Met Ala Arg Gly
 505 510

aaa 1653

<210> 68

<211> 510

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

Met Ala Thr Asp Thr His Ala Ala Ser Phe Asp Asp Asp Tyr Val Pro
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Pro Gln Glu Pro Ser Asp Ser Phe Ala Asp Asp Ala His Val Asp Val
 20 25 30

Pro Ala Pro Ala Phe Glu Asp Phe Ser Pro Ala Gln Ala Phe Gly Gln

35					40					45						
Gly	Thr	Arg	Gly	Gly	Asp	Ser	Gln	Gly	Phe	Lys	Lys	Arg	Gly	Arg	Lys	
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Asp	Glu	Ser	Arg	Glu	Tyr	Arg	Asp	Phe	Arg	Gln	Pro	Pro	Tyr	Asp	Asn	
65					70					75					80	
Asp	Ala	Glu	Met	Gly	Val	Leu	Gly	Ala	Met	Leu	Leu	Ser	Pro	Thr	Thr	
85					90					95						
Val	Ile	Asp	Ile	Leu	Asp	Ile	Leu	Thr	Pro	Glu	Asp	Phe	Tyr	Arg	Pro	
100					105					110						
Ser	His	Gln	Leu	Ile	Phe	Gln	Ala	Ile	Ile	Asp	Leu	Phe	Ser	Asp	Asn	
115					120					125						
Arg	Asp	Ile	Asp	Pro	Val	Ile	Val	Ser	Gly	Arg	Leu	Asp	Arg	Thr	Asn	
130					135					140						
Asp	Leu	Asp	Arg	Val	Gly	Gly	Gly	Ala	Tyr	Leu	His	Asp	Leu	Ile	Gln	
145					150					155					160	
Ser	Val	Pro	Thr	Ala	Ala	Asn	Ala	Arg	Tyr	Tyr	Ala	Glu	Ile	Val	Ser	
165					170					175						
Glu	Lys	Ala	Val	Leu	Arg	Arg	Leu	Val	Asp	Ala	Gly	Thr	Arg	Val	Val	
180					185					190						
Gln	Leu	Gly	Tyr	Glu	Gly	Asp	Glu	Gly	Ala	Glu	Ile	Asp	Ala	Val	Ile	
195					200					205						
Asp	Arg	Ala	Gln	Gln	Glu	Val	Phe	Ala	Val	Ser	Gln	Lys	Asn	Gln	Ser	
210					215					220						
Glu	Asp	Tyr	Ala	Val	Leu	Ala	Asp	Ile	Leu	Asp	Glu	Thr	Met	Ala	Glu	
225					230					235					240	
Leu	Glu	Met	Leu	Asn	Asp	Gly	Gly	Ile	Ala	Thr	Gly	Ile	Pro	Thr	Gly	
245					250					255						
Phe	Lys	Asp	Leu	Asp	Asp	Leu	Thr	Asn	Gly	Leu	Arg	Gly	Gly	Gln	Met	
260					265					270						
Ile	Ile	Val	Ala	Ala	Arg	Pro	Gly	Val	Gly	Lys	Ser	Thr	Ile	Ala	Leu	
275					280					285						
Asp	Phe	Met	Arg	Ser	Ala	Ser	Ile	Lys	Asn	Asn	Met	Ala	Ser	Val	Ile	
290					295					300						
Phe	Ser	Leu	Glu	Met	Ser	Lys	Ser	Glu	Ile	Val	Met	Arg	Leu	Leu	Ser	
305					310					315					320	
Ala	Glu	Thr	Glu	Ile	Arg	Leu	Ala	Asp	Met	Arg	Gly	Gly	Lys	Met	Asp	
325					330					335						
Glu	Thr	Ala	Trp	Glu	Lys	Met	Val	Gln	Lys	Leu	Asp	Lys	Val	Ala	Gln	
340					345					350						
Ala	Pro	Leu	Phe	Ile	Asp	Asp	Ser	Ala	Asn	Leu	Thr	Met	Met	Glu	Ile	
355					360					365						

Arg Ser Lys Ala Arg Lys Leu Lys Gln Lys His Asp Leu Lys Met Ile
 370 375 380
 Val Val Asp Tyr Leu Gln Leu Met Ser Ser Gly Lys Arg Val Glu Ser
 385 390 395 400
 Arg Gln Gln Glu Val Ser Glu Phe Ser Arg Gln Leu Lys Leu Leu Ala
 405 410 415
 Lys Glu Leu Asp Val Pro Leu Ile Ala Ile Ser Gln Leu Asn Arg Gly
 420 425 430
 Pro Glu Ser Arg Thr Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu
 435 440 445
 Ser Gly Ser Leu Glu Gln Asp Ala Asp Ile Val Met Leu Leu Tyr Arg
 450 455 460
 Pro Asp Ser Gln Asp Lys Asp Asp Glu Arg Ala Gly Glu Ala Asp Ile
 465 470 475 480
 Ile Leu Ala Lys His Arg Gly Gly Pro Ile Asp Thr Val Gln Val Ala
 485 490 495
 His Gln Leu His Tyr Ser Arg Phe Val Asp Met Ala Arg Gly
 500 505 510

<210> 69

<211> 421

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(421)

<223> RXA01866

<400> 69

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 tggattaaag ccagcctgat tcttcgatct cagctaccac ttg aaa ccc ggc cac 115
 Leu Lys Pro Gly His
 1 5

 cgc gat gac ggc gtc aca gtc ctc atc ccc att cca gtg ctg ggt gga 163
 Arg Asp Asp Gly Val Thr Val Leu Ile Pro Ile Pro Val Leu Gly Gly
 10 15 20

 ctt gat acc gaa ggc ttc gat tgg cta gtt cca ggc tta agg ctt gat 211
 Leu Asp Thr Glu Gly Phe Asp Trp Leu Val Pro Gly Leu Arg Leu Asp
 25 30 35

 ttg gtg acc gag tta atc cgc acc atg cct aag gct tta cga cgc acc 259
 Leu Val Thr Glu Leu Ile Arg Thr Met Pro Lys Ala Leu Arg Arg Thr
 40 45 50

 gtt gtc cct gcc ccg gat ttc gcc gag cgg gtc ttg ccg tta ctg cgt 307
 Val Val Pro Ala Pro Asp Phe Ala Glu Arg Val Leu Pro Leu Leu Arg
 55 60 65

ccc tac atg aca cca ctg acc acc caa ctt gcc gat gca ctc cat acc 355
 Pro Tyr Met Thr Pro Leu Thr Thr Gln Leu Ala Asp Ala Leu His Thr
 70 75 80 85

ctg ggc ggc caa gga atc aac gcc tct gat ttc gat cct gcc aaa ctc 403
 Leu Gly Gly Gln Gly Ile Asn Ala Ser Asp Phe Asp Pro Ala Lys Leu
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<213> Corynebacterium glutamicum

<400> 70

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Pro Val Leu Gly Gly Leu Asp Thr Glu Gly Phe Asp Trp Leu Val Pro
 20 25 30

Gly Leu Arg Leu Asp Leu Val Thr Glu Leu Ile Arg Thr Met Pro Lys
 35 40 45

Ala Leu Arg Arg Thr Val Val Pro Ala Pro Asp Phe Ala Glu Arg Val
 50 55 60

Leu Pro Leu Leu Arg Pro Tyr Met Thr Pro Leu Thr Thr Gln Leu Ala
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Asp Ala Leu His Thr Leu Gly Gly Gln Gly Ile Asn Ala Ser Asp Phe
 85 90 95

Asp Pro Ala Lys Leu Pro Asp His Leu Arg Ile
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<222> (1)..(492)

<223> RXA01867

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 Pro Glu Trp Val Glu Lys Ala Ala Gly Pro Leu Leu Lys His Gln Tyr
 1 5 10 15

tct gaa ccg tat tgg tcc tca aag cgt ggc gct gcc atg gtg cac cgc 96
 Ser Glu Pro Tyr Trp Ser Ser Lys Arg Gly Ala Ala Met Val His Arg
 20 25 30

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aaa tca acg ctc ttc ggt gtg aca att gtt gcc gtc aag gta gtt ccc 144
Lys Ser Thr Leu Phe Gly Val Thr Ile Val Ala Val Lys Val Val Pro
      35              40              45

tac cac acg gtt gat ccc gtg gct gcg cgc gat atg ttc atc cgc cat 192
Tyr His Thr Val Asp Pro Val Ala Ala Arg Asp Met Phe Ile Arg His
      50              55              60

gcc ctc atc gaa ggc gat tgg tcc act cac cac cgc ttc tac cac gac 240
Ala Leu Ile Glu Gly Asp Trp Ser Thr His His Arg Phe Tyr His Asp
      65              70              75              80

aac gtg gcc aaa ttg gag gca atc gga gaa ctt gaa gcc aag gcg cgt 288
Asn Val Ala Lys Leu Glu Ala Ile Gly Glu Leu Glu Ala Lys Ala Arg
      85              90              95

cgc cgc gac atc gtc gta gat gaa gac acc ctg ttt gat ttc tac gat 336
Arg Arg Asp Ile Val Val Asp Glu Asp Thr Leu Phe Asp Phe Tyr Asp
      100              105              110

gcc aag ctt cca agc aac gcc acc acc acc cgc aat ttc gat tcc tgg 384
Ala Lys Leu Pro Ser Asn Ala Thr Thr Thr Arg Asn Phe Asp Ser Trp
      115              120              125

tgg aag aaa aca tca cgc gtc aca cca gat ctt ctc gat ttc gac cca 432
Trp Lys Lys Thr Ser Arg Val Thr Pro Asp Leu Leu Asp Phe Asp Pro
      130              135              140

gat agt ctg atc aag gaa gac gct ggg gcg tta cga aga agc ctt tcc 480
Asp Ser Leu Ile Lys Glu Asp Ala Gly Ala Leu Arg Arg Ser Leu Ser
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cga caa gtg gat taaagccagc ctgattcttc gat 515
Arg Gln Val Asp

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 <212> PRT
 <213> *Corynebacterium glutamicum*

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Lys Ser Thr Leu Phe Gly Val Thr Ile Val Ala Val Lys Val Val Pro
      35              40              45

Tyr His Thr Val Asp Pro Val Ala Ala Arg Asp Met Phe Ile Arg His
      50              55              60

Ala Leu Ile Glu Gly Asp Trp Ser Thr His His Arg Phe Tyr His Asp
      65              70              75              80

Asn Val Ala Lys Leu Glu Ala Ile Gly Glu Leu Glu Ala Lys Ala Arg
      85              90              95

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Arg Arg Asp Ile Val Val Asp Glu Asp Thr Leu Phe Asp Phe Tyr Asp
 100 105 110

Ala Lys Leu Pro Ser Asn Ala Thr Thr Thr Arg Asn Phe Asp Ser Trp
 115 120 125

Trp Lys Lys Thr Ser Arg Val Thr Pro Asp Leu Leu Asp Phe Asp Pro
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Asp Ser Leu Ile Lys Glu Asp Ala Gly Ala Leu Arg Arg Ser Leu Ser
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Arg Gln Val Asp

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<220>

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<222> (101)..(2335)

<223> RXN03166

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 Met Thr Thr Ser Glu
 1 5

act gcc cca tca aag gct tcc ctg tat gaa ctt tta gag ggc gta tcc 163
 Thr Ala Pro Ser Lys Ala Ser Leu Tyr Glu Leu Leu Glu Gly Val Ser
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ctc tcc gac gag cgc acg ttt agg cgc cga ctg tcc aaa gcc cgc gcg 211
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 25 30 35

ccc aag gcg ctt ggt gcg att aag gct gat atc gat aag gca cgc ttg 259
 Pro Lys Ala Leu Gly Ala Ile Lys Ala Asp Ile Asp Lys Ala Arg Leu
 40 45 50

ctt atc gac gaa aag agc cag tta att ccg tct atc acc tac cca gaa 307
 Leu Ile Asp Glu Lys Ser Gln Leu Ile Pro Ser Ile Thr Tyr Pro Glu
 55 60 65

aac ctt ccg gtg agt tcc cgg cgc gat gat atc gcc gag gct atc cgt 355
 Asn Leu Pro Val Ser Ser Arg Arg Asp Asp Ile Ala Glu Ala Ile Arg
 70 75 80 85

gat aat cag gtg gtt att atc gcc ggt gag act ggt tcg ggt aag acg 403
 Asp Asn Gln Val Val Ile Ile Ala Gly Glu Thr Gly Ser Gly Lys Thr
 90 95 100

act cag att cct aag att tgt ttg gac cta ggc cgt ggc cgg cgt ggg 451
 Thr Gln Ile Pro Lys Ile Cys Leu Asp Leu Gly Arg Gly Arg Arg Gly
 105 110 115

ctc att ggc cac aca cag cca cgt cga tta gca gct agg acc gtc gcc	499
Leu Ile Gly His Thr Gln Pro Arg Arg Leu Ala Ala Arg Thr Val Ala	
120 125 130	
gag cgc atc gcc gat gaa ttg ggg caa gac atc ggc gaa tcg gtg ggt	547
Glu Arg Ile Ala Asp Glu Leu Gly Gln Asp Ile Gly Glu Ser Val Gly	
135 140 145	
tat gcg att cgt ttt gat gat cga gtt tcc tcg cat aca tcc gtg aag	595
Tyr Ala Ile Arg Phe Asp Asp Arg Val Ser Ser His Thr Ser Val Lys	
150 155 160 165	
ttg atg acg gat ggt att ttg ctt gct gaa atg cag cgg gat cgt ttc	643
Leu Met Thr Asp Gly Ile Leu Leu Ala Glu Met Gln Arg Asp Arg Phe	
170 175 180	
ctc aat gcg tat gac acc atc atc atc gat gag gcg cat gaa cgt tcc	691
Leu Asn Ala Tyr Asp Thr Ile Ile Ile Asp Glu Ala His Glu Arg Ser	
185 190 195	
ctc aac att gac ttc att ctg ggt tat ttg cgc cag ttg ttg cct aag	739
Leu Asn Ile Asp Phe Ile Leu Gly Tyr Leu Arg Gln Leu Leu Pro Lys	
200 205 210	
cgc cct gat ctt aaa gtc att att acc tcc gca acg att gac cct gag	787
Arg Pro Asp Leu Lys Val Ile Ile Thr Ser Ala Thr Ile Asp Pro Glu	
215 220 225	
cgt ttc gcg gag cac ttt gct gat gct tct gga aaa cca gca cca att	835
Arg Phe Ala Glu His Phe Ala Asp Ala Ser Gly Lys Pro Ala Pro Ile	
230 235 240 245	
atc gag gtc tcc ggc cgc acc ttc ccg gta gag atc cgt tat cgc cca	883
Ile Glu Val Ser Gly Arg Thr Phe Pro Val Glu Ile Arg Tyr Arg Pro	
250 255 260	
ctt gag gta tta gac ggc gat aaa att atc gat acc gat ccc ctt gac	931
Leu Glu Val Leu Asp Gly Asp Lys Ile Ile Asp Thr Asp Pro Leu Asp	
265 270 275	
ggc ttg tgt tct gct ttg gaa gag ctc atg gct gaa ggc gac ggc gat	979
Gly Leu Cys Ser Ala Leu Glu Glu Leu Met Ala Glu Gly Asp Gly Asp	
280 285 290	
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Ile Leu Cys Phe Phe Ala Gly Glu Arg Asp Ile Arg Asp Ala Met Glu	
295 300 305	
gca atc gag gcc cga cgc tgg aaa ggt gtg gaa gtc act ccc ctg ttt	1075
Ala Ile Glu Ala Arg Arg Trp Lys Gly Val Glu Val Thr Pro Leu Phe	
310 315 320 325	
ggc cgc ctg tcc aac cag gag cag cac cgt gta ttt agc ccg cac tct	1123
Gly Arg Leu Ser Asn Gln Glu Gln His Arg Val Phe Ser Pro His Ser	
330 335 340	
ggt cga cgc att gtg ctt tcc acc aat atc gca gag aca tcc ctg acg	1171
Gly Arg Arg Ile Val Leu Ser Thr Asn Ile Ala Glu Thr Ser Leu Thr	
345 350 355	
gtt ccg ggc att cac tac gtg gtt gat acc ggt acg gcg cgt atc tct	1219

Val	Pro	Gly	Ile	His	Tyr	Val	Val	Asp	Thr	Gly	Thr	Ala	Arg	Ile	Ser		
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cgt	tat	tca	gtg	cgc	acc	aag	gtg	cag	cgc	ctt	ccg	att	gag	aac	att	1267	
Arg	Tyr	Ser	Val	Arg	Thr	Lys	Val	Gln	Arg	Leu	Pro	Ile	Glu	Asn	Ile		
	375					380					385						
tcc	cag	gcc	agc	gca	aac	cag	cgt	tct	ggg	cgt	tgt	ggg	cgt	gtc	gca	1315	
Ser	Gln	Ala	Ser	Ala	Asn	Gln	Arg	Ser	Gly	Arg	Cys	Gly	Arg	Val	Ala		
390					395				400					405			
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Asp	Gly	Ile	Ala	Ile	Arg	Leu	Tyr	Ser	Glu	Asp	Asp	Phe	Asn	Ser	Arg		
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Pro	Glu	Phe	Thr	Asp	Pro	Glu	Ile	Leu	Arg	Thr	Asn	Leu	Ala	Ser	Val		
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Ile	Leu	Arg	Met	Ala	Ser	Leu	Arg	Leu	Gly	Asp	Ile	Asn	Asp	Phe	Pro		
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Phe	Val	Gln	Ala	Pro	Glu	Gln	Arg	Ser	Ile	Arg	Asp	Gly	Ile	Leu	Leu		
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ctc	cac	gag	ttg	ggc	gca	ctc	acc	gac	gac	acc	caa	gcc	gat	ggg	tca	1555	
Leu	His	Glu	Leu	Gly	Ala	Leu	Thr	Asp	Asp	Thr	Gln	Ala	Asp	Gly	Ser		
470					475					480					485		
ccg	cag	ctc	acc	cag	atc	ggg	aaa	gac	tta	gcc	aac	atc	cca	gtc	gat	1603	
Pro	Gln	Leu	Thr	Gln	Ile	Gly	Lys	Asp	Leu	Ala	Asn	Ile	Pro	Val	Asp		
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ccc	cgc	atg	gcc	cgc	atg	ctc	gta	gaa	gcc	aac	act	cta	ggc	tgc	ctg	1651	
Pro	Arg	Met	Ala	Arg	Met	Leu	Val	Glu	Ala	Asn	Thr	Leu	Gly	Cys	Leu		
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cat	tct	gtc	atg	gtc	att	gtg	tcc	gct	ctg	acg	att	caa	gat	gtt	cgc	1699	
His	Ser	Val	Met	Val	Ile	Val	Ser	Ala	Leu	Thr	Ile	Gln	Asp	Val	Arg		
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gaa	cgc	ccc	ctg	gaa	ttc	caa	gcc	caa	gct	gat	caa	gcc	cac	gct	agg	1747	
Glu	Arg	Pro	Leu	Glu	Phe	Gln	Ala	Gln	Ala	Asp	Gln	Ala	His	Ala	Arg		
	535					540					545						
ttc	aag	gac	acc	acc	tca	gat	ttc	tta	ggc	ttt	ttg	aaa	ctg	tgg	gag	1795	
Phe	Lys	Asp	Thr	Thr	Ser	Asp	Phe	Leu	Gly	Phe	Leu	Lys	Leu	Trp	Glu		
550					555					560					565		
tac	atc	gcc	gat	cag	cgc	aat	caa	agc	agc	ggc	aat	tcc	ttc	cgc	aag	1843	
Tyr	Ile	Ala	Asp	Gln	Arg	Asn	Gln	Ser	Ser	Gly	Asn	Ser	Phe	Arg	Lys		
				570				575						580			
cag	atg	aaa	aaa	gaa	ttc	ctc	cac	tac	atg	cgt	atc	cgc	gag	tgg	tgg	1891	
Gln	Met	Lys	Lys	Glu	Phe	Leu	His	Tyr	Met	Arg	Ile	Arg	Glu	Trp	Trp		
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gat	ttg	gtg	cgc	caa	tta	gag	cag	att	ggc	cag	caa	ctt	ggg	tgg	gca	1939	
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Lys Lys Glu Gln Val Ala Gly Thr Ala Ser Pro Asp Ile Ile His Gln			
615	620	625	
tcc ttg ctc acc ggt ctg ttc tcg caa atc ggt tcc cgt gat ggt gag			2035
Ser Leu Leu Thr Gly Leu Phe Ser Gln Ile Gly Ser Arg Asp Gly Glu			
630	635	640	645
agc aaa gaa ttc act gga gcc aga ggt acc aaa ttc ttg gtc ttt cct			2083
Ser Lys Glu Phe Thr Gly Ala Arg Gly Thr Lys Phe Leu Val Phe Pro			
650	655	660	
ggg tct gcg cta acc aag aag ccg cca cag ttc atc atg gct ggc caa			2131
Gly Ser Ala Leu Thr Lys Lys Pro Pro Gln Phe Ile Met Ala Gly Gln			
665	670	675	
ttg gta gaa acc tca cgt ttg tgg gct cgc gat gta gcc aag att gaa			2179
Leu Val Glu Thr Ser Arg Leu Trp Ala Arg Asp Val Ala Lys Ile Glu			
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cca gag tgg gtg gaa aaa gca gcc ggc cca ttg ctc aag cac caa tac			2227
Pro Glu Trp Val Glu Lys Ala Ala Gly Pro Leu Leu Lys His Gln Tyr			
695	700	705	
tct gaa ccg tat tgg tcc tca aag cgt ggc ggc tgc cat ggt gca ccg			2275
Ser Glu Pro Tyr Trp Ser Ser Lys Arg Gly Gly Cys His Gly Ala Pro			
710	715	720	725
caa atc aac gct ctt cgg tgt gac aat tgt tgc cgt caa ggt agt tcc			2323
Gln Ile Asn Ala Leu Arg Cys Asp Asn Cys Cys Arg Gln Gly Ser Ser			
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Leu Pro His Gly			
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<212> PRT

<213> Corynebacterium glutamicum

<400> 74

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Asp Lys Ala Arg Leu Leu Ile Asp Glu Lys Ser Gln Leu Ile Pro Ser			
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Ile Thr Tyr Pro Glu Asn Leu Pro Val Ser Ser Arg Arg Asp Asp Ile			
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Ala Glu Ala Ile Arg Asp Asn Gln Val Val Ile Ile Ala Gly Glu Thr			

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Arg	Gly	Arg	Arg	Gly	Leu	Ile	Gly	His	Thr	Gln	Pro	Arg	Arg	Leu	Ala	
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Ala	Arg	Thr	Val	Ala	Glu	Arg	Ile	Ala	Asp	Glu	Leu	Gly	Gln	Asp	Ile	
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Gly	Glu	Ser	Val	Gly	Tyr	Ala	Ile	Arg	Phe	Asp	Asp	Arg	Val	Ser	Ser	
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His	Thr	Ser	Val	Lys	Leu	Met	Thr	Asp	Gly	Ile	Leu	Leu	Ala	Glu	Met	
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Gln	Arg	Asp	Arg	Phe	Leu	Asn	Ala	Tyr	Asp	Thr	Ile	Ile	Ile	Asp	Glu	
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Ala	His	Glu	Arg	Ser	Leu	Asn	Ile	Asp	Phe	Ile	Leu	Gly	Tyr	Leu	Arg	
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Gln	Leu	Leu	Pro	Lys	Arg	Pro	Asp	Leu	Lys	Val	Ile	Ile	Thr	Ser	Ala	
				210					215					220		
Thr	Ile	Asp	Pro	Glu	Arg	Phe	Ala	Glu	His	Phe	Ala	Asp	Ala	Ser	Gly	
				225					230					235		
Lys	Pro	Ala	Pro	Ile	Ile	Glu	Val	Ser	Gly	Arg	Thr	Phe	Pro	Val	Glu	
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Ile	Arg	Tyr	Arg	Pro	Leu	Glu	Val	Leu	Asp	Gly	Asp	Lys	Ile	Ile	Asp	
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Thr	Asp	Pro	Leu	Asp	Gly	Leu	Cys	Ser	Ala	Leu	Glu	Glu	Leu	Met	Ala	
				275					280					285		
Glu	Gly	Asp	Gly	Asp	Ile	Leu	Cys	Phe	Phe	Ala	Gly	Glu	Arg	Asp	Ile	
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Arg	Asp	Ala	Met	Glu	Ala	Ile	Glu	Ala	Arg	Arg	Trp	Lys	Gly	Val	Glu	
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Glu	Thr	Ser	Leu	Thr	Val	Pro	Gly	Ile	His	Tyr	Val	Val	Asp	Thr	Gly	
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Pro	Ile	Glu	Asn	Ile	Ser	Gln	Ala	Ser	Ala	Asn	Gln	Arg	Ser	Gly	Arg	
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Cys	Gly	Arg	Val	Ala	Asp	Gly	Ile	Ala	Ile	Arg	Leu	Tyr	Ser	Glu	Asp	
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Asp Phe Asn Ser Arg Pro Glu Phe Thr Asp Pro Glu Ile Leu Arg Thr
420 425 430

Asn Leu Ala Ser Val Ile Leu Arg Met Ala Ser Leu Arg Leu Gly Asp
435 440 445

Ile Asn Asp Phe Pro Phe Val Gln Ala Pro Glu Gln Arg Ser Ile Arg
450 455 460

Asp Gly Ile Leu Leu Leu His Glu Leu Gly Ala Leu Thr Asp Asp Thr
465 470 475 480

Gln Ala Asp Gly Ser Pro Gln Leu Thr Gln Ile Gly Lys Asp Leu Ala
485 490 495

Asn Ile Pro Val Asp Pro Arg Met Ala Arg Met Leu Val Glu Ala Asn
500 505 510

Thr Leu Gly Cys Leu His Ser Val Met Val Ile Val Ser Ala Leu Thr
515 520 525

Ile Gln Asp Val Arg Glu Arg Pro Leu Glu Phe Gln Ala Gln Ala Asp
530 535 540

Gln Ala His Ala Arg Phe Lys Asp Thr Thr Ser Asp Phe Leu Gly Phe
545 550 555 560

Leu Lys Leu Trp Glu Tyr Ile Ala Asp Gln Arg Asn Gln Ser Ser Gly
565 570 575

Asn Ser Phe Arg Lys Gln Met Lys Lys Glu Phe Leu His Tyr Met Arg
580 585 590

Ile Arg Glu Trp Trp Asp Leu Val Arg Gln Leu Glu Gln Ile Gly Gln
595 600 605

Gln Leu Gly Trp Ala Lys Lys Glu Gln Val Ala Gly Thr Ala Ser Pro
610 615 620

Asp Ile Ile His Gln Ser Leu Leu Thr Gly Leu Phe Ser Gln Ile Gly
625 630 635 640

Ser Arg Asp Gly Glu Ser Lys Glu Phe Thr Gly Ala Arg Gly Thr Lys
645 650 655

Phe Leu Val Phe Pro Gly Ser Ala Leu Thr Lys Lys Pro Pro Gln Phe
660 665 670

Ile Met Ala Gly Gln Leu Val Glu Thr Ser Arg Leu Trp Ala Arg Asp
675 680 685

Val Ala Lys Ile Glu Pro Glu Trp Val Glu Lys Ala Ala Gly Pro Leu
690 695 700

Leu Lys His Gln Tyr Ser Glu Pro Tyr Trp Ser Ser Lys Arg Gly Gly
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Cys His Gly Ala Pro Gln Ile Asn Ala Leu Arg Cys Asp Asn Cys Cys
725 730 735

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<211> 1939

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<220>

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<222> (92)..(1939)

<223> FRXA00361

<400> 75

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Met Thr Thr Ser Glu Thr Ala
1 5

cca tca aag gct tcc ctg tat gaa ctt tta gag ggc gta tcc ctc tcc 160
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Asp Glu Arg Thr Phe Arg Arg Arg Leu Ser Lys Ala Arg Ala Pro Lys
25 30 35

gcg ctt ggt gcg att aag gct gat atc gat aag gca cgc ttg ctt atc 256
Ala Leu Gly Ala Ile Lys Ala Asp Ile Asp Lys Ala Arg Leu Leu Ile
40 45 50 55

gac gaa aag agc cag tta att ccg tct atc acc tac cca gaa aac ctt 304
Asp Glu Lys Ser Gln Leu Ile Pro Ser Ile Thr Tyr Pro Glu Asn Leu
60 65 70

ccg gtg agt tcc cgg cgc gat gat atc gcc gag gct atc cgt gat aat 352
Pro Val Ser Ser Arg Arg Asp Asp Ile Ala Glu Ala Ile Arg Asp Asn
75 80 85

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Gln Val Val Ile Ile Ala Gly Glu Thr Gly Ser Gly Lys Thr Thr Gln
90 95 100

att cct aag att tgt ttg gac cta ggc cgt ggc cgg cgt ggg ctc att 448
Ile Pro Lys Ile Cys Leu Asp Leu Gly Arg Gly Arg Arg Gly Leu Ile
105 110 115

ggc cac aca cag cca cgt cga tta gca gct agg acc gtc gcc gag cgc 496
Gly His Thr Gln Pro Arg Arg Leu Ala Ala Arg Thr Val Ala Glu Arg
120 125 130 135

atc gcc gat gaa ttg ggg caa gac atc ggc gaa tcg gtg ggt tat gcg 544
Ile Ala Asp Glu Leu Gly Gln Asp Ile Gly Glu Ser Val Gly Tyr Ala
140 145 150

att cgt ttt gat gat cga gtt tcc tcg cat aca tcc gtg aag ttg atg 592
Ile Arg Phe Asp Asp Arg Val Ser Ser His Thr Ser Val Lys Leu Met
155 160 165

acg gat ggt att ttg ctt gct gaa atg cag cgg gat cgt ttc ctc aat 640

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Ala	Tyr	Asp	Thr	Ile	Ile	Ile	Asp	Glu	Ala	His	Glu	Arg	Ser	Leu	Asn		
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att	gac	ttc	att	ctg	ggt	tat	ttg	cgc	cag	ttg	ttg	cct	aag	cgc	cct	736	
Ile	Asp	Phe	Ile	Leu	Gly	Tyr	Leu	Arg	Gln	Leu	Leu	Pro	Lys	Arg	Pro		
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gat	ctt	aaa	gtc	att	att	acc	tcc	gca	acg	att	gac	cct	gag	cgt	ttc	784	
Asp	Leu	Lys	Val	Ile	Ile	Thr	Ser	Ala	Thr	Ile	Asp	Pro	Glu	Arg	Phe		
			220						225					230			
gcg	gag	cac	ttt	gct	gat	gct	tct	gga	aaa	cca	gca	cca	att	atc	gag	832	
Ala	Glu	His	Phe	Ala	Asp	Ala	Ser	Gly	Lys	Pro	Ala	Pro	Ile	Ile	Glu		
			235					240					245				
gtc	tcc	ggc	cgc	acc	ttc	ccg	gta	gag	atc	cgt	tat	cgc	cca	ctt	gag	880	
Val	Ser	Gly	Arg	Thr	Phe	Pro	Val	Glu	Ile	Arg	Tyr	Arg	Pro	Leu	Glu		
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gta	tta	gac	ggc	gat	aaa	att	atc	gat	acc	gat	ccc	ctt	gac	ggc	ttg	928	
Val	Leu	Asp	Gly	Asp	Lys	Ile	Ile	Asp	Thr	Asp	Pro	Leu	Asp	Gly	Leu		
	265					270					275						
tgt	tct	gct	ttg	gaa	gag	ctc	atg	gct	gaa	ggc	gac	ggc	gat	atc	ctc	976	
Cys	Ser	Ala	Leu	Glu	Glu	Leu	Met	Ala	Glu	Gly	Asp	Gly	Asp	Ile	Leu		
280					285					290					295		
tgc	ttc	ttt	gcc	ggt	gag	cgt	gat	atc	cgc	gat	gcc	atg	gag	gca	atc	1024	
Cys	Phe	Phe	Ala	Gly	Glu	Arg	Asp	Ile	Arg	Asp	Ala	Met	Glu	Ala	Ile		
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gag	gcc	cga	cgc	tgg	aaa	ggt	gtg	gaa	gtc	act	ccc	ctg	ttt	ggc	cgc	1072	
Glu	Ala	Arg	Arg	Trp	Lys	Gly	Val	Glu	Val	Thr	Pro	Leu	Phe	Gly	Arg		
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ctg	tcc	aac	cag	gag	cag	cac	cgt	gta	ttt	agc	ccg	cac	tct	ggt	cga	1120	
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Arg	Ile	Val	Leu	Ser	Thr	Asn	Ile	Ala	Glu	Thr	Ser	Leu	Thr	Val	Pro		
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Gly	Ile	His	Tyr	Val	Val	Asp	Thr	Gly	Thr	Ala	Arg	Ile	Ser	Arg	Tyr		
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tca	gtg	cgc	acc	aag	gtg	cag	cgc	ctt	ccg	att	gag	aac	att	tcc	cag	1264	
Ser	Val	Arg	Thr	Lys	Val	Gln	Arg	Leu	Pro	Ile	Glu	Asn	Ile	Ser	Gln		
				380					385					390			
gcc	agc	gca	aac	cag	cgt	tct	ggt	cgt	tgt	ggt	cgt	gtc	gca	gac	ggt	1312	
Ala	Ser	Ala	Asn	Gln	Arg	Ser	Gly	Arg	Cys	Gly	Arg	Val	Ala	Asp	Gly		
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Ile	Ala	Ile	Arg	Leu	Tyr	Ser	Glu	Asp	Asp	Phe	Asn	Ser	Arg	Pro	Glu		

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cgc atg gcg tcg ctg cgt ctt ggc gat att aat gat ttc ccc ttc gtc Arg Met Ala Ser Leu Arg Leu Gly Asp Ile Asn Asp Phe Pro Phe Val 440 445 450 455			1456
caa gcc cca gag caa cgc tcc atc agg gat ggt att ttg ctg ctc cac Gln Ala Pro Glu Gln Arg Ser Ile Arg Asp Gly Ile Leu Leu Leu His 460 465 470			1504
gag ttg ggc gca ctc acc gac gac acc caa gcc gat ggt tca ccg cag Glu Leu Gly Ala Leu Thr Asp Asp Thr Gln Ala Asp Gly Ser Pro Gln 475 480 485			1552
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atg gcc cgc atg ctc gta gaa gcc aac act cta ggc tgc ctg cat tct Met Ala Arg Met Leu Val Glu Ala Asn Thr Leu Gly Cys Leu His Ser 505 510 515			1648
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35 40 45
Asp Lys Ala Arg Leu Leu Ile Asp Glu Lys Ser Gln Leu Ile Pro Ser
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Ile Thr Tyr Pro Glu Asn Leu Pro Val Ser Ser Arg Arg Asp Asp Ile
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Ala Glu Ala Ile Arg Asp Asn Gln Val Val Ile Ile Ala Gly Glu Thr
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Gly Ser Gly Lys Thr Thr Gln Ile Pro Lys Ile Cys Leu Asp Leu Gly
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Arg Gly Arg Arg Gly Leu Ile Gly His Thr Gln Pro Arg Arg Leu Ala
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Ala Arg Thr Val Ala Glu Arg Ile Ala Asp Glu Leu Gly Gln Asp Ile
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Gly Glu Ser Val Gly Tyr Ala Ile Arg Phe Asp Asp Arg Val Ser Ser
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His Thr Ser Val Lys Leu Met Thr Asp Gly Ile Leu Leu Ala Glu Met
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Gln Arg Asp Arg Phe Leu Asn Ala Tyr Asp Thr Ile Ile Ile Asp Glu
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Ala His Glu Arg Ser Leu Asn Ile Asp Phe Ile Leu Gly Tyr Leu Arg
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Gln Leu Leu Pro Lys Arg Pro Asp Leu Lys Val Ile Ile Thr Ser Ala
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Thr Ile Asp Pro Glu Arg Phe Ala Glu His Phe Ala Asp Ala Ser Gly
225 230 235 240
Lys Pro Ala Pro Ile Ile Glu Val Ser Gly Arg Thr Phe Pro Val Glu
245 250 255
Ile Arg Tyr Arg Pro Leu Glu Val Leu Asp Gly Asp Lys Ile Ile Asp
260 265 270
Thr Asp Pro Leu Asp Gly Leu Cys Ser Ala Leu Glu Glu Leu Met Ala
275 280 285
Glu Gly Asp Gly Asp Ile Leu Cys Phe Phe Ala Gly Glu Arg Asp Ile
290 295 300
Arg Asp Ala Met Glu Ala Ile Glu Ala Arg Arg Trp Lys Gly Val Glu
305 310 315 320

Val Thr Pro Leu Phe Gly Arg Leu Ser Asn Gln Glu Gln His Arg Val
325 330 335

Phe Ser Pro His Ser Gly Arg Arg Ile Val Leu Ser Thr Asn Ile Ala
340 345 350

Glu Thr Ser Leu Thr Val Pro Gly Ile His Tyr Val Val Asp Thr Gly
355 360 365

Thr Ala Arg Ile Ser Arg Tyr Ser Val Arg Thr Lys Val Gln Arg Leu
370 375 380

Pro Ile Glu Asn Ile Ser Gln Ala Ser Ala Asn Gln Arg Ser Gly Arg
385 390 395 400

Cys Gly Arg Val Ala Asp Gly Ile Ala Ile Arg Leu Tyr Ser Glu Asp
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Asp Phe Asn Ser Arg Pro Glu Phe Thr Asp Pro Glu Ile Leu Arg Thr
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Asn Leu Ala Ser Val Ile Leu Arg Met Ala Ser Leu Arg Leu Gly Asp
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Ile Asn Asp Phe Pro Phe Val Gln Ala Pro Glu Gln Arg Ser Ile Arg
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Asp Gly Ile Leu Leu Leu His Glu Leu Gly Ala Leu Thr Asp Asp Thr
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Gln Ala Asp Gly Ser Pro Gln Leu Thr Gln Ile Gly Lys Asp Leu Ala
485 490 495

Asn Ile Pro Val Asp Pro Arg Met Ala Arg Met Leu Val Glu Ala Asn
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Thr Leu Gly Cys Leu His Ser Val Met Val Ile Val Ser Ala Leu Thr
515 520 525

Ile Gln Asp Val Arg Glu Arg Pro Leu Glu Phe Gln Ala Gln Ala Asp
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Gln Ala His Ala Arg Phe Lys Asp Thr Thr Ser Asp Phe Leu Gly Phe
545 550 555 560

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Asn Ser Phe Arg Lys Gln Met Lys Lys Glu Phe Leu His Tyr Met Arg
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Met Ser Ser Arg Ile
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Gly Asn Phe Leu Ile Asn Arg Ile Ser Thr Gly Leu Pro Val Glu Asn
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Ile Ile Pro His Leu Gln Glu Ala Phe Ser Ala Gly Pro Lys Asn Leu
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gtc att cag gcc cct ccc ggc aca gga aaa acg aca ctt ctc ccc cca 259
Val Ile Gln Ala Pro Pro Gly Thr Gly Lys Thr Thr Leu Leu Pro Pro
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Leu Val Ala Asn Ile Leu Cys Asn Glu Gly Ala Gly Asn Ala Thr Pro
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Thr Lys Val Leu Val Thr Ala Pro Arg Arg Val Ala Val Arg Ala Ala
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Met Thr Pro Gly Val Leu Ile Arg Gln Leu Leu Asn Asn Pro Glu Leu
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ccc ggc atc ggc gct gtg att atc gat gaa gtc cac gaa cgt caa ctc 547
Pro Gly Ile Gly Ala Val Ile Ile Asp Glu Val His Glu Arg Gln Leu
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Asp Ser Asp Leu Leu Gly Met Leu Ala Glu Leu Ser Gln Leu Arg
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Asp Asp Phe Ser Leu Ile Ala Met Ser Ala Thr Leu Asp Ser Asp Lys
170 175 180

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185 190 195

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Phe Pro Leu Asp Ile Ser Tyr Ala Pro Ala Arg Ala Pro Arg Leu Asn	
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Ala Lys Gly Val Asp Trp Asp Phe Leu Asp His Met Ala Gln Lys Thr	
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His Asp Ala Val Thr His Ser Glu His Ser Ala Leu Ile Phe Val Pro	
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Gly Val Arg Glu Ile Asp Arg Val Met Ser Thr Leu Lys Ser Leu Gly	
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cat aat aat gtt ttc cca ctt cat ggc caa ctc agc ccg acc gaa caa	931
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Asp Arg Ala Leu Ala Pro Ser Gln Gln Gln Arg Ile Ile Val Ser Thr	
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Pro Val Ala Glu Ser Ser Leu Thr Val Pro Gly Val Arg Ile Gly Val	
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Asp Ser Gly Leu Ser Arg Ser Pro Lys Arg Asp Ser Ala Arg Gly Met	
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Thr Gly Leu Ile Thr Ser Ser Cys Ala Gln Ala Ser Ala Gly Gln Arg	
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Ala Gly Arg Ala Gly Arg Glu Gly Pro Gly Gln Ile Ile Arg Cys Tyr	
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Ser Glu Glu Asp Phe Ser His Phe Pro Arg Phe Val Thr Pro Glu Ile	
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Thr Ser Pro Ala Asp Leu Pro Leu Leu Asp Gln Pro Pro His Ala Ala	
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Trp Thr Ala Ala Gln Gln Ile Leu Arg Leu Ile Gly Ala Leu Glu Gly	
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Ile	Leu	Ala	Val	Val	Ser	Glu	Asn	Pro	Gln	Gly	Asp	Val	Glu	Lys	Gln	
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caa	ccc	gac	aag	cgt	gaa	gtg	gaa	cgc	ctt	cgc	cgt	ttg	gca	cct	gcg	1555
Gln	Pro	Asp	Lys	Arg	Glu	Val	Glu	Arg	Leu	Arg	Arg	Leu	Ala	Pro	Ala	
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Gly	Thr	Arg	Ala	Arg	Leu	Met	Asp	Ser	Asp	Leu	Lys	Asp	Ala	Glu	Trp	
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Ile	Ser	Val	Ala	Ala	Ile	Asn	Arg	Ser	Gln	Asn	Ser	Ala	Ile	Ile	Arg	
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Val	Glu	Glu	Thr	Arg	Ala	Ile	Phe	Val	Asn	Gly	Lys	Val	Gln	Ala	Arg	
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Lys	Val	Lys	Ala	Ala	Gly	Ala	Ile	Glu	Leu	Ser	Ser	Thr	Pro	Thr	Lys	
			585					590					595			
cca	aca	ccc	gcc	gaa	gcc	tcg	gaa	aca	atc	gcc	aca	gcc	ctt	gcc	aaa	1939
Pro	Thr	Pro	Ala	Glu	Ala	Ser	Glu	Thr	Ile	Ala	Thr	Ala	Leu	Ala	Lys	
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Gly	Gly	Ile	Asp	Leu	Phe	His	Phe	Ser	Asp	Lys	Ala	Ala	Ser	Leu	Arg	
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Ile	Glu	Thr	Ala	Asp	Pro	His	Leu	Trp	Leu	Ser	Pro	Glu	Ile	Glu	Ala	
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ctc	agc	cac	gga	aca	cga	cta	aac	aac	atc	gat	atg	tat	ccc	gca	ctc	2131
Leu	Ser	His	Gly	Thr	Arg	Leu	Asn	Asn	Ile	Asp	Met	Tyr	Pro	Ala	Leu	
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 680 685 690

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 760 765 770

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Gly Pro Lys Asn Leu Val Ile Gln Ala Pro Pro Gly Thr Gly Lys Thr
 35 40 45

Thr Leu Leu Pro Pro Leu Val Ala Asn Ile Leu Cys Asn Glu Gly Ala
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Gly Asn Ala Thr Pro Thr Lys Val Leu Val Thr Ala Pro Arg Arg Val
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Ala Val Arg Ala Ala Ala Arg Arg Leu Ala Gln Leu Asp Asp Ser Gln
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Leu Gly Thr Lys Val Gly Phe Ser Val Arg Gly Glu His Ile Ser Gly
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Ser His Val Gln Phe Met Thr Pro Gly Val Leu Ile Arg Gln Leu Leu
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Asn Asn Pro Glu Leu Pro Gly Ile Gly Ala Val Ile Ile Asp Glu Val
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Leu Asp Ser Asp Lys Phe Ala Asn Leu Leu Asp Ala Gln Val Leu Ser
180 185 190

Val Glu Ala Pro Ile Phe Pro Leu Asp Ile Ser Tyr Ala Pro Ala Arg
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210 215 220

Met Ala Gln Lys Thr His Asp Ala Val Thr His Ser Glu His Ser Ala
225 230 235 240

Leu Ile Phe Val Pro Gly Val Arg Glu Ile Asp Arg Val Met Ser Thr
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Leu Lys Ser Leu Gly His Asn Asn Val Phe Pro Leu His Gly Gln Leu
260 265 270

Ser Pro Thr Glu Gln Asp Arg Ala Leu Ala Pro Ser Gln Gln Gln Arg
275 280 285

Ile Ile Val Ser Thr Pro Val Ala Glu Ser Ser Leu Thr Val Pro Gly
290 295 300

Val Arg Ile Gly Val Asp Ser Gly Leu Ser Arg Ser Pro Lys Arg Asp
305 310 315 320

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 Tyr Leu Leu Ala Ser Gly Thr Arg Ala Arg Leu Met Asp Ser Asp Leu
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 Lys Asp Ala Glu Trp Ile Ser Val Ala Ala Ile Asn Arg Ser Gln Asn
 530 535 540
 Ser Ala Ile Ile Arg Ala Ala Ala Arg Ile Ser Glu Asp Asp Ala Ile
 545 550 555 560
 Asp Ile Ile Gly Val Val Glu Glu Thr Arg Ala Ile Phe Val Asn Gly
 565 570 575
 Lys Val Gln Ala Arg Lys Val Lys Ala Ala Gly Ala Ile Glu Leu Ser
 580 585 590
 Ser Thr Pro Thr Lys Pro Thr Pro Ala Glu Ala Ser Glu Thr Ile Ala
 595 600 605
 Thr Ala Leu Ala Lys Gly Gly Ile Asp Leu Phe His Phe Ser Asp Lys
 610 615 620
 Ala Ala Ser Leu Arg Asp Arg Leu Lys Phe Ile His Glu His Arg Gly
 625 630 635 640
 Glu Pro Trp Pro Asp Ile Glu Thr Ala Asp Pro His Leu Trp Leu Ser
 645 650 655
 Pro Glu Ile Glu Ala Leu Ser His Gly Thr Arg Leu Asn Asn Ile Asp
 660 665 670
 Met Tyr Pro Ala Leu Gln Arg Leu Leu Pro Trp Pro Glu Ala Thr Asn
 675 680 685
 Phe Glu Glu Phe Ala Pro Ser His Leu Ser Val Pro Ser Gly Asn Gln
 690 695 700
 His Arg Leu Asp Tyr Ser Ser Gly Arg Pro Val Ile Arg Val Lys Leu
 705 710 715 720
 Gln Glu Cys Phe Gly Leu Glu Glu Ser Pro Gln Leu Cys Gly Ile Pro
 725 730 735
 Val Gln Phe His Leu Leu Ser Pro Ala Gly Arg Pro Leu Ala Val Thr
 740 745 750
 Asp Asp Leu Arg Ser Phe Trp Ser Gly Pro Tyr Ser Gln Val Arg Ala
 755 760 765
 Glu Met Arg Gly Arg Tyr Pro Lys His Pro Trp Pro Glu Asp Pro Trp

770

775

780

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<213> Corynebacterium glutamicum

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<222> (101)..(2488)

<223> FRXA02293

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gatgtgttca ctcagcaaatt tcttaatgta caggcaattg atg agt tca aga att 115
 Met Ser Ser Arg Ile
 1 5

ggc aat ttt ctt ata aat cgc att tcc acg ggc ctg ccc gta gaa aat 163
 Gly Asn Phe Leu Ile Asn Arg Ile Ser Thr Gly Leu Pro Val Glu Asn
 10 15 20

att atc cct cac ctg caa gaa gct ttt tcg gcc gga cct aaa aac ctt 211
 Ile Ile Pro His Leu Gln Glu Ala Phe Ser Ala Gly Pro Lys Asn Leu
 25 30 35

gtc att cag gcc cct ccc ggc aca gga aaa acg aca ctt ctc ccc cca 259
 Val Ile Gln Ala Pro Pro Gly Thr Gly Lys Thr Thr Leu Leu Pro Pro
 40 45 50

tta gta gct aac atc tta tgt aat gaa gga gcg gga aat gcc acc cca 307
 Leu Val Ala Asn Ile Leu Cys Asn Glu Gly Ala Gly Asn Ala Thr Pro
 55 60 65

acc aag gtt tta gta acg gca cct cgt cgt gtg gcc gtc cga gca gca 355
 Thr Lys Val Leu Val Thr Ala Pro Arg Arg Val Ala Val Arg Ala Ala
 70 75 80 85

gct cgc aga ctc gcc caa cta gat gat agc cag ctc gga aca aaa gtg 403
 Ala Arg Arg Leu Ala Gln Leu Asp Asp Ser Gln Leu Gly Thr Lys Val
 90 95 100

gga ttc agc gtg cgt ggt gaa cat att tca ggc tcc cac gtg caa ttt 451
 Gly Phe Ser Val Arg Gly Glu His Ile Ser Gly Ser His Val Gln Phe
 105 110 115

atg acc ccc ggt gtg tta atc cgc cag ctc tta aac aac cca gaa tta 499
 Met Thr Pro Gly Val Leu Ile Arg Gln Leu Leu Asn Asn Pro Glu Leu
 120 125 130

ccc ggc atc ggc gct gtg att atc gat gaa gtc cac gaa cgt caa ctc 547
 Pro Gly Ile Gly Ala Val Ile Ile Asp Glu Val His Glu Arg Gln Leu
 135 140 145

gat tcc gat cta ctg cta gga atg ctt gct gaa ctc agt caa ctg cgc 595
 Asp Ser Asp Leu Leu Leu Gly Met Leu Ala Glu Leu Ser Gln Leu Arg

150	155	160	165	
gac gat ttc tcc ctc atc gcc atg tcc gca acc tta gat tca gat aaa				643
Asp Asp Phe Ser Leu Ile Ala Met Ser Ala Thr Leu Asp Ser Asp Lys	170	175	180	
ttc gca aac tta tta gac gct cag gtc ctt agt gtt gaa gca ccg att				691
Phe Ala Asn Leu Leu Asp Ala Gln Val Leu Ser Val Glu Ala Pro Ile	185	190	195	
ttc ccc tta gac att tct tat gct cca gcc cgc gcg cct cgc ctc aat				739
Phe Pro Leu Asp Ile Ser Tyr Ala Pro Ala Arg Ala Pro Arg Leu Asn	200	205	210	
gca aaa ggt gtc gac tgg gat ttc ctc gac cac atg gcg cag aaa act				787
Ala Lys Gly Val Asp Trp Asp Phe Leu Asp His Met Ala Gln Lys Thr	215	220	225	
cac gat gcg gtg aca cat tca gag cac tct gca ctc att ttc gtc cca				835
His Asp Ala Val Thr His Ser Glu His Ser Ala Leu Ile Phe Val Pro	230	235	240	245
ggt gtg cgt gaa att gat cga gta atg agc acg ctc aaa tcg ctc ggc				883
Gly Val Arg Glu Ile Asp Arg Val Met Ser Thr Leu Lys Ser Leu Gly	250	255	260	
cat aat aat gtt ttc cca ctt cat ggc caa ctc agc ccg acc gaa caa				931
His Asn Asn Val Phe Pro Leu His Gly Gln Leu Ser Pro Thr Glu Gln	265	270	275	
gac cgc gcc ctc gca ccg tca caa cag cag cgc atc att gtc tcc act				979
Asp Arg Ala Leu Ala Pro Ser Gln Gln Gln Arg Ile Ile Val Ser Thr	280	285	290	
ccc gtt gcg gaa agc tcc cta act gtg cct gga gtt cgc atc ggg gtg				1027
Pro Val Ala Glu Ser Ser Leu Thr Val Pro Gly Val Arg Ile Gly Val	295	300	305	
gat tcc ggc ctc tca cga agc ccc aaa cga gac tct gcc cgc ggc atg				1075
Asp Ser Gly Leu Ser Arg Ser Pro Lys Arg Asp Ser Ala Arg Gly Met	310	315	320	325
aca gga ctg atc acc agc agt tgc gcg cag gct tca gca ggc caa cgc				1123
Thr Gly Leu Ile Thr Ser Ser Cys Ala Gln Ala Ser Ala Gly Gln Arg	330	335	340	
gca ggt cgc gct ggc cgt gaa gga cca gga caa ata atc aga tgc tat				1171
Ala Gly Arg Ala Gly Arg Glu Gly Pro Gly Gln Ile Ile Arg Cys Tyr	345	350	355	
tcc gaa gaa gac ttc tcc cac ttc cca cga ttt gtg aca cca gaa atc				1219
Ser Glu Glu Asp Phe Ser His Phe Pro Arg Phe Val Thr Pro Glu Ile	360	365	370	
agc tcc gct gac ctc acc caa gca gcc ctc tgg ctc gcc caa tgg gga				1267
Ser Ser Ala Asp Leu Thr Gln Ala Ala Leu Trp Leu Ala Gln Trp Gly	375	380	385	
acg tca cct gcg gat tta ccg ctt ctt gat caa ccc cct cac gca gcc				1315
Thr Ser Pro Ala Asp Leu Pro Leu Leu Asp Gln Pro Pro His Ala Ala	390	395	400	405

tgg acg gct gca caa cag atc ctg cgc ctc atc ggc gcg ctt gaa ggt	1363
Trp Thr Ala Ala Gln Gln Ile Leu Arg Leu Ile Gly Ala Leu Glu Gly	
410 415 420	
gac gct atc acg agc ctg gga cat cgc tta tcg acg ctt ccc ctc tgc	1411
Asp Ala Ile Thr Ser Leu Gly His Arg Leu Ser Thr Leu Pro Leu Cys	
425 430 435	
cct caa ctc agc gct tct ctc ctc cgc ttc ggt gaa caa tcc gca aaa	1459
Pro Gln Leu Ser Ala Ser Leu Leu Arg Phe Gly Glu Gln Ser Ala Lys	
440 445 450	
atc ttg gcg gtg gtg tcc gaa aac ccg cag ggg gac gtc gaa aag caa	1507
Ile Leu Ala Val Val Ser Glu Asn Pro Gln Gly Asp Val Glu Lys Gln	
455 460 465	
caa ccc gac aag cgt gaa gtg gaa cgc ctt cgc cgt ttg gca cct gcg	1555
Gln Pro Asp Lys Arg Glu Val Glu Arg Leu Arg Arg Leu Ala Pro Ala	
470 475 480 485	
tcg gtt gga aaa gcg agt gcg ggg caa atc gta ggc gct gca ttc ccg	1603
Ser Val Gly Lys Ala Ser Ala Gly Gln Ile Val Gly Ala Ala Phe Pro	
490 495 500	
cag ctc atc ggc cga aaa ata gac aat gga gaa tac ctt tta gcc agt	1651
Gln Leu Ile Gly Arg Lys Ile Asp Asn Gly Glu Tyr Leu Leu Ala Ser	
505 510 515	
gga acc cgc gca cgc ctc atg gat tca gat ctc aaa gat gcc gaa tgg	1699
Gly Thr Arg Ala Arg Leu Met Asp Ser Asp Leu Lys Asp Ala Glu Trp	
520 525 530	
atc tcc gtt gct gca att aac cgc tca caa aat tct gcc atc atc cgc	1747
Ile Ser Val Ala Ala Ile Asn Arg Ser Gln Asn Ser Ala Ile Ile Arg	
535 540 545	
gcc gcc gcc cgc att tca gag gac gat gcc ata gac atc atc gga gtc	1795
Ala Ala Ala Arg Ile Ser Glu Asp Asp Ala Ile Asp Ile Ile Gly Val	
550 555 560 565	
gtg gaa gaa acc cgc gcg att ttt gtc aac gga aaa gtc caa gcc cgg	1843
Val Glu Glu Thr Arg Ala Ile Phe Val Asn Gly Lys Val Gln Ala Arg	
570 575 580	
aag gtc aaa gca gca ggc gcg atc gaa tta agt tcc act ccg aca aaa	1891
Lys Val Lys Ala Ala Gly Ala Ile Glu Leu Ser Ser Thr Pro Thr Lys	
585 590 595	
cca aca ccc gcc gaa gcc tcg gaa aca atc gcc aca gcc ctt gcc aaa	1939
Pro Thr Pro Ala Glu Ala Ser Glu Thr Ile Ala Thr Ala Leu Ala Lys	
600 605 610	
ggc gga atc gac cta ttc cac ttc tcc gac aaa gcg gca tcc ttg cgt	1987
Gly Gly Ile Asp Leu Phe His Phe Ser Asp Lys Ala Ala Ser Leu Arg	
615 620 625	
gac cga ctg aaa ttc atc cac gaa cac cgt ggc gaa ccc tgg cca gat	2035
Asp Arg Leu Lys Phe Ile His Glu His Arg Gly Glu Pro Trp Pro Asp	
630 635 640 645	

att gaa act gcg gac ccg cac ctg tgg tta tct cca gaa att gag gcg 2083
 Ile Glu Thr Ala Asp Pro His Leu Trp Leu Ser Pro Glu Ile Glu Ala
 650 655 660

ctc agc cac gga aca cga cta aac aat atc gat atg tat ccc gca ctc 2131
 Leu Ser His Gly Thr Arg Leu Asn Asn Ile Asp Met Tyr Pro Ala Leu
 665 670 675

cag cga ctt ctc ccc tgg cct gaa gca acc aac ttt gaa gaa ttc gct 2179
 Gln Arg Leu Leu Pro Trp Pro Glu Ala Thr Asn Phe Glu Glu Phe Ala
 680 685 690

cct tcc cac cta tcc gta ccc agc ggg aat cag cac cga cta gat tat 2227
 Pro Ser His Leu Ser Val Pro Ser Gly Asn Gln His Arg Leu Asp Tyr
 695 700 705

tca tca ggc agg cca gtt ata cga gtg aaa tta caa gaa tgc ttc gga 2275
 Ser Ser Gly Arg Pro Val Ile Arg Val Lys Leu Gln Glu Cys Phe Gly
 710 715 720 725

tta gaa gaa tcc ccg cag ctc tgc gga atc ccg gtg caa ttt cat ctc 2323
 Leu Glu Glu Ser Pro Gln Leu Cys Gly Ile Pro Val Gln Phe His Leu
 730 735 740

ctg tca cct gcg gga aga cct ctt gca gtt acc gat gac ctg cgt agt 2371
 Leu Ser Pro Ala Gly Arg Pro Leu Ala Val Thr Asp Asp Leu Arg Ser
 745 750 755

ttc tgg tct ggc ccg tac agc caa gtc cgt gca gaa atg cgg ggc cgg 2419
 Phe Trp Ser Gly Pro Tyr Ser Gln Val Arg Ala Glu Met Arg Gly Arg
 760 765 770

tac ccc aaa cac ccg tgg ccg gag gat cca tgg acc gct cct gcc act 2467
 Tyr Pro Lys His Pro Trp Pro Glu Asp Pro Trp Thr Ala Pro Ala Thr
 775 780 785

gcg cgc acc aag aat cgc atg tagttttggc acgacttgat gtg 2511
 Ala Arg Thr Lys Asn Arg Met
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Gly Pro Lys Asn Leu Val Ile Gln Ala Pro Pro Gly Thr Gly Lys Thr
 35 40 45

Thr Leu Leu Pro Pro Leu Val Ala Asn Ile Leu Cys Asn Glu Gly Ala
 50 55 60

Gly Asn Ala Thr Pro Thr Lys Val Leu Val Thr Ala Pro Arg Arg Val
 65 70 75 80

Ala Val Arg Ala Ala Ala Arg Arg Leu Ala Gln Leu Asp Asp Ser Gln
85 90 95

Leu Gly Thr Lys Val Gly Phe Ser Val Arg Gly Glu His Ile Ser Gly
100 105 110

Ser His Val Gln Phe Met Thr Pro Gly Val Leu Ile Arg Gln Leu Leu
115 120 125

Asn Asn Pro Glu Leu Pro Gly Ile Gly Ala Val Ile Ile Asp Glu Val
130 135 140

His Glu Arg Gln Leu Asp Ser Asp Leu Leu Leu Gly Met Leu Ala Glu
145 150 155 160

Leu Ser Gln Leu Arg Asp Asp Phe Ser Leu Ile Ala Met Ser Ala Thr
165 170 175

Leu Asp Ser Asp Lys Phe Ala Asn Leu Leu Asp Ala Gln Val Leu Ser
180 185 190

Val Glu Ala Pro Ile Phe Pro Leu Asp Ile Ser Tyr Ala Pro Ala Arg
195 200 205

Ala Pro Arg Leu Asn Ala Lys Gly Val Asp Trp Asp Phe Leu Asp His
210 215 220

Met Ala Gln Lys Thr His Asp Ala Val Thr His Ser Glu His Ser Ala
225 230 235 240

Leu Ile Phe Val Pro Gly Val Arg Glu Ile Asp Arg Val Met Ser Thr
245 250 255

Leu Lys Ser Leu Gly His Asn Asn Val Phe Pro Leu His Gly Gln Leu
260 265 270

Ser Pro Thr Glu Gln Asp Arg Ala Leu Ala Pro Ser Gln Gln Gln Arg
275 280 285

Ile Ile Val Ser Thr Pro Val Ala Glu Ser Ser Leu Thr Val Pro Gly
290 295 300

Val Arg Ile Gly Val Asp Ser Gly Leu Ser Arg Ser Pro Lys Arg Asp
305 310 315 320

Ser Ala Arg Gly Met Thr Gly Leu Ile Thr Ser Ser Cys Ala Gln Ala
325 330 335

Ser Ala Gly Gln Arg Ala Gly Arg Ala Gly Arg Glu Gly Pro Gly Gln
340 345 350

Ile Ile Arg Cys Tyr Ser Glu Glu Asp Phe Ser His Phe Pro Arg Phe
355 360 365

Val Thr Pro Glu Ile Ser Ser Ala Asp Leu Thr Gln Ala Ala Leu Trp
370 375 380

Leu Ala Gln Trp Gly Thr Ser Pro Ala Asp Leu Pro Leu Leu Asp Gln
385 390 395 400

Pro Pro His Ala Ala Trp Thr Ala Ala Gln Gln Ile Leu Arg Leu Ile
405 410 415

Gly Ala Leu Glu Gly Asp Ala Ile Thr Ser Leu Gly His Arg Leu Ser
420 425 430

Thr Leu Pro Leu Cys Pro Gln Leu Ser Ala Ser Leu Leu Arg Phe Gly
435 440 445

Glu Gln Ser Ala Lys Ile Leu Ala Val Val Ser Glu Asn Pro Gln Gly
450 455 460

Asp Val Glu Lys Gln Gln Pro Asp Lys Arg Glu Val Glu Arg Leu Arg
465 470 475 480

Arg Leu Ala Pro Ala Ser Val Gly Lys Ala Ser Ala Gly Gln Ile Val
485 490 495

Gly Ala Ala Phe Pro Gln Leu Ile Gly Arg Lys Ile Asp Asn Gly Glu
500 505 510

Tyr Leu Leu Ala Ser Gly Thr Arg Ala Arg Leu Met Asp Ser Asp Leu
515 520 525

Lys Asp Ala Glu Trp Ile Ser Val Ala Ala Ile Asn Arg Ser Gln Asn
530 535 540

Ser Ala Ile Ile Arg Ala Ala Ala Arg Ile Ser Glu Asp Asp Ala Ile
545 550 555 560

Asp Ile Ile Gly Val Val Glu Glu Thr Arg Ala Ile Phe Val Asn Gly
565 570 575

Lys Val Gln Ala Arg Lys Val Lys Ala Ala Gly Ala Ile Glu Leu Ser
580 585 590

Ser Thr Pro Thr Lys Pro Thr Pro Ala Glu Ala Ser Glu Thr Ile Ala
595 600 605

Thr Ala Leu Ala Lys Gly Gly Ile Asp Leu Phe His Phe Ser Asp Lys
610 615 620

Ala Ala Ser Leu Arg Asp Arg Leu Lys Phe Ile His Glu His Arg Gly
625 630 635 640

Glu Pro Trp Pro Asp Ile Glu Thr Ala Asp Pro His Leu Trp Leu Ser
645 650 655

Pro Glu Ile Glu Ala Leu Ser His Gly Thr Arg Leu Asn Asn Ile Asp
660 665 670

Met Tyr Pro Ala Leu Gln Arg Leu Leu Pro Trp Pro Glu Ala Thr Asn
675 680 685

Phe Glu Glu Phe Ala Pro Ser His Leu Ser Val Pro Ser Gly Asn Gln
690 695 700

His Arg Leu Asp Tyr Ser Ser Gly Arg Pro Val Ile Arg Val Lys Leu
705 710 715 720

Gln Glu Cys Phe Gly Leu Glu Glu Ser Pro Gln Leu Cys Gly Ile Pro

725	730	735
Val Gln Phe His Leu Leu Ser Pro Ala Gly Arg Pro Leu Ala Val Thr		
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Asp Asp Leu Arg Ser Phe Trp Ser Gly Pro Tyr Ser Gln Val Arg Ala		
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Glu Met Arg Gly Arg Tyr Pro Lys His Pro Trp Pro Glu Asp Pro Trp		
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 Met Ser Ala Pro Glu
 1 5
 tca ccc aca aat acc acc cca gat ccg ctc aat gct tcc acg gaa gag 163
 Ser Pro Thr Asn Thr Thr Pro Asp Pro Leu Asn Ala Ser Thr Glu Glu
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 ttg ctt act gct gcc gtt gaa gcg ttg ggc ggt gcc cgt cgt gct gga 211
 Leu Leu Thr Ala Ala Val Glu Ala Leu Gly Gly Ala Arg Arg Ala Gly
 25 30 35
 cag gaa gca atg gct aag gct gtg acc aag gct ttt gat aca gag cgt 259
 Gln Glu Ala Met Ala Lys Ala Val Thr Lys Ala Phe Asp Thr Glu Arg
 40 45 50
 cac ttg gcg gtg cag gcg ggt acg ggt acg ggt aag tct ttg gct tat 307
 His Leu Ala Val Gln Ala Gly Thr Gly Thr Gly Lys Ser Leu Ala Tyr
 55 60 65
 ctt gtt ccg tcg att cgt cat gcg cag aag tct gat tcc acg gtc att 355
 Leu Val Pro Ser Ile Arg His Ala Gln Lys Ser Asp Ser Thr Val Ile
 70 75 80 85
 gtg tct act gcg acg atc gcg ttg cag cgc cag ttg gtc aat agg gat 403
 Val Ser Thr Ala Thr Ile Ala Leu Gln Arg Gln Leu Val Asn Arg Asp
 90 95 100
 ctc ccc cgc ttg gtg gat gcg ttg gaa ccc ttg atg gaa cgt cgc ccg 451
 Leu Pro Arg Leu Val Asp Ala Leu Glu Pro Leu Met Glu Arg Arg Pro
 105 110 115
 act ttt gcg att atg aag ggc cgt tcc aat tat ttg tgc atg aat aag 499

Thr	Phe	Ala	Ile	Met	Lys	Gly	Arg	Ser	Asn	Tyr	Leu	Cys	Met	Asn	Lys	
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Val	Ala	Arg	Gln	Glu	Glu	Leu	Asn	Gln	Glu	Asp	Ala	Leu	Ile	Glu	Gln	
135						140				145						
gag	gat	atc	tcg	tgg	tta	ggc	aag	cac	att	gtg	cgc	ctt	aat	gag	tgg	595
Glu	Asp	Ile	Ser	Trp	Leu	Gly	Lys	His	Ile	Val	Arg	Leu	Asn	Glu	Trp	
150					155				160						165	
gcc	aat	gag	act	gag	act	ggc	gat	cgt	gat	gat	ttg	gat	ccg	ggc	gtt	643
Ala	Asn	Glu	Thr	Glu	Thr	Gly	Asp	Arg	Asp	Asp	Leu	Asp	Pro	Gly	Val	
				170				175						180		
cct	gat	ctt	gcg	tgg	aag	cag	gta	agt	gtt	act	gcc	cgt	gag	tgc	att	691
Pro	Asp	Leu	Ala	Trp	Lys	Gln	Val	Ser	Val	Thr	Ala	Arg	Glu	Cys	Ile	
		185						190				195				
ggc	gcg	tca	agg	tgc	ccg	cat	ggc	gag	gat	tgt	ttc	gct	gag	att	gcc	739
Gly	Ala	Ser	Arg	Cys	Pro	His	Gly	Glu	Asp	Cys	Phe	Ala	Glu	Ile	Ala	
		200				205						210				
cgc	ggg	aag	gca	aag	gag	gct	gat	gtg	gtg	gtc	acc	aac	cat	gcg	tta	787
Arg	Gly	Lys	Ala	Lys	Glu	Ala	Asp	Val	Val	Val	Thr	Asn	His	Ala	Leu	
		215				220				225						
ctt	gct	att	gat	gcg	ttg	tcg	gat	gtt	tct	gtg	ctt	cct	gaa	cat	gat	835
Leu	Ala	Ile	Asp	Ala	Leu	Ser	Asp	Val	Ser	Val	Leu	Pro	Glu	His	Asp	
230					235				240						245	
gtg	gtg	gtc	atc	gat	gag	gcc	cat	gag	cta	gat	ggc	cgc	atc	act	gct	883
Val	Val	Val	Ile	Asp	Glu	Ala	His	Glu	Leu	Asp	Gly	Arg	Ile	Thr	Ala	
				250				255						260		
gtg	gcg	tcg	gct	gag	atc	acg	gtg	aat	tcg	ctc	aat	tta	gct	gct	cgc	931
Val	Ala	Ser	Ala	Glu	Ile	Thr	Val	Asn	Ser	Leu	Asn	Leu	Ala	Ala	Arg	
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cgt	gcg	tcc	aag	ttg	gat	tcc	gat	aag	cgg	gaa	gaa	cgc	gtc	cag	gaa	979
Arg	Ala	Ser	Lys	Leu	Asp	Ser	Asp	Lys	Arg	Glu	Glu	Arg	Val	Gln	Glu	
		280				285						290				
atc	gct	ggc	gat	ttg	gaa	acc	ttg	ttg	caa	acc	atg	cag	ccg	ggc	cgg	1027
Ile	Ala	Gly	Asp	Leu	Glu	Thr	Leu	Leu	Gln	Thr	Met	Gln	Pro	Gly	Arg	
		295				300				305						
tgg	aat	gac	atg	gat	gag	ggc	tcc	aaa	ggc	aca	ctg	gtg	gca	ttg	aag	1075
Trp	Asn	Asp	Met	Asp	Glu	Gly	Ser	Lys	Gly	Thr	Leu	Val	Ala	Leu	Lys	
310					315				320						325	
gac	gcg	ttg	tgg	gca	ttg	cgt	gct	cag	atc	gcg	gga	gca	cct	gag	ggc	1123
Asp	Ala	Leu	Trp	Ala	Leu	Arg	Ala	Gln	Ile	Ala	Gly	Ala	Pro	Glu	Gly	
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360	365	370	
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cac gat gat cgt cgc ggg gat tcc ctc aat gtg gcg ccg ctg tcg gtt His Asp Asp Arg Arg Gly Asp Ser Leu Asn Val Ala Pro Leu Ser Val 390 395 400 405			1315
gca ggg ctg ttg cat gag aaa ctg ttc gcg gaa aac acc gtg gtt ttg Ala Gly Leu Leu His Glu Lys Leu Phe Ala Glu Asn Thr Val Val Leu 410 415 420			1363
gcc agt gcg acg ctg acc att ggt ggc aat ttc aac gca atg gct gcc Ala Ser Ala Thr Leu Thr Ile Gly Gly Asn Phe Asn Ala Met Ala Ala 425 430 435			1411
agc tgg ggt ttg ccg aaa ggg tcg tgg gat tcc atg gat gcc ggc acg Ser Trp Gly Leu Pro Lys Gly Ser Trp Asp Ser Met Asp Ala Gly Thr 440 445 450			1459
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cct ttt gat gtg ctc tgc cag gga gat gac aat act gcc gcg ctg gtg Pro Phe Asp Val Leu Cys Gln Gly Asp Asp Asn Thr Ala Ala Leu Val 520 525 530			1699
aag aag ttt tcc gac agc gaa aac acg tgc ctt ttt ggc act ctc acg Lys Lys Phe Ser Asp Ser Glu Asn Thr Cys Leu Phe Gly Thr Leu Thr 535 540 545			1747
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att gac cgc atc ccg ttc ccc cgc ccc gac gac ccg ctg ctg cag gcc Ile Asp Arg Ile Pro Phe Pro Arg Pro Asp Asp Pro Leu Leu Gln Ala 570 575 580			1843
cgc aag gag gcc gcc gat gcc gaa ggc cgc aac ggt ttc atg gag gtc Arg Lys Glu Ala Ala Asp Ala Glu Gly Arg Asn Gly Phe Met Glu Val 585 590 595			1891
gca gcc acc cac gcg gcg ttg ttg atg gcg cag ggc gcg ggc cgg ttg Ala Ala Thr His Ala Ala Leu Leu Met Ala Gln Gly Ala Gly Arg Leu 600 605 610			1939

ttg cgg cac gtc ggc gac cgc ggc gtg gta gca gtg cta gac cac cgc 1987
 Leu Arg His Val Gly Asp Arg Gly Val Val Ala Val Leu Asp His Arg
 615 620 625

tta tcg acg aaa cgt tac ggc ggt ttc ctg cgc ttc tcc atg ccc aga 2035
 Leu Ser Thr Lys Arg Tyr Gly Gly Phe Leu Arg Phe Ser Met Pro Arg
 630 635 640 645

ttt tgg gaa acc acc aac cca gag acc gta cgc gcg gca ctc aaa cga 2083
 Phe Trp Glu Thr Thr Asn Pro Glu Thr Val Arg Ala Ala Leu Lys Arg
 650 655 660

ttg gtg act aag taaaactaac tgctactgac gct 2118
 Leu Val Thr Lys
 665

<210> 82

<211> 665

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

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 20 25 30

Ala Arg Arg Ala Gly Gln Glu Ala Met Ala Lys Ala Val Thr Lys Ala
 35 40 45

Phe Asp Thr Glu Arg His Leu Ala Val Gln Ala Gly Thr Gly Thr Gly
 50 55 60

Lys Ser Leu Ala Tyr Leu Val Pro Ser Ile Arg His Ala Gln Lys Ser
 65 70 75 80

Asp Ser Thr Val Ile Val Ser Thr Ala Thr Ile Ala Leu Gln Arg Gln
 85 90 95

Leu Val Asn Arg Asp Leu Pro Arg Leu Val Asp Ala Leu Glu Pro Leu
 100 105 110

Met Glu Arg Arg Pro Thr Phe Ala Ile Met Lys Gly Arg Ser Asn Tyr
 115 120 125

Leu Cys Met Asn Lys Val Ala Arg Gln Glu Glu Leu Asn Gln Glu Asp
 130 135 140

Ala Leu Ile Glu Gln Glu Asp Ile Ser Trp Leu Gly Lys His Ile Val
 145 150 155 160

Arg Leu Asn Glu Trp Ala Asn Glu Thr Glu Thr Gly Asp Arg Asp Asp
 165 170 175

Leu Asp Pro Gly Val Pro Asp Leu Ala Trp Lys Gln Val Ser Val Thr
 180 185 190

Ala Arg Glu Cys Ile Gly Ala Ser Arg Cys Pro His Gly Glu Asp Cys

195					200					205					
Phe	Ala	Glu	Ile	Ala	Arg	Gly	Lys	Ala	Lys	Glu	Ala	Asp	Val	Val	Val
210						215					220				
Thr	Asn	His	Ala	Leu	Leu	Ala	Ile	Asp	Ala	Leu	Ser	Asp	Val	Ser	Val
225					230					235					240
Leu	Pro	Glu	His	Asp	Val	Val	Val	Ile	Asp	Glu	Ala	His	Glu	Leu	Asp
				245					250					255	
Gly	Arg	Ile	Thr	Ala	Val	Ala	Ser	Ala	Glu	Ile	Thr	Val	Asn	Ser	Leu
			260					265					270		
Asn	Leu	Ala	Ala	Arg	Arg	Ala	Ser	Lys	Leu	Asp	Ser	Asp	Lys	Arg	Glu
		275					280					285			
Glu	Arg	Val	Gln	Glu	Ile	Ala	Gly	Asp	Leu	Glu	Thr	Leu	Leu	Gln	Thr
		290				295					300				
Met	Gln	Pro	Gly	Arg	Trp	Asn	Asp	Met	Asp	Glu	Gly	Ser	Lys	Gly	Thr
305					310					315					320
Leu	Val	Ala	Leu	Lys	Asp	Ala	Leu	Trp	Ala	Leu	Arg	Ala	Gln	Ile	Ala
				325					330					335	
Gly	Ala	Pro	Glu	Gly	Glu	Ala	Ala	Asn	Asp	Pro	Glu	Arg	Phe	Ala	Glu
			340					345					350		
Arg	Gln	Asn	Leu	Ser	Asn	His	Leu	Met	Glu	Ile	His	Asp	Ala	Asn	Val
		355					360					365			
Arg	Ile	Leu	Glu	Val	Phe	Ala	Glu	Glu	Asp	Pro	Ser	Lys	Gln	Tyr	Asp
		370				375					380				
Val	Val	Trp	His	Asn	His	Asp	Asp	Arg	Arg	Gly	Asp	Ser	Leu	Asn	Val
385					390					395					400
Ala	Pro	Leu	Ser	Val	Ala	Gly	Leu	Leu	His	Glu	Lys	Leu	Phe	Ala	Glu
				405					410					415	
Asn	Thr	Val	Val	Leu	Ala	Ser	Ala	Thr	Leu	Thr	Ile	Gly	Gly	Asn	Phe
			420					425					430		
Asn	Ala	Met	Ala	Ala	Ser	Trp	Gly	Leu	Pro	Lys	Gly	Ser	Trp	Asp	Ser
		435					440					445			
Met	Asp	Ala	Gly	Thr	Pro	Phe	Asp	Pro	Ala	Lys	Ser	Gly	Ile	Leu	Tyr
		450				455						460			
Thr	Ala	Arg	His	Leu	Pro	Asp	Pro	Gly	Arg	Asp	Gly	Leu	Pro	Glu	Glu
465					470					475					480
Thr	Leu	Asp	Glu	Ile	Tyr	Glu	Leu	Ile	Thr	Ala	Ala	Gly	Gly	Arg	Thr
			485						490					495	
Leu	Gly	Leu	Phe	Ser	Ser	Lys	Arg	Ala	Ala	Glu	Gln	Ala	Thr	Lys	Ala
			500					505					510		
Met	Arg	Leu	Arg	Leu	Pro	Phe	Asp	Val	Leu	Cys	Gln	Gly	Asp	Asp	Asn
			515				520					525			

Thr Ala Ala Leu Val Lys Lys Phe Ser Asp Ser Glu Asn Thr Cys Leu
 530 535 540
 Phe Gly Thr Leu Thr Leu Trp Gln Gly Val Asp Val Pro Gly Arg Ser
 545 550 555 560
 Leu Ser Leu Val Leu Ile Asp Arg Ile Pro Phe Pro Arg Pro Asp Asp
 565 570 575
 Pro Leu Leu Gln Ala Arg Lys Glu Ala Ala Asp Ala Glu Gly Arg Asn
 580 585 590
 Gly Phe Met Glu Val Ala Ala Thr His Ala Ala Leu Leu Met Ala Gln
 595 600 605
 Gly Ala Gly Arg Leu Leu Arg His Val Gly Asp Arg Gly Val Val Ala
 610 615 620
 Val Leu Asp His Arg Leu Ser Thr Lys Arg Tyr Gly Gly Phe Leu Arg
 625 630 635 640
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 Ala Ala Leu Lys Arg Leu Val Thr Lys
 660 665

<210> 83

<211> 1365

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1342)

<223> RXN01374

<400> 83

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 attcgcaaatt actttgttaa gacgcgttaa tctttaacct atg tct gaa tca ggt 115
 Met Ser Glu Ser Gly
 1 5
 gcg cta agt tct act gac tct cta tcc ccg ggt gtc acc att gaa gtc 163
 Ala Leu Ser Ser Thr Asp Ser Leu Ser Pro Gly Val Thr Ile Glu Val
 10 15 20
 cga gat gaa att tgg ctg gtt act cac gtt act cgc tcc aca gat ggt 211
 Arg Asp Glu Ile Trp Leu Val Thr His Val Thr Arg Ser Thr Asp Gly
 25 30 35
 ttt agg gtt aaa gct cgt ggt ctc tct gat tat gtg cgg gac cac gaa 259
 Phe Arg Val Lys Ala Arg Gly Leu Ser Asp Tyr Val Arg Asp His Glu
 40 45 50
 gct acg ttc ttc acc gca ctt gat aaa gat ttg aag gtc att gac cct 307
 Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu Lys Val Ile Asp Pro
 55 60 65

acc cag gtc acc gtc agt ctt gat gat tcc tcc aat tac cgt cgc acc	355
Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser Asn Tyr Arg Arg Thr	
70 75 80 85	
cgc ctg tgg ttg gag gcc acc atg cgt aaa act ccg gta ccg ctc tat	403
Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr Pro Val Pro Leu Tyr	
90 95 100	
caa gag tca ctt tcc gtg gca gat caa atg ctc gcc gat cca ctg gag	451
Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu Ala Asp Pro Leu Glu	
105 110 115	
tac caa tta gca gcc gtg cgc aaa acc ctc tct agt gct aac ttg cgc	499
Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser Ser Ala Asn Leu Arg	
120 125 130	
ccc cgc gtg ctt att gct gat gcc gtg gga ctt ggc aaa acc cta gaa	547
Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu Gly Lys Thr Leu Glu	
135 140 145	
atg ggc atg atc ttg gcg gaa ctt atc cgc cgt ggc cgt ggt gag cgc	595
Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg Gly Arg Gly Glu Arg	
150 155 160 165	
att ttg gta gtc acc ccg cgc cac att atg gag cag ttc cag cag gaa	643
Ile Leu Val Val Thr Pro Arg His Ile Met Glu Gln Phe Gln Glu	
170 175 180	
atg tgg acc cgt ttt gcc atc ccg ctc gtt cgt cta gat tcc gtg ggc	691
Met Trp Thr Arg Phe Ala Ile Pro Leu Val Arg Leu Asp Ser Val Gly	
185 190 195	
atc cag caa gtg cgc caa aaa ttg cca gca tca cgc aac cct ttt act	739
Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser Arg Asn Pro Phe Thr	
200 205 210	
tat ttc ccg cgc gtg att gtc tct atg gat act ttg aaa tct ccg aag	787
Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr Leu Lys Ser Pro Lys	
215 220 225	
tac cgc gcg caa cta gaa aag gtg cac tgg gat gcg gtg gtt ata gat	835
Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp Ala Val Val Ile Asp	
230 235 240 245	
gaa atc cac aat gca acc aat gct ggc acc caa aat aat gag cta gcc	883
Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln Asn Asn Glu Leu Ala	
250 255 260	
ggc aca ctt ggg cct act gcc gag gct ctt att ttg gcc tct gcc acc	931
Gly Thr Leu Gly Pro Thr Ala Glu Ala Leu Ile Leu Ala Ser Ala Thr	
265 270 275	
ccg cac aat ggt gat cca gaa tcc ttt aag gag atc ttg cgt ttg ctt	979
Pro His Asn Gly Asp Pro Glu Ser Phe Lys Glu Ile Leu Arg Leu Leu	
280 285 290	
gat ccc acc gct gtg atg cct gat ggc acc att gat gcc gaa gct gca	1027
Asp Pro Thr Ala Val Met Pro Asp Gly Thr Ile Asp Ala Glu Ala Ala	
295 300 305	

cag cgt ctg atc att cgt cgc cat cgc aat agc cct gag gtt tca ggt 1075
 Gln Arg Leu Ile Ile Arg Arg His Arg Asn Ser Pro Glu Val Ser Gly
 310 315 320 325
 ttt gtg ggc gaa aaa tgg gct cca cgc aat gag cct cag aac ttc ctg 1123
 Phe Val Gly Glu Lys Trp Ala Pro Arg Asn Glu Pro Gln Asn Phe Leu
 330 335 340
 gtc gct gcg tca aaa gaa gaa aac ggc gtt gct gca gaa ctc aac cat 1171
 Val Ala Ala Ser Lys Glu Glu Asn Gly Val Ala Ala Glu Leu Asn His
 345 350 355
 gtg tgg att tca cca ggt gcg agc aat ccg atc aag gat cgc ctc ttc 1219
 Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile Lys Asp Arg Leu Phe
 360 365 370
 ccc ctg gac att ggt gaa ggc ttt tct ctc ctc ccc tgc agc ctt ggg 1267
 Pro Leu Asp Ile Gly Glu Gly Phe Ser Leu Leu Pro Cys Ser Leu Gly
 375 380 385
 cga aac agt gtc caa tcg cct caa aaa ggc ctc tgc acc aga aga aaa 1315
 Arg Asn Ser Val Gln Ser Pro Gln Lys Gly Leu Cys Thr Arg Arg Lys
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 acg cgc cct aga aac cct ttc aca act taattctgcg atcaccccg 1362
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 aga 1365

<210> 84

<211> 414

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

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 20 25 30

Arg Ser Thr Asp Gly Phe Arg Val Lys Ala Arg Gly Leu Ser Asp Tyr
 35 40 45

Val Arg Asp His Glu Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu
 50 55 60

Lys Val Ile Asp Pro Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser
 65 70 75 80

Asn Tyr Arg Arg Thr Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr
 85 90 95

Pro Val Pro Leu Tyr Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu
 100 105 110

Ala Asp Pro Leu Glu Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser
 115 120 125

Ser Ala Asn Leu Arg Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu
 130 135 140
 Gly Lys Thr Leu Glu Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg
 145 150 155 160
 Gly Arg Gly Glu Arg Ile Leu Val Val Thr Pro Arg His Ile Met Glu
 165 170 175
 Gln Phe Gln Gln Glu Met Trp Thr Arg Phe Ala Ile Pro Leu Val Arg
 180 185 190
 Leu Asp Ser Val Gly Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser
 195 200 205
 Arg Asn Pro Phe Thr Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr
 210 215 220
 Leu Lys Ser Pro Lys Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp
 225 230 235 240
 Ala Val Val Ile Asp Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln
 245 250 255
 Asn Asn Glu Leu Ala Gly Thr Leu Gly Pro Thr Ala Glu Ala Leu Ile
 260 265 270
 Leu Ala Ser Ala Thr Pro His Asn Gly Asp Pro Glu Ser Phe Lys Glu
 275 280 285
 Ile Leu Arg Leu Leu Asp Pro Thr Ala Val Met Pro Asp Gly Thr Ile
 290 295 300
 Asp Ala Glu Ala Ala Gln Arg Leu Ile Ile Arg Arg His Arg Asn Ser
 305 310 315 320
 Pro Glu Val Ser Gly Phe Val Gly Glu Lys Trp Ala Pro Arg Asn Glu
 325 330 335
 Pro Gln Asn Phe Leu Val Ala Ala Ser Lys Glu Glu Asn Gly Val Ala
 340 345 350
 Ala Glu Leu Asn His Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile
 355 360 365
 Lys Asp Arg Leu Phe Pro Leu Asp Ile Gly Glu Gly Phe Ser Leu Leu
 370 375 380
 Pro Cys Ser Leu Gly Arg Asn Ser Val Gln Ser Pro Gln Lys Gly Leu
 385 390 395 400
 Cys Thr Arg Arg Lys Thr Arg Pro Arg Asn Pro Phe Thr Thr
 405 410

<210> 85

<211> 982

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> FRXA01374

<400> 85

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attcgcaaat actttgttaa gacgcgttaa tctttaacct atg tct gaa tca ggt 115
                                         Met Ser Glu Ser Gly
                                         1       5

gcg cta agt tct act gac tct cta tcc ccg ggt gtc acc att gaa gtc 163
Ala Leu Ser Ser Thr Asp Ser Leu Ser Pro Gly Val Thr Ile Glu Val
                        10                        15                        20

cga gat gaa att tgg ctg gtt act cac gtt act cgc tcc aca gat ggt 211
Arg Asp Glu Ile Trp Leu Val Thr His Val Thr Arg Ser Thr Asp Gly
                        25                        30                        35

ttt agg gtt aaa gct cgt ggt ctc tct gat tat gtg cgg gac cac gaa 259
Phe Arg Val Lys Ala Arg Gly Leu Ser Asp Tyr Val Arg Asp His Glu
                        40                        45                        50

gct acg ttc ttc acc gca ctt gat aaa gat ttg aag gtc att gac cct 307
Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu Lys Val Ile Asp Pro
                        55                        60                        65

acc cag gtc acc gtc agt ctt gat gat tcc tcc aat tac cgt cgc acc 355
Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser Asn Tyr Arg Arg Thr
                        70                        75                        80                        85

cgc ctg tgg ttg gag gcc acc atg cgt aaa act ccg gta ccg ctc tat 403
Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr Pro Val Pro Leu Tyr
                        90                        95                        100

caa gag tca ctt tcc gtg gca gat caa atg ctc gcc gat cca ctg gag 451
Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu Ala Asp Pro Leu Glu
                        105                        110                        115

tac caa tta gca gcc gtg cgc aaa acc ctc tct agt gct aac ttg cgc 499
Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser Ser Ala Asn Leu Arg
                        120                        125                        130

ccc cgc gtg ctt att gct gat gcc gtg gga ctt ggc aaa acc cta gaa 547
Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu Gly Lys Thr Leu Glu
                        135                        140                        145

atg ggc atg atc ttg gcg gaa ctt atc cgc cgt ggc cgt ggt gag cgc 595
Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg Gly Arg Gly Glu Arg
                        150                        155                        160                        165

att ttg gta gtc acc ccg cgc cac att atg gag cag ttc cag cag gaa 643
Ile Leu Val Val Thr Pro Arg His Ile Met Glu Gln Phe Gln Gln Glu
                        170                        175                        180

atg tgg acc cgt ttt gcc atc ccg ctc gtt cgt cta gat tcc gtg ggc 691
Met Trp Thr Arg Phe Ala Ile Pro Leu Val Arg Leu Asp Ser Val Gly
                        185                        190                        195

atc cag caa gtg cgc caa aaa ttg cca gca tca cgc aac cct ttt act 739
Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser Arg Asn Pro Phe Thr

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200	205	210	
tat ttc ccg cgc gtg att gtc tct atg gat act ttg aaa tct ccg aag			787
Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr Leu Lys Ser Pro Lys			
215	220	225	
tac cgc gcg caa cta gaa aag gtg cac tgg gat gcg gtg gtt ata gat			835
Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp Ala Val Val Ile Asp			
230	235	240	245
gaa atc cac aat gca acc aat gct ggc acc caa aat aat gag cta gcc			883
Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln Asn Asn Glu Leu Ala			
250	255	260	
cgc aca ctt gcg cct act gcc gag gct ctt att ttg gcc tct gcc acc			931
Arg Thr Leu Ala Pro Thr Ala Glu Ala Leu Ile Leu Ala Ser Ala Thr			
265	270	275	
ccg cac aat ggt gat cca gaa tcc ttt aag gag atc ttg cgt ttg ctt			979
Pro His Asn Gly Asp Pro Glu Ser Phe Lys Glu Ile Leu Arg Leu Leu			
280	285	290	
gat			982
Asp			

<210> 86

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

Met Ser Glu Ser Gly Ala Leu Ser Ser Thr Asp Ser Leu Ser Pro Gly
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Val Thr Ile Glu Val Arg Asp Glu Ile Trp Leu Val Thr His Val Thr
20 25 30

Arg Ser Thr Asp Gly Phe Arg Val Lys Ala Arg Gly Leu Ser Asp Tyr
35 40 45

Val Arg Asp His Glu Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu
50 55 60

Lys Val Ile Asp Pro Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser
65 70 75 80

Asn Tyr Arg Arg Thr Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr
85 90 95

Pro Val Pro Leu Tyr Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu
100 105 110

Ala Asp Pro Leu Glu Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser
115 120 125

Ser Ala Asn Leu Arg Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu
130 135 140

Gly Lys Thr Leu Glu Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg

145		150		155		160
Gly Arg Gly Glu Arg Ile Leu Val Val Thr Pro Arg His Ile Met Glu						
		165		170		175
Gln Phe Gln Gln Glu Met Trp Thr Arg Phe Ala Ile Pro Leu Val Arg						
		180		185		190
Leu Asp Ser Val Gly Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser						
		195		200		205
Arg Asn Pro Phe Thr Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr						
		210		215		220
Leu Lys Ser Pro Lys Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp						
		225		230		240
Ala Val Val Ile Asp Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln						
		245		250		255
Asn Asn Glu Leu Ala Arg Thr Leu Ala Pro Thr Ala Glu Ala Leu Ile						
		260		265		270
Leu Ala Ser Ala Thr Pro His Asn Gly Asp Pro Glu Ser Phe Lys Glu						
		275		280		285
Ile Leu Arg Leu Leu Asp						
		290				

<210> 87.
 <211> 2517
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2494)
 <223> RXN00817

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 tcagtcccat ttatacagcc cagcgaaagg gggtaaattc ttg act acc ccc gat 115
 Leu Thr Thr Pro Asp
 1 5
 ttt gag agt gaa aag act caa gct atg agg ccc agc ttt ggt gaa gag 163
 Phe Glu Ser Glu Lys Thr Gln Ala Met Arg Pro Ser Phe Gly Glu Glu
 10 15 20
 ctg gcc gca atc gtt tcc aaa cgt tac tcc gaa tcg acg ctc act cat 211
 Leu Ala Ala Ile Val Ser Lys Arg Tyr Ser Glu Ser Thr Leu Thr His
 25 30 35
 atg gtg acg ttg ccc gca tcg aaa gct aaa tac gtc gat tgg ccg agt 259
 Met Val Thr Leu Pro Ala Ser Lys Ala Lys Tyr Val Asp Trp Pro Ser
 40 45 50
 tgg gta cct gct agc ctg cgc gat gcg ttg gtg aat cgt ggt atc aat 307
 Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val Asn Arg Gly Ile Asn

55	60	65	
aag ctc ttt tcc cac cag gag cag acc gca cat ctg gcg tgg aat ggc			355
Lys Leu Phe Ser His Gln Glu Gln Thr Ala His Leu Ala Trp Asn Gly			
70	75	80	85
cag cat gtg gtg gtt gcc acc ggt aca tct tcg gga aaa tct ttg ggt			403
Gln His Val Val Val Ala Thr Gly Thr Ser Ser Gly Lys Ser Leu Gly			
	90	95	100
tat cag ctg ccc att ttg tca gcg ctc ggc acg gat cct acc gcc tgt			451
Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr Asp Pro Thr Ala Cys			
	105	110	115
gcg ttg tat cta act ccc acc aag gct ttg gga tct gat cag cta acc			499
Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly Ser Asp Gln Leu Thr			
	120	125	130
tcc acg tcc acg ttg ctg cgc gac att ccg gat ttc cac ccg att aat			547
Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp Phe His Pro Ile Asn			
	135	140	145
ccg gcg ccc tac gat ggc gat acc ccc tcc gag gcg ccg tcc ggc atc			595
Pro Ala Pro Tyr Asp Gly Asp Thr Pro Ser Glu Ala Arg Ser Gly Ile			
150	155	160	165
cgc gat ttg agt cgt ttt gtg ttc acc aat ccg gat atg gtg cat gcg			643
Arg Asp Leu Ser Arg Phe Val Phe Thr Asn Pro Asp Met Val His Ala			
	170	175	180
tcg atg ctg gcg aat cat ccc cgc tgg gcc agg ttg ttg cgc cat ttg			691
Ser Met Leu Ala Asn His Pro Arg Trp Ala Arg Leu Leu Arg His Leu			
	185	190	195
aag ttc atc gtg att gat gaa tgc cat gcc tac cgt ggt gtg ttt ggc			739
Lys Phe Ile Val Ile Asp Glu Cys His Ala Tyr Arg Gly Val Phe Gly			
	200	205	210
gcg aac gtg tcg atg gtg ctt cgt cgt cta ctg cgc atc gcc gcg ttt			787
Ala Asn Val Ser Met Val Leu Arg Arg Leu Leu Arg Ile Ala Ala Phe			
	215	220	225
tat gga tcc cac ccg acg gtc att ttg gcg tcc gcg acc agc tcc gat			835
Tyr Gly Ser His Pro Thr Val Ile Leu Ala Ser Ala Thr Ser Ser Asp			
230	235	240	245
ccg gaa att cat gct tcc aga ttg ttg ggc gcg ccg gtt aaa gca gtg			883
Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala Pro Val Lys Ala Val			
	250	255	260
acg gaa gat ggc gcc ccg acg ggt gaa cgc acc gtt ttg ctg tgg gag			931
Thr Glu Asp Gly Ala Pro Thr Gly Glu Arg Thr Val Leu Leu Trp Glu			
	265	270	275
ccc ggt ttc atc gaa ggc gcc gag ggc gag aac ggc gcg ccg gtg cgt			979
Pro Gly Phe Ile Glu Gly Ala Glu Gly Glu Asn Gly Ala Pro Val Arg			
	280	285	290
cgc gca gcc agc acc gaa gca gca aac att atg gcc acg ctc att tcc			1027
Arg Ala Ala Ser Thr Glu Ala Ala Asn Ile Met Ala Thr Leu Ile Ser			
	295	300	305

gag ggt gca cgc acg ttg acg ttc gtc cgt tca cgt cga caa gca gaa	1075
Glu Gly Ala Arg Thr Leu Thr Phe Val Arg Ser Arg Arg Gln Ala Glu	
310 315 320 325	
atc gtt gcc ctg cgc gcg cag gaa gag ctc agc acg ctg ggc cgc ccc	1123
Ile Val Ala Leu Arg Ala Gln Glu Glu Leu Ser Thr Leu Gly Arg Pro	
330 335 340	
gat ttc gcc cgg cgc gtc gcg tcc tac cgg gcg ggg tac ttg gcg gag	1171
Asp Phe Ala Arg Arg Val Ala Ser Tyr Arg Ala Gly Tyr Leu Ala Glu	
345 350 355	
gac cgc cgt agg ttg gag aga ttg ctt gac gac ggc acc ctc ctc ggt	1219
Asp Arg Arg Arg Leu Glu Arg Leu Leu Asp Asp Gly Thr Leu Leu Gly	
360 365 370	
gtt gct tcc acc aat gcg ctt gaa ctg ggc att gat gtc ggt gga ctg	1267
Val Ala Ser Thr Asn Ala Leu Glu Leu Gly Ile Asp Val Gly Gly Leu	
375 380 385	
gat gct gtg gtc acg gct ggt ttt cca gga act gtg gcg tcg ttt tgg	1315
Asp Ala Val Val Thr Ala Gly Phe Pro Gly Thr Val Ala Ser Phe Trp	
390 395 400 405	
cag cag gcg ggg cga gct ggt cgg cgt ggg cag ggt tcg ttg gtg gtg	1363
Gln Gln Ala Gly Arg Ala Gly Arg Arg Gly Gln Gly Ser Leu Val Val	
410 415 420	
ctt gtt gct cgt gat gag ccg atg gat acg tat ttg gtg cat cat ccg	1411
Leu Val Ala Arg Asp Glu Pro Met Asp Thr Tyr Leu Val His His Pro	
425 430 435	
gca gcc ctg ttg gag aag ccg gtt gag gct gcg gtg ttt gat ccg acg	1459
Ala Ala Leu Leu Glu Lys Pro Val Glu Ala Ala Val Phe Asp Pro Thr	
440 445 450	
aat ccg cat gtt att cgg ggt cat gtt tat tgc gct gcg gtg gaa aag	1507
Asn Pro His Val Ile Arg Gly His Val Tyr Cys Ala Ala Val Glu Lys	
455 460 465	
cct ctg aca gag gcg gag gtc gcg gcg ttt ggt gcc caa aag gtg gtg	1555
Pro Leu Thr Glu Ala Glu Val Ala Ala Phe Gly Ala Gln Lys Val Val	
470 475 480 485	
gag aag ctc gag att gaa ggg ctg ttg cgc aag cgt ccg cgt ggc tgg	1603
Glu Lys Leu Glu Ile Glu Gly Leu Leu Arg Lys Arg Pro Arg Gly Trp	
490 495 500	
ttt gcg gtg gaa aag ccc atg tca gag gat ccg gat gag ctg agt cct	1651
Phe Ala Val Glu Lys Pro Met Ser Glu Asp Pro Asp Glu Leu Ser Pro	
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gat tcg gca cac cag cag gtg agt ttg cgt ggt ggg tct ggt tcg gag	1699
Asp Ser Ala His Gln Gln Val Ser Leu Arg Gly Gly Ser Gly Ser Glu	
520 525 530	
ttc atg att gtt gat atc act gac ggc cgg ttg tta ggc acc atc gat	1747
Phe Met Ile Val Asp Ile Thr Asp Gly Arg Leu Leu Gly Thr Ile Asp	
535 540 545	

tcc gcg aag gcg atg tcg cag act cat ccc ggc gcg gtg tat ctc cac	1795
Ser Ala Lys Ala Met Ser Gln Thr His Pro Gly Ala Val Tyr Leu His	
550 555 560 565	
cag ggt gaa tcc ttt gtc att gat gag ttg gat ttg gag gag aat ctg	1843
Gln Gly Glu Ser Phe Val Ile Asp Glu Leu Asp Leu Glu Glu Asn Leu	
570 575 580	
gca ctg gcc agg cct gag ctg cct gat tac acc acc tat gcc aga agt	1891
Ala Leu Ala Arg Pro Glu Leu Pro Asp Tyr Thr Thr Tyr Ala Arg Ser	
585 590 595	
gac acg gac atc agg att acc tct gcc ccg ttg gag gac gag gtt ttt	1939
Asp Thr Asp Ile Arg Ile Thr Ser Ala Pro Leu Glu Asp Glu Val Phe	
600 605 610	
gat gct ggt ggt ggt ttg tgg gtc gcc aac gta gag gtg cag gtc acc	1987
Asp Ala Gly Gly Gly Leu Trp Val Ala Asn Val Glu Val Gln Val Thr	
615 620 625	
gac cgt gtg act ggc tat gtc acc cgc ctt agt gat ggc acc acg ttg	2035
Asp Arg Val Thr Gly Tyr Val Thr Arg Leu Ser Asp Gly Thr Thr Leu	
630 635 640 645	
gat gcg act ccg ttg tat ctt cct cct caa att ctt cag act cgt gcg	2083
Asp Ala Thr Pro Leu Tyr Leu Pro Pro Gln Ile Leu Gln Thr Arg Ala	
650 655 660	
gtg gcg tac acg att gat ccg ttg gcg ttg gaa gcg atg ggc att ccc	2131
Val Ala Tyr Thr Ile Asp Pro Leu Ala Leu Glu Ala Met Gly Ile Pro	
665 670 675	
gcc gct gat att ccc ggt gct ctt cac gca gcg gag cat gcg gcg att	2179
Ala Ala Asp Ile Pro Gly Ala Leu His Ala Ala Glu His Ala Ala Ile	
680 685 690	
ggt atg ttg ccg ctg ctt gcg acg tgt gat cgt tgg gat atc ggc ggc	2227
Gly Met Leu Pro Leu Leu Ala Thr Cys Asp Arg Trp Asp Ile Gly Gly	
695 700 705	
gta tcc acg gca ctt cat gcg gat acg ggc tac ccc act gtg ttt gtc	2275
Val Ser Thr Ala Leu His Ala Asp Thr Gly Tyr Pro Thr Val Phe Val	
710 715 720 725	
tat gac ggt atg gac ggc gga gct ggt ttt gcg gat act ggt ttt cga	2323
Tyr Asp Gly Met Asp Gly Gly Ala Gly Phe Ala Asp Thr Gly Phe Arg	
730 735 740	
cgt ttc gcc cag tgg att gag gcc aca ttt gag gtc gtc cgc agc tgt	2371
Arg Phe Ala Gln Trp Ile Glu Ala Thr Phe Glu Val Val Arg Ser Cys	
745 750 755	
agc tgt gaa tct ggg tgc ccg agc tgt gtg cag tcc ccg aaa tgc ggc	2419
Ser Cys Glu Ser Gly Cys Pro Ser Cys Val Gln Ser Pro Lys Cys Gly	
760 765 770	
aat gga aac aat ccg ttg gat aag gca ggt gcc atc aag tta ctg ggt	2467
Asn Gly Asn Asn Pro Leu Asp Lys Ala Gly Ala Ile Lys Leu Leu Gly	
775 780 785	
gcg atg gtg acc ttg ttg gga acc tca taaaggctcct gcttttgcgt	2514

Ala Met Val Thr Leu Leu Gly Thr Ser
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ggg

2517

<210> 88

<211> 798

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

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20 25 30

Ser Thr Leu Thr His Met Val Thr Leu Pro Ala Ser Lys Ala Lys Tyr
35 40 45

Val Asp Trp Pro Ser Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val
50 55 60

Asn Arg Gly Ile Asn Lys Leu Phe Ser His Gln Glu Gln Thr Ala His
65 70 75 80

Leu Ala Trp Asn Gly Gln His Val Val Val Ala Thr Gly Thr Ser Ser
85 90 95

Gly Lys Ser Leu Gly Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr
100 105 110

Asp Pro Thr Ala Cys Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly
115 120 125

Ser Asp Gln Leu Thr Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp
130 135 140

Phe His Pro Ile Asn Pro Ala Pro Tyr Asp Gly Asp Thr Pro Ser Glu
145 150 155 160

Ala Arg Ser Gly Ile Arg Asp Leu Ser Arg Phe Val Phe Thr Asn Pro
165 170 175

Asp Met Val His Ala Ser Met Leu Ala Asn His Pro Arg Trp Ala Arg
180 185 190

Leu Leu Arg His Leu Lys Phe Ile Val Ile Asp Glu Cys His Ala Tyr
195 200 205

Arg Gly Val Phe Gly Ala Asn Val Ser Met Val Leu Arg Arg Leu Leu
210 215 220

Arg Ile Ala Ala Phe Tyr Gly Ser His Pro Thr Val Ile Leu Ala Ser
225 230 235 240

Ala Thr Ser Ser Asp Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala
245 250 255

Pro Val Lys Ala Val Thr Glu Asp Gly Ala Pro Thr Gly Glu Arg Thr

260					265					270					
Val	Leu	Leu	Trp	Glu	Pro	Gly	Phe	Ile	Glu	Gly	Ala	Glu	Gly	Glu	Asn
	275						280					285			
Gly	Ala	Pro	Val	Arg	Arg	Ala	Ala	Ser	Thr	Glu	Ala	Ala	Asn	Ile	Met
	290					295					300				
Ala	Thr	Leu	Ile	Ser	Glu	Gly	Ala	Arg	Thr	Leu	Thr	Phe	Val	Arg	Ser
305					310					315					320
Arg	Arg	Gln	Ala	Glu	Ile	Val	Ala	Leu	Arg	Ala	Gln	Glu	Glu	Leu	Ser
				325					330					335	
Thr	Leu	Gly	Arg	Pro	Asp	Phe	Ala	Arg	Arg	Val	Ala	Ser	Tyr	Arg	Ala
			340					345					350		
Gly	Tyr	Leu	Ala	Glu	Asp	Arg	Arg	Arg	Leu	Glu	Arg	Leu	Leu	Asp	Asp
	355						360					365			
Gly	Thr	Leu	Leu	Gly	Val	Ala	Ser	Thr	Asn	Ala	Leu	Glu	Leu	Gly	Ile
	370					375					380				
Asp	Val	Gly	Gly	Leu	Asp	Ala	Val	Val	Thr	Ala	Gly	Phe	Pro	Gly	Thr
385					390					395					400
Val	Ala	Ser	Phe	Trp	Gln	Gln	Ala	Gly	Arg	Ala	Gly	Arg	Arg	Gly	Gln
				405					410					415	
Gly	Ser	Leu	Val	Val	Leu	Val	Ala	Arg	Asp	Glu	Pro	Met	Asp	Thr	Tyr
			420					425					430		
Leu	Val	His	His	Pro	Ala	Ala	Leu	Leu	Glu	Lys	Pro	Val	Glu	Ala	Ala
		435					440					445			
Val	Phe	Asp	Pro	Thr	Asn	Pro	His	Val	Ile	Arg	Gly	His	Val	Tyr	Cys
	450					455					460				
Ala	Ala	Val	Glu	Lys	Pro	Leu	Thr	Glu	Ala	Glu	Val	Ala	Ala	Phe	Gly
465						470					475				480
Ala	Gln	Lys	Val	Val	Glu	Lys	Leu	Glu	Ile	Glu	Gly	Leu	Leu	Arg	Lys
				485					490					495	
Arg	Pro	Arg	Gly	Trp	Phe	Ala	Val	Glu	Lys	Pro	Met	Ser	Glu	Asp	Pro
			500					505					510		
Asp	Glu	Leu	Ser	Pro	Asp	Ser	Ala	His	Gln	Gln	Val	Ser	Leu	Arg	Gly
	515						520					525			
Gly	Ser	Gly	Ser	Glu	Phe	Met	Ile	Val	Asp	Ile	Thr	Asp	Gly	Arg	Leu
	530					535					540				
Leu	Gly	Thr	Ile	Asp	Ser	Ala	Lys	Ala	Met	Ser	Gln	Thr	His	Pro	Gly
545					550					555					560
Ala	Val	Tyr	Leu	His	Gln	Gly	Glu	Ser	Phe	Val	Ile	Asp	Glu	Leu	Asp
				565					570					575	
Leu	Glu	Glu	Asn	Leu	Ala	Leu	Ala	Arg	Pro	Glu	Leu	Pro	Asp	Tyr	Thr
			580					585					590		

Thr Tyr Ala Arg Ser Asp Thr Asp Ile Arg Ile Thr Ser Ala Pro Leu
 595 600 605
 Glu Asp Glu Val Phe Asp Ala Gly Gly Gly Leu Trp Val Ala Asn Val
 610 615 620
 Glu Val Gln Val Thr Asp Arg Val Thr Gly Tyr Val Thr Arg Leu Ser
 625 630 635 640
 Asp Gly Thr Thr Leu Asp Ala Thr Pro Leu Tyr Leu Pro Pro Gln Ile
 645 650 655
 Leu Gln Thr Arg Ala Val Ala Tyr Thr Ile Asp Pro Leu Ala Leu Glu
 660 665 670
 Ala Met Gly Ile Pro Ala Ala Asp Ile Pro Gly Ala Leu His Ala Ala
 675 680 685
 Glu His Ala Ala Ile Gly Met Leu Pro Leu Leu Ala Thr Cys Asp Arg
 690 695 700
 Trp Asp Ile Gly Gly Val Ser Thr Ala Leu His Ala Asp Thr Gly Tyr
 705 710 715 720
 Pro Thr Val Phe Val Tyr Asp Gly Met Asp Gly Gly Ala Gly Phe Ala
 725 730 735
 Asp Thr Gly Phe Arg Arg Phe Ala Gln Trp Ile Glu Ala Thr Phe Glu
 740 745 750
 Val Val Arg Ser Cys Ser Cys Glu Ser Gly Cys Pro Ser Cys Val Gln
 755 760 765
 Ser Pro Lys Cys Gly Asn Gly Asn Asn Pro Leu Asp Lys Ala Gly Ala
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 Ile Lys Leu Leu Gly Ala Met Val Thr Leu Leu Gly Thr Ser
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<210> 89

<211> 610

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(610)

<223> FRXA00809

<400> 89

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 Leu Thr Thr Pro Asp
 1 5

ttt gag agt gaa aag act caa gct atg agg ccc agc ttt ggt gaa gag 163
 Phe Glu Ser Glu Lys Thr Gln Ala Met Arg Pro Ser Phe Gly Glu Glu
 10 15 20

ctg gcc gca atc gtt tcc aaa cgt tac tcc gaa tcg acg ctc act cat 211
 Leu Ala Ala Ile Val Ser Lys Arg Tyr Ser Glu Ser Thr Leu Thr His
 25 30 35

atg gtg acg ttg ccc gca tcg aaa gct aaa tac gtc gat tgg ccg agt 259
 Met Val Thr Leu Pro Ala Ser Lys Ala Lys Tyr Val Asp Trp Pro Ser
 40 45 50

tgg gta cct gct agc ctg cgc gat gcg ttg gtg aat cgt ggt atc aat 307
 Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val Asn Arg Gly Ile Asn
 55 60 65

aag ctc ttt tcc cac cag gag cag acc gca cat ctg gcg tgg aat ggc 355
 Lys Leu Phe Ser His Gln Glu Gln Thr Ala His Leu Ala Trp Asn Gly
 70 75 80 85

cag cat gtg gtg gtt gcc acc ggt aca tct tcg gga aaa tct ttg ggt 403
 Gln His Val Val Val Ala Thr Gly Thr Ser Ser Gly Lys Ser Leu Gly
 90 95 100

tat cag ctg ccc att ttg tca gcg ctc ggc acg gat cct acc gcc tgt 451
 Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr Asp Pro Thr Ala Cys
 105 110 115

gcg ttg tat cta act ccc acc aag gct ttg gga tct gat cag cta acc 499
 Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly Ser Asp Gln Leu Thr
 120 125 130

tcc acg tcc acg ttg ctg cgc gac att ccg gat ttc cac ccg att aat 547
 Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp Phe His Pro Ile Asn
 135 140 145

ccg gcg ccc tac gat ggc gat acc ccc tcc gag gcg cgg tcc ggc atc 595
 Pro Ala Pro Tyr Asp Gly Asp Thr Pro Ser Glu Ala Arg Ser Gly Ile
 150 155 160 165

cgc gat ttg agt cgt 610
 Arg Asp Leu Ser Arg
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<210> 90

<211> 170

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

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Ser Phe Gly Glu Glu Leu Ala Ala Ile Val Ser Lys Arg Tyr Ser Glu
 20 25 30

Ser Thr Leu Thr His Met Val Thr Leu Pro Ala Ser Lys Ala Lys Tyr
 35 40 45

Val Asp Trp Pro Ser Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val
 50 55 60

Asn Arg Gly Ile Asn Lys Leu Phe Ser His Gln Glu Gln Thr Ala His

65	70	75	80
Leu Ala Trp Asn Gly Gln His Val Val Val Ala Thr Gly Thr Ser Ser			
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Gly Lys Ser Leu Gly Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr			
	100	105	110
Asp Pro Thr Ala Cys Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly			
	115	120	125
Ser Asp Gln Leu Thr Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp			
	130	135	140
Phe His Pro Ile Asn Pro Ala Pro Tyr Asp Gly Asp Thr Pro Ser Glu			
	145	150	155
Ala Arg Ser Gly Ile Arg Asp Leu Ser Arg			
	165	170	

<210> 91
 <211> 1733
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1710)
 <223> FRXA00817

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gat ccg gaa att cat gct tcc aga ttg ttg ggc gcg ccg gtt aaa gca	96
Asp Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala Pro Val Lys Ala	
20 25 30	
gtg acg gaa gat ggc gcc ccg acg ggt gaa cgc acc gtt ttg ctg tgg	144
Val Thr Glu Asp Gly Ala Pro Thr Gly Glu Arg Thr Val Leu Leu Trp	
35 40 45	
gag ccc ggt ttc atc gaa ggc gcc gag ggc gag aac ggc gcg ccg gtg	192
Glu Pro Gly Phe Ile Glu Gly Ala Glu Gly Glu Asn Gly Ala Pro Val	
50 55 60	
cgt cgc gca gcc agc acc gaa gca gca aac att atg gcc acg ctc att	240
Arg Arg Ala Ala Ser Thr Glu Ala Ala Asn Ile Met Ala Thr Leu Ile	
65 70 75 80	
tcc gag ggt gca cgc acg ttg acg ttc gtc cgt tca cgt cga caa gca	288
Ser Glu Gly Ala Arg Thr Leu Thr Phe Val Arg Ser Arg Arg Gln Ala	
85 90 95	
gaa atc gtt gcc ctg cgc gcg cag gaa gag ctc agc acg ctg ggc cgc	336
Glu Ile Val Ala Leu Arg Ala Gln Glu Glu Leu Ser Thr Leu Gly Arg	
100 105 110	
ccc gat ttc gcc cgg cgc gtc gcg tcc tac cgg gcg ggg tac ttg gcg	384

Pro Asp Phe Ala Arg Arg Val Ala Ser Tyr Arg Ala Gly Tyr Leu Ala	
115 120 125	
gag gac cgc cgt agg ttg gag aga ttg ctt gac gac ggc acc ctc ctc	432
Glu Asp Arg Arg Arg Leu Glu Arg Leu Leu Asp Asp Gly Thr Leu Leu	
130 135 140	
ggt gtt gct tcc acc aat gcg ctt gaa ctg ggc att gat gtc ggt gga	480
Gly Val Ala Ser Thr Asn Ala Leu Glu Leu Gly Ile Asp Val Gly Gly	
145 150 155 160	
ctg gat gct gtg gtc acg gct ggt ttt cca gga act gtg gcg tcg ttt	528
Leu Asp Ala Val Val Thr Ala Gly Phe Pro Gly Thr Val Ala Ser Phe	
165 170 175	
tgg cag cag gcg ggg cga gct ggt cgg cgt ggg cag ggt tcg ttg gtg	576
Trp Gln Gln Ala Gly Arg Ala Gly Arg Arg Gly Gln Gly Ser Leu Val	
180 185 190	
gtg ctt gtt gct cgt gat gag ccg atg gat acg tat ttg gtg cat cat	624
Val Leu Val Ala Arg Asp Glu Pro Met Asp Thr Tyr Leu Val His His	
195 200 205	
ccg gca gcc ctg ttg gag aag ccg gtt gag gct gcg gtg ttt gat ccg	672
Pro Ala Ala Leu Leu Glu Lys Pro Val Glu Ala Ala Val Phe Asp Pro	
210 215 220	
acg aat ccg cat gtt att cgg ggt cat gtt tat tgc gct gcg gtg gaa	720
Thr Asn Pro His Val Ile Arg Gly His Val Tyr Cys Ala Ala Val Glu	
225 230 235 240	
aag cct ctg aca gag gcg gag gtc gcg gcg ttt ggt gcc caa aag gtg	768
Lys Pro Leu Thr Glu Ala Glu Val Ala Ala Phe Gly Ala Gln Lys Val	
245 250 255	
gtg gag aag ctc gag att gaa ggg ctg ttg cgc aag cgt ccg cgt ggc	816
Val Glu Lys Leu Glu Ile Glu Gly Leu Leu Arg Lys Arg Pro Arg Gly	
260 265 270	
tgg ttt gcg gtg gaa aag ccc atg tca gag gat ccg gat gag ctg agt	864
Trp Phe Ala Val Glu Lys Pro Met Ser Glu Asp Pro Asp Glu Leu Ser	
275 280 285	
cct gat tcg gca cac cag cag gtg agt ttg cgt ggt ggg tct ggt tcg	912
Pro Asp Ser Ala His Gln Gln Val Ser Leu Arg Gly Gly Ser Gly Ser	
290 295 300	
gag ttc atg att gtt gat atc act gac ggc cgg ttg tta ggc acc atc	960
Glu Phe Met Ile Val Asp Ile Thr Asp Gly Arg Leu Leu Gly Thr Ile	
305 310 315 320	
gat tcc gcg aag gcg atg tcg cag act cat ccc ggc gcg gtg tat ctc	1008
Asp Ser Ala Lys Ala Met Ser Gln Thr His Pro Gly Ala Val Tyr Leu	
325 330 335	
cac cag ggt gaa tcc ttt gtc att gat gag ttg gat ttg gag gag aat	1056
His Gln Gly Glu Ser Phe Val Ile Asp Glu Leu Asp Leu Glu Glu Asn	
340 345 350	
ctg gca ctg gcc agg cct gag ctg cct gat tac acc acc tat gcc aga	1104
Leu Ala Leu Ala Arg Pro Glu Leu Pro Asp Tyr Thr Thr Tyr Ala Arg	

355	360	365	
agt gac acg gac atc agg att acc tct gcc ccg ttg gag gac gag gtt Ser Asp Thr Asp Ile Arg Ile Thr Ser Ala Pro Leu Glu Asp Glu Val 370 375 380			1152
ttt gat gct ggt ggt ggt ttg tgg gtc gcc aac gta gag gtg cag gtc Phe Asp Ala Gly Gly Gly Leu Trp Val Ala Asn Val Glu Val Gln Val 385 390 395 400			1200
acc gac cgt gtg act ggc tat gtc acc cgc ctt agt gat ggc acc acg Thr Asp Arg Val Thr Gly Tyr Val Thr Arg Leu Ser Asp Gly Thr Thr 405 410 415			1248
ttg gat gcg act ccg ttg tat ctt cct cct caa att ctt cag act cgt Leu Asp Ala Thr Pro Leu Tyr Leu Pro Pro Gln Ile Leu Gln Thr Arg 420 425 430			1296
gcg gtg gcg tac acg att gat ccg ttg gcg ttg gaa gcg atg ggc att Ala Val Ala Tyr Thr Ile Asp Pro Leu Ala Leu Glu Ala Met Gly Ile 435 440 445			1344
ccc gcc gct gat att ccc ggt gct ctt cac gca gcg gag cat gcg gcg Pro Ala Ala Asp Ile Pro Gly Ala Leu His Ala Ala Glu His Ala Ala 450 455 460			1392
att ggt atg ttg ccg ctg ctt gcg acg tgt gat cgt tgg gat atc ggc Ile Gly Met Leu Pro Leu Leu Ala Thr Cys Asp Arg Trp Asp Ile Gly 465 470 475 480			1440
ggc gta tcc acg gca ctt cat gcg gat acg ggc tac ccc act gtg ttt Gly Val Ser Thr Ala Leu His Ala Asp Thr Gly Tyr Pro Thr Val Phe 485 490 495			1488
gtc tat gac ggt atg gac ggc gga gct ggt ttt gcg gat act ggt ttt Val Tyr Asp Gly Met Asp Gly Gly Ala Gly Phe Ala Asp Thr Gly Phe 500 505 510			1536
cga cgt ttc gcc cag tgg att gag gcc aca ttt gag gtc gtc cgc agc Arg Arg Phe Ala Gln Trp Ile Glu Ala Thr Phe Glu Val Val Arg Ser 515 520 525			1584
tgt agc tgt gaa tct ggg tgc ccg agc tgt gtg cag tcc ccg aaa tgc Cys Ser Cys Glu Ser Gly Cys Pro Ser Cys Val Gln Ser Pro Lys Cys 530 535 540			1632
ggc aat gga aac aat ccg ttg gat aag gca ggt gcc atc aag tta ctg Gly Asn Gly Asn Asn Pro Leu Asp Lys Ala Gly Ala Ile Lys Leu Leu 545 550 555 560			1680
ggg ggc atg gtg acc ttg ttg gga acc tca taaaggctcct gcttttgcgt Gly Ala Met Val Thr Leu Leu Gly Thr Ser 565 570			1730
ggg			1733

<210> 92

<211> 570

<212> PRT

<213> Corynebacterium glutamicum

<400> 92

Phe Tyr Gly Ser His Pro Thr Val Ile Leu Ala Ser Ala Thr Ser Ser
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 Asp Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala Pro Val Lys Ala
 20 25 30
 Val Thr Glu Asp Gly Ala Pro Thr Gly Glu Arg Thr Val Leu Leu Trp
 35 40 45
 Glu Pro Gly Phe Ile Glu Gly Ala Glu Gly Glu Asn Gly Ala Pro Val
 50 55 60
 Arg Arg Ala Ala Ser Thr Glu Ala Ala Asn Ile Met Ala Thr Leu Ile
 65 70 75 80
 Ser Glu Gly Ala Arg Thr Leu Thr Phe Val Arg Ser Arg Arg Gln Ala
 85 90 95
 Glu Ile Val Ala Leu Arg Ala Gln Glu Glu Leu Ser Thr Leu Gly Arg
 100 105 110
 Pro Asp Phe Ala Arg Arg Val Ala Ser Tyr Arg Ala Gly Tyr Leu Ala
 115 120 125
 Glu Asp Arg Arg Arg Leu Glu Arg Leu Leu Asp Asp Gly Thr Leu Leu
 130 135 140
 Gly Val Ala Ser Thr Asn Ala Leu Glu Leu Gly Ile Asp Val Gly Gly
 145 150 155 160
 Leu Asp Ala Val Val Thr Ala Gly Phe Pro Gly Thr Val Ala Ser Phe
 165 170 175
 Trp Gln Gln Ala Gly Arg Ala Gly Arg Arg Gly Gln Gly Ser Leu Val
 180 185 190
 Val Leu Val Ala Arg Asp Glu Pro Met Asp Thr Tyr Leu Val His His
 195 200 205
 Pro Ala Ala Leu Leu Glu Lys Pro Val Glu Ala Ala Val Phe Asp Pro
 210 215 220
 Thr Asn Pro His Val Ile Arg Gly His Val Tyr Cys Ala Ala Val Glu
 225 230 235 240
 Lys Pro Leu Thr Glu Ala Glu Val Ala Ala Phe Gly Ala Gln Lys Val
 245 250 255
 Val Glu Lys Leu Glu Ile Glu Gly Leu Leu Arg Lys Arg Pro Arg Gly
 260 265 270
 Trp Phe Ala Val Glu Lys Pro Met Ser Glu Asp Pro Asp Glu Leu Ser
 275 280 285
 Pro Asp Ser Ala His Gln Gln Val Ser Leu Arg Gly Gly Ser Gly Ser
 290 295 300
 Glu Phe Met Ile Val Asp Ile Thr Asp Gly Arg Leu Leu Gly Thr Ile
 305 310 315 320

Asp Ser Ala Lys Ala Met Ser Gln Thr His Pro Gly Ala Val Tyr Leu
325 330 335

His Gln Gly Glu Ser Phe Val Ile Asp Glu Leu Asp Leu Glu Glu Asn
340 345 350

Leu Ala Leu Ala Arg Pro Glu Leu Pro Asp Tyr Thr Thr Tyr Ala Arg
355 360 365

Ser Asp Thr Asp Ile Arg Ile Thr Ser Ala Pro Leu Glu Asp Glu Val
370 375 380

Phe Asp Ala Gly Gly Gly Leu Trp Val Ala Asn Val Glu Val Gln Val
385 390 395 400

Thr Asp Arg Val Thr Gly Tyr Val Thr Arg Leu Ser Asp Gly Thr Thr
405 410 415

Leu Asp Ala Thr Pro Leu Tyr Leu Pro Pro Gln Ile Leu Gln Thr Arg
420 425 430

Ala Val Ala Tyr Thr Ile Asp Pro Leu Ala Leu Glu Ala Met Gly Ile
435 440 445

Pro Ala Ala Asp Ile Pro Gly Ala Leu His Ala Ala Glu His Ala Ala
450 455 460

Ile Gly Met Leu Pro Leu Leu Ala Thr Cys Asp Arg Trp Asp Ile Gly
465 470 475 480

Gly Val Ser Thr Ala Leu His Ala Asp Thr Gly Tyr Pro Thr Val Phe
485 490 495

Val Tyr Asp Gly Met Asp Gly Gly Ala Gly Phe Ala Asp Thr Gly Phe
500 505 510

Arg Arg Phe Ala Gln Trp Ile Glu Ala Thr Phe Glu Val Val Arg Ser
515 520 525

Cys Ser Cys Glu Ser Gly Cys Pro Ser Cys Val Gln Ser Pro Lys Cys
530 535 540

Gly Asn Gly Asn Asn Pro Leu Asp Lys Ala Gly Ala Ile Lys Leu Leu
545 550 555 560

Gly Ala Met Val Thr Leu Leu Gly Thr Ser
565 570

<210> 93

<211> 4683

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(4660)

<223> RXN00103

<400> 93

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Lys Asp Val Gln Val Asp Glu Trp Tyr Glu Thr Ile Arg Lys Ala Tyr	
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 Ala Ala Val Ser Ile Lys Asp Val Gln Val Asp Glu Trp Tyr Glu Thr
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 Ala Ser Pro Thr Pro Val Gln Glu Gly Thr Trp Glu Ala Val Ser Lys
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 Gly Lys Asn Ala Leu Val Val Ala Pro Thr Gly Ser Gly Lys Thr Leu
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 Ala Ala Phe Leu Trp Ala Leu Asp Ser Leu Thr Glu Gln Thr Gly Gln
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 Lys Val Leu Tyr Ile Ser Pro Leu Lys Ala Leu Gly Val Asp Val Glu
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Ser Phe Tyr Pro Lys His Arg Ser Asp Leu Val Gln Thr Ala Val Thr	
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Val Gln Arg Met Lys Glu Gly Leu Ile Glu Glu Ile His Val Pro Lys	
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Lys Asp Val Gln Val Asp Glu Trp Tyr Glu Thr Ile Arg Lys Ala Tyr	
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Ala	His	Asp	Asn	Leu	Ile	Ala	Phe	Leu	Gln	Glu	Gln	Glu	Glu	Ser	Thr		
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Gln	Arg	Ala	Ala	Gln	Leu	Leu	Asp	Val	Ala	Arg	Lys	Tyr	Pro	Ser	Phe		
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ccg	atc	att	ttg	gaa	aca	gtg	cgc	gaa	tgt	ctt	caa	gat	gtt	tac	gat	2611	
Pro	Ile	Ile	Leu	Glu	Thr	Val	Arg	Glu	Cys	Leu	Gln	Asp	Val	Tyr	Asp		
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Ala Leu Gln Ser Ala Pro Val Ile Glu Gly Arg Tyr Arg Gln Gly Val			
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Asp Val Gln Glu Tyr Cys Ala Thr Glu Val Leu Ser Ile Ile Arg Arg			
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Arg Ser Leu Ala Ala Ala Arg Lys Gln Thr Arg Pro Val Ser Gln Ser			
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Ser Val Ser Lys Asp Glu Arg Ala Thr Thr Glu Thr Met Leu Lys Glu
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Asp Met Gly Ala Val Asp Leu Val Ile Gln Val Glu Ser Pro Pro Ser
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Val Ala Ser Gly Leu Gln Arg Val Gly Arg Ala Gly His Thr Val Gly
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Ser Val Ile Asp Leu Val Ser Gly Val Tyr Pro Ser Thr Asp Phe Ala
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Glu Leu Lys Pro Arg Val Val Tyr Asp Arg Val Ser Gly Val Leu Glu
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Pro Phe Trp Thr Gly Asp Ala Ala Gly Arg Pro Ala Glu Leu Gly Lys
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Ala Leu Gly Ala Phe Arg Arg Ser Thr Leu Thr Asp Pro Ser Ser Ser
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Gln Glu Glu Ser Thr Gly Val Leu Pro Asp Glu Lys Thr Leu Val Leu
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Glu Arg Phe Lys Asp Glu Leu Gly Asp Trp Arg Ile Val Leu His Thr

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Gln Val Gly Asn Ser Ala Leu Phe Ala Ser Arg Phe Arg Glu Cys Ala 770 775 780		
Ala Arg Ala Leu Leu Leu Pro Arg Arg Asn Pro Gly Lys Arg Ala Pro 785 790 795 800		
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Lys Tyr Pro Ser Phe Pro Ile Ile Leu Glu Thr Val Arg Glu Cys Leu 820 825 830		
Gln Asp Val Tyr Asp Leu Pro Ala Leu Lys Asn Leu Ile Glu Asp Leu 835 840 845		
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Leu Leu Asp Pro Asp Ile Ile Ala Glu Val His Gln Gln Leu Arg Arg 915 920 925		
Gln Gly Asp Arg Ala Ala Arg Asn Asn Glu Glu Leu Ala Asp Ser Leu 930 935 940		
Arg Ile Leu Gly Pro Ile Pro Leu Asp Glu Leu Gly Glu His Ile Thr 945 950 955 960		
Phe Glu Asn Pro Asp Leu Glu Asp Arg Ala Met Thr Val Arg Ile Asn 965 970 975		
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Gly Gln Ala Gly Ser Arg Asp Pro Trp Ile Ser Leu Leu Pro Val Asp
1170 1175 1180

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 Met Ser Ser Leu Ile
 1 5
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 Pro Val His Ala Ala Gly Ser Ile Gln Glu Gly Ile Thr Glu Tyr Leu
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 Thr Thr Ser Phe Ser Leu Ala Asp Lys Gln Val Ala Thr Glu Leu Lys
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Arg Phe Leu Gly His Gly Asp Ser Gly Met Phe His Gly Pro Tyr Val	
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Arg Ala Arg Leu Pro Tyr Ala Gln Ala Gln Glu Trp Glu Asn Val Leu	
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agt tgg tta cct gag aac ttt gtg ccc tat cac cat caa aaa gcg gcg	355
Ser Trp Leu Pro Glu Asn Phe Val Pro Tyr His His Gln Lys Ala Ala	
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Phe Gln Arg Leu Ser Ser Leu Asp Asn Arg Gly Lys Asp Arg Arg Pro	
90 95 100	
gat ccc acc ttg gtg gta act gga acg ggt tcc ggt aag acg gaa tct	451
Asp Pro Thr Leu Val Val Thr Gly Thr Gly Ser Gly Lys Thr Glu Ser	
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Phe Leu Tyr Pro Ile Leu Asp His Ala Leu Arg Leu Arg Lys Arg Gly	
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Gln Gln Gly Ile Lys Ala Leu Leu Leu Tyr Pro Met Asn Ala Leu Ala	
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Asn Asp Gln Ala Asp Arg Leu Ala Arg Leu Ile His Asn Asn Pro Ala	
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Leu Lys Gly Val Thr Ala Gly Ile Tyr Thr Gly Glu Ala Lys Gly Asn	
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Arg Thr Gln Met Gly Glu Arg Glu Leu Ile Asn Asp Pro Gln Ala Met	
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Gln Leu Leu Leu Arg Ser Val Asp Arg Glu Met Trp Gln Lys Ser Ala	
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Ser Gly Asp Ser Gly Ser Pro Met Leu Asp Phe Ala Tyr Thr Ile Phe	
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Val Ser Glu Pro Arg Glu Leu Pro Thr Val Glu Asp Ile Glu Val Val	
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Cys Phe Arg Val Phe Cys Glu Lys Val Trp Leu Cys Glu Ala Asp Leu	
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His Ala Ala Ile Ser Ala Tyr Ala Ala His Asp Leu Thr Ala Ala Ile	
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Leu Gln His Ala Ala Asp Ser Thr Pro Leu Ser Arg Arg Asp Gln Asp	
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Glu Val Thr Ala Leu Pro Glu Leu Val Leu Gly Ala Thr Ala Arg Ile	
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Met Ala Phe Val Arg Ala Glu Tyr Gly Lys Val Ala Ala Trp Gly Ala	
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Lys Arg Leu Pro Gly Val Glu Thr His Leu Trp Val Arg Glu Val Ser	
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Trp Ser Asp Asp Gly Pro Ala Glu Asp Ala Asn Thr Gln Gln Trp Leu	
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Leu	Glu	Gln	Gly	Thr	Asn	Ile	Pro	Val	Leu	Glu	Glu	Gln	Lys	Ile	Arg		
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ctc	aac	tcc	ttt	gaa	caa	ccc	cat	aaa	caa	aga	gcg	ctt	ctc	gac	gcc	1795	
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Thr	Ser	Glu	Gln	Arg	Ala	Ala	Ile	Glu	Gln	Gly	Arg	Ser	Val	Ala	Gly		
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ccg	cga	gga	gtt	gat	ggc	acc	tca	gca	gtg	ctg	tgg	ttc	cat	agc	gcc	1891	
Pro	Arg	Gly	Val	Asp	Gly	Thr	Ser	Ala	Val	Leu	Trp	Phe	His	Ser	Ala		
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agc	aat	gaa	ctc	agc	acg	cgc	caa	ccc	agc	cca	gaa	gaa	gaa	caa	tca	1939	
Ser	Asn	Glu	Leu	Ser	Thr	Arg	Gln	Pro	Ser	Pro	Glu	Glu	Glu	Gln	Ser		
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ggg	tct	tct	atc	gca	gtg	ctc	acc	cac	ttt	ggc	cct	gag	gca	gac	gat	1987	
Gly	Ser	Ser	Ile	Ala	Val	Leu	Thr	His	Phe	Gly	Pro	Glu	Ala	Asp	Asp		
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ctc	tcc	gcc	aaa	cag	acc	tgc	cct	tcc	tgt	ggg	gat	gtt	gat	tcc	atc	2035	
Leu	Ser	Ala	Lys	Gln	Thr	Cys	Pro	Ser	Cys	Gly	Asp	Val	Asp	Ser	Ile		
630					635					640					645		
cggt	tat	atc	gga	tcg	gga	atc	tct	acc	ctg	ctc	tct	gtc	tca	ctc	tcc	2083	
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aat	ctt	ttt	ggg	atg	gcc	gat	ttg	gat	agc	gct	gag	aaa	aag	acg	ctg	2131	
Asn	Leu	Phe	Gly	Met	Ala	Asp	Leu	Asp	Ser	Ala	Glu	Lys	Lys	Thr	Leu		
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gtc	ttt	gcc	gat	tcc	gtg	caa	gat	gcc	gcg	cac	cgc	gcc	ggg	tac	gtc	2179	
Val	Phe	Ala	Asp	Ser	Val	Gln	Asp	Ala	Ala	His	Arg	Ala	Gly	Tyr	Val		
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caa	gca	cggt	tcc	cggt	gct	ttt	gcc	ctt	cggt	acc	tat	acc	cggt	cggt	gca	2227	
Gln	Ala	Arg	Ser	Arg	Ala	Phe	Ala	Leu	Arg	Thr	Tyr	Thr	Arg	Arg	Ala		
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gtg	ggg	gat	aat	gaa	gtc	acc	ttg	cca	tca	atc	tcc	cggt	gcgt	ctgt	atgt	2275	
Val	Gly	Asp	Asn	Glu	Val	Thr	Leu	Pro	Ser	Ile	Ser	Arg	Ala	Leu	Met		
710					715					720					725		
gat	aac	gcc	acc	tct	ggg	cggt	acc	cggt	tat	gag	ctc	cta	ccc	cct	gac	2323	
Asp	Asn	Ala	Thr	Ser	Gly	Arg	Thr	Arg	Tyr	Glu	Leu	Leu	Pro	Pro	Asp		
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ctg	acc	gat	ctt	gat	att	tac	aaa	cct	tat	tgg	cac	ccc	gat	gcc	agc	2371	
Leu	Thr	Asp	Leu	Asp	Ile	Tyr	Lys	Pro	Tyr	Trp	His	Pro	Asp	Ala	Ser		
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Lys	Ala	Glu	Arg	Arg	Glu	Ala	Ser	Arg	Asn	Val	His	Lys	Arg	Leu	Ser		

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Leu Ala Leu Thr Gly Ala	Leu Ser Ala Phe Val	Asp Leu Pro Lys Gly	
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Val Ala Leu Ser Ala Ala	Ala Glu Ala Leu Tyr	Ala Ile Glu Val Pro	
810	815	820	
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Thr Leu Asp Ile Glu Asp	Glu Asn Leu Arg Leu	Arg Trp Val Gln Gly	
825	830	835	
gcc ctg gaa ctt ttg cgc	gcc cgc ggg ggc atc	aac cat gag tgg ttt	2659
Ala Leu Glu Leu Leu Arg	Ala Arg Gly Gly Ile	Asn His Glu Trp Phe	
840	845	850	
ggc gcc tac ctg cgc acc	gat ggc aac ccc tat	atg ctt aac cgc cgc	2707
Gly Ala Tyr Leu Arg Thr	Asp Gly Asn Pro Tyr	Met Leu Asn Arg Arg	
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Gln Ala Arg Ala Glu Gly	Ile Pro Gly Phe Val	Arg Gly Gly Ala Pro	
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Glu Phe Pro Arg Val Gly	Ser Ala Leu Ser Gly	Ser Leu Arg Ser Ser	
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Thr Gly Thr Thr Pro Leu	Gly Ser Pro Arg Gly	Arg Tyr Ala Ser Trp	
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Ser Thr Asp Ser Gly Gly	Lys Ile Tyr Cys Leu	Glu Ala Glu Arg Ile	
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Arg Ile Phe Ser Glu Asp	His Pro Glu Val Leu	Glu Cys Ser Val Cys	
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His Ala Gln Thr Gly Val	Thr Asp His Val Arg	Asp Phe Leu Asp Gly	
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aac ttc acc ctg gtt gat gat tcc gta gaa ctt aat gtg gcg gtt act	4099
Asn Phe Thr Leu Val Asp Asp Ser Val Glu Leu Asn Val Ala Val Thr	
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tcg ttc aac ccc cag gaa gtg gaa ttt gat acc aag aat cat gcc tac	4147
Ser Phe Asn Pro Gln Glu Val Glu Phe Asp Thr Lys Asn His Ala Tyr	
1335 1340 1345	
tcg cgt ggg atc tct gca gcg ctt ttt gag ctc gct ccc ggt gcg acc	4195
Ser Arg Gly Ile Ser Ala Ala Leu Phe Glu Leu Ala Pro Gly Ala Thr	
1350 1355 1360 1365	
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Phe Tyr Ala Gln Gly Ile Ala Ala Lys Val Asp Ser Ile Glu Ile Gly	
1370 1375 1380	
gaa cat ggc tct gcc att gag caa tgg cgg ttg tgc ccc gtg tgc tcg	4291
Glu His Gly Ser Ala Ile Glu Gln Trp Arg Leu Cys Pro Val Cys Ser	
1385 1390 1395	
cac tcc gaa atc ctc cag ccg ggt gtc tct aca ccg gga tcg tgt cct	4339
His Ser Glu Ile Leu Gln Pro Gly Val Ser Thr Pro Gly Ser Cys Pro	
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acc tgt ggc tcc ccc gcc ttt gcc gat aag gga caa atc cta gag gta	4387
Thr Cys Gly Ser Pro Ala Phe Ala Asp Lys Gly Gln Ile Leu Glu Val	
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gtg caa atg cgt aag gtt tcc tcc gca gtg gag aaa act cgc gct gcc	4435
Val Gln Met Arg Lys Val Ser Ser Ala Val Glu Lys Thr Arg Ala Ala	
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att agc gat gac cgt gaa gat cgc ttt agc acc cgc ttt aac cag cac	4483
Ile Ser Asp Asp Arg Glu Asp Arg Phe Ser Thr Arg Phe Asn Gln His	
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Val Ser Phe Val Val Pro Pro Asp Gly His Gly Lys Ser Trp Tyr Leu	
1465 1470 1475	
aat gat ggt ttt ggc att gag cat ctg ccc aag gtg gaa tta cgc tgg	4579
Asn Asp Gly Phe Gly Ile Glu His Leu Pro Lys Val Glu Leu Arg Trp	
1480 1485 1490	
ctg aac tta gga att ggc aat ggc caa aag cgt cgg ctc ggt ggc ttt	4627

Leu	Asn	Leu	Gly	Ile	Gly	Asn	Gly	Gln	Lys	Arg	Arg	Leu	Gly	Gly	Phe	
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gaa	gtc	acc	agc	cca	cta	ttt	aat	gtg	tgc	cgc	cac	tgt	gga	cat	tta	4675
Glu	Val	Thr	Ser	Pro	Leu	Phe	Asn	Val	Cys	Arg	His	Cys	Gly	His	Leu	
1510					1515					1520					1525	
gat	tcc	gag	gca	gga	gct	aac	tca	cgc	tgg	gat	cac	cga	ccc	tgg	tgc	4723
Asp	Ser	Glu	Ala	Gly	Ala	Asn	Ser	Arg	Trp	Asp	His	Arg	Pro	Trp	Cys	
				1530					1535					1540		
cca	cac	cgt	tat	gag	caa	aaa	gaa	gat	acc	gta	tct	ttc	gct	ttg	ggc	4771
Pro	His	Arg	Tyr	Glu	Gln	Lys	Glu	Asp	Thr	Val	Ser	Phe	Ala	Leu	Gly	
			1545					1550					1555			
cgt	act	ctt	aaa	acc	caa	ggc	gtg	ctc	atg	ctg	ctg	ccc	gaa	tat	ttt	4819
Arg	Thr	Leu	Lys	Thr	Gln	Gly	Val	Leu	Met	Leu	Leu	Pro	Glu	Tyr	Phe	
		1560					1565					1570				
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Gly	Ser	Glu	Ala	Asp	Ser	Met	Val	Val	Thr	Ser	Leu	Ile	Ala	Ala	Ile	
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Lys	Leu	Gly	Phe	Arg	Glu	Val	Leu	Gly	Gly	Asp	Pro	Asp	His	Leu	Asp	
1590					1595					1600					1605	
gtc	acc	agt	gtg	cag	gtc	ccc	cgt	act	tct	ggc	gat	ggc	gca	ctt	gat	4963
Val	Thr	Ser	Val	Gln	Val	Pro	Arg	Thr	Ser	Gly	Asp	Gly	Ala	Leu	Asp	
				1610					1615					1620		
gcc	ctt	ttg	ctg	cac	gat	cag	gtt	cca	gga	ggc	aca	ggc	tat	ctt	aac	5011
Ala	Leu	Leu	Leu	His	Asp	Gln	Val	Pro	Gly	Gly	Thr	Gly	Tyr	Leu	Asn	
			1625					1630					1635			
caa	ttt	gcc	gat	cct	aca	aag	gtt	cct	gaa	ctt	att	tcc	cga	gct	tgg	5059
Gln	Phe	Ala	Asp	Pro	Thr	Lys	Val	Pro	Glu	Leu	Ile	Ser	Arg	Ala	Trp	
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gag	cgg	gtg	tct	agg	tgc	caa	tgc	cag	tat	gat	gaa	acg	ctg	gcc	tgc	5107
Glu	Arg	Val	Ser	Arg	Cys	Gln	Cys	Gln	Tyr	Asp	Glu	Thr	Leu	Ala	Cys	
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Pro	Glu	Cys	Leu	Leu	Pro	Tyr	Thr	Arg	Thr	Asp	Thr	Leu	Leu	His	Thr	
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ttc	cgc	gca	act	gca	gaa	aaa	tcc	ttg	cgc	gca	att	ttg	ctc	aat	agc	5203
Phe	Arg	Ala	Thr	Ala	Glu	Lys	Ser	Leu	Arg	Ala	Ile	Leu	Leu	Asn	Ser	
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tcg	cgc	ccc	gaa	gaa	atc	act	gac	ctt	tct	gca	gta	ccg	gac	tgg	act	5251
Ser	Arg	Pro														

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Leu Val Asp Arg Val Asn Gly Ser Asn Ser Tyr Val Asp Ile Glu Met			
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agc tcc ggt gtg cgc tgg cgg atg agc gaa caa gtt gat cgt gga tat			5443
Ser Ser Gly Val Arg Trp Arg Met Ser Glu Gln Val Asp Arg Gly Tyr			
	1770	1775	1780
aca cgc cct gat ttc tgg ttt gaa ccg ctc aac ggc aac tat ccc acc			5491
Thr Arg Pro Asp Phe Trp Phe Glu Pro Leu Asn Gly Asn Tyr Pro Thr			
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gtg gct gtt ttt acc gat ggc gct gcg ttc cat atc tct tca gct aac			5539
Val Ala Val Phe Thr Asp Gly Ala Ala Phe His Ile Ser Ser Ala Asn			
	1800	1805	1810
tac cgt ctt gat ggc gat att cag aaa cgg atg aaa cta gcg ctc gat			5587
Tyr Arg Leu Asp Gly Asp Ile Gln Lys Arg Met Lys Leu Ala Leu Asp			
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cca gac aat att ttg ccg tgg aat atc act agc tta gac ctc gac cgc			5635
Pro Asp Asn Ile Leu Pro Trp Asn Ile Thr Ser Leu Asp Leu Asp Arg			
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Phe Ser Asn Pro Ala Ala Gln Gly Glu Glu Pro Ala Trp Phe Ser Pro			
	1850	1855	1860
atc ggc agg cag ctc agc aaa gca aat ttg att ctt gat cca caa tca			5731
Ile Gly Arg Gln Leu Ser Lys Ala Asn Leu Ile Leu Asp Pro Gln Ser			
	1865	1870	1875
act gca ctc ctg gca gca acg cct atg gat caa ctc ttg gca ttt tta			5779
Thr Ala Leu Leu Ala Ala Thr Pro Met Asp Gln Leu Leu Ala Phe Leu			
	1880	1885	1890
gat aat ccc gcg gca tcc tcg tgg aag gag ttt gct cat atc gct gct			5827
Asp Asn Pro Ala Ala Ser Ser Trp Lys Glu Phe Ala His Ile Ala Ala			
	1895	1900	1905
gct cac atg ctt ggg cat aat cca caa aaa aat ggc gac gga att gtt			5875
Ala His Met Leu Gly His Asn Pro Gln Lys Asn Gly Asp Gly Ile Val			
	1910	1915	1920
ggt acc ttc cgc aat aag att tcc ttg cgg gcc acc atg gtt aat cgg			5923
Gly Thr Phe Arg Asn Lys Ile Ser Leu Arg Ala Thr Met Val Asn Arg			
	1930	1935	1940
gaa ctg cgc gcc cgc caa ttg tgg ctt gct ccc acc act cca gaa gag			5971
Glu Leu Arg Ala Arg Gln Leu Trp Leu Ala Pro Thr Thr Pro Glu Glu			
	1945	1950	1955
ctg gaa gtg gat acc tgg act gcc ttc ctc aat ttg gcc aac ctc atg			6019
Leu Glu Val Asp Thr Trp Thr Ala Phe Leu Asn Leu Ala Asn Leu Met			
	1960	1965	1970
tgg ctg gca ccg gaa tcc gta tac gta agc act aat ggt tca ccg cat			6067
Trp Leu Ala Pro Glu Ser Val Tyr Val Ser Thr Asn Gly Ser Pro His			
	1975	1980	1985

aaa att gat att gtg cct gct cca gca gct ccg ctt gtt gtt gaa gtt 6115
 Lys Ile Asp Ile Val Pro Ala Pro Ala Ala Pro Leu Val Val Glu Val
 1990 1995 2000 2005

cct gaa ttg tgg gct ccc atc ttg gat ggc ttt acc gcc gat gaa gat 6163
 Pro Glu Leu Trp Ala Pro Ile Leu Asp Gly Phe Thr Ala Asp Glu Asp
 2010 2015 2020

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 2025 2030 2035

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 Val Pro Glu Thr Thr Gly Asp Glu Leu Ser Ser Ile Pro Thr Ile Ala
 2040 2045 2050

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 Thr Trp Pro Ser Val Lys Ile Ala Leu Leu Tyr Glu Ser Asp Pro Asp
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 Glu Pro Leu Glu Asp Asp Leu Lys Ala Glu Gly Trp Thr Leu Leu Phe
 2070 2075 2080 2085

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Ala Thr Glu Leu Lys Arg Phe Leu Gly His Gly Asp Ser Gly Met Phe
 35 40 45

His Gly Pro Tyr Val Arg Ala Arg Leu Pro Tyr Ala Gln Ala Gln Glu
 50 55 60

Trp Glu Asn Val Leu Ser Trp Leu Pro Glu Asn Phe Val Pro Tyr His
 65 70 75 80

His Gln Lys Ala Ala Phe Gln Arg Leu Ser Ser Leu Asp Asn Arg Gly
 85 90 95

Lys Asp Arg Arg Pro Asp Pro Thr Leu Val Val Thr Gly Thr Gly Ser
 100 105 110

Gly Lys Thr Glu Ser Phe Leu Tyr Pro Ile Leu Asp His Ala Leu Arg
 115 120 125

Leu Arg Lys Arg Gly Gln Gln Gly Ile Lys Ala Leu Leu Leu Tyr Pro
 130 135 140
 Met Asn Ala Leu Ala Asn Asp Gln Ala Asp Arg Leu Ala Arg Leu Ile
 145 150 155 160
 His Asn Asn Pro Ala Leu Lys Gly Val Thr Ala Gly Ile Tyr Thr Gly
 165 170 175
 Glu Ala Lys Gly Asn Arg Thr Gln Met Gly Glu Arg Glu Leu Ile Asn
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 Asp Pro Gln Ala Met Arg Val Ser Pro Pro Asp Ile Leu Leu Thr Asn
 195 200 205
 Tyr Lys Met Leu Asp Gln Leu Leu Leu Arg Ser Val Asp Arg Glu Met
 210 215 220
 Trp Gln Lys Ser Ala Thr Ser Leu Gln Tyr Leu Val Leu Asp Glu Phe
 225 230 235 240
 His Thr Tyr Asp Gly Ala Gln Gly Thr Asp Val Ala Leu Leu Leu Arg
 245 250 255
 Arg Leu Gly Leu Met Leu Lys Ser Gln Gln Pro Ala Asn Phe Leu Asp
 260 265 270
 Asp Ser Ala Met His Arg Pro Leu Gly Ile Ile Thr Pro Val Ala Thr
 275 280 285
 Ser Ala Thr Leu Gly Ser Gly Asp Ser Gly Ser Pro Met Leu Asp Phe
 290 295 300
 Ala Tyr Thr Ile Phe Gly Glu Arg Phe Pro Ala Asp Ala Ile Val Gly
 305 310 315 320
 Glu Thr Arg Leu Glu Leu Asp Gln Trp Arg Ala Glu Ile Ala Gln Asn
 325 330 335
 Phe Gly Ala Pro Ala Val Ser Glu Pro Arg Glu Leu Pro Thr Val Glu
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 Asp Ile Glu Val Val Leu Asp Thr Ile Ala Thr Ala Gln His Glu Asp
 355 360 365
 Asp Tyr Ala Gln Leu Cys Phe Arg Val Phe Cys Glu Lys Val Trp Leu
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 Cys Glu Ala Asp Leu His Ala Ala Ile Ser Ala Tyr Ala Ala His Asp
 385 390 395 400
 Leu Thr Ala Ala Ile Leu Gln His Ala Ala Asp Ser Thr Pro Leu Ser
 405 410 415
 Arg Arg Asp Gln Asp Glu Val Thr Ala Leu Pro Glu Leu Val Leu Gly
 420 425 430
 Ala Thr Ala Arg Ile Leu Gly Glu Val Lys Ala Ala Glu Phe Ile Ser
 435 440 445

His Ala Leu Ala Ala Met Ala Phe Val Arg Ala Glu Tyr Gly Lys Val
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Ala Ala Trp Gly Ala Lys Arg Leu Pro Gly Val Glu Thr His Leu Trp
465 470 475 480

Val Arg Glu Val Ser Arg Ile Asp Arg Ala Leu Gly Val Gly Asp Glu
485 490 495

Gln Ser Met Phe Arg Trp Ser Asp Asp Gly Pro Ala Glu Asp Ala Asn
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Thr Gln Gln Trp Leu Pro Ala Cys Tyr Cys Arg Ser Cys Gly Arg Ser
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Gly Trp Met Val Ser Leu Glu Gln Gly Thr Asn Ile Pro Val Leu Glu
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Glu Gln Lys Ile Arg Leu Asn Ser Phe Glu Gln Pro His Lys Gln Arg
545 550 555 560

Ala Leu Leu Asp Ala Thr Ser Glu Gln Arg Ala Ala Ile Glu Gln Gly
565 570 575

Arg Ser Val Ala Gly Pro Arg Gly Val Asp Gly Thr Ser Ala Val Leu
580 585 590

Trp Phe His Ser Ala Ser Asn Glu Leu Ser Thr Arg Gln Pro Ser Pro
595 600 605

Glu Glu Glu Gln Ser Gly Ser Ser Ile Ala Val Leu Thr His Phe Gly
610 615 620

Pro Glu Ala Asp Asp Leu Ser Ala Lys Gln Thr Cys Pro Ser Cys Gly
625 630 635 640

Asp Val Asp Ser Ile Arg Tyr Ile Gly Ser Gly Ile Ser Thr Leu Leu
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Ser Val Ser Leu Ser Asn Leu Phe Gly Met Ala Asp Leu Asp Ser Ala
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Glu Lys Lys Thr Leu Val Phe Ala Asp Ser Val Gln Asp Ala Ala His
675 680 685

Arg Ala Gly Tyr Val Gln Ala Arg Ser Arg Ala Phe Ala Leu Arg Thr
690 695 700

Tyr Thr Arg Arg Ala Val Gly Asp Asn Glu Val Thr Leu Pro Ser Ile
705 710 715 720

Ser Arg Ala Leu Met Asp Asn Ala Thr Ser Gly Arg Thr Arg Tyr Glu
725 730 735

Leu Leu Pro Pro Asp Leu Thr Asp Leu Asp Ile Tyr Lys Pro Tyr Trp
740 745 750

His Pro Asp Ala Ser Lys Ala Glu Arg Arg Glu Ala Ser Arg Asn Val
755 760 765

His Lys Arg Leu Ser Phe Asp Leu Ala Leu Glu Phe Gly Gln Arg Ala

770 775 780

Asp Leu Pro Arg Ser Leu Ala Leu Thr Gly Ala Leu Ser Ala Phe Val
785 790 795 800

Asp Leu Pro Lys Gly Val Ala Leu Ser Ala Ala Ala Glu Ala Leu Tyr
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Ala Ile Glu Val Pro Thr Leu Asp Ile Glu Asp Glu Asn Leu Arg Leu
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Arg Trp Val Gln Gly Ala Leu Glu Leu Leu Arg Ala Arg Gly Gly Ile
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Asn His Glu Trp Phe Gly Ala Tyr Leu Arg Thr Asp Gly Asn Pro Tyr
 850 855 860

Met Leu Asn Arg Arg Gln Ala Arg Ala Glu Gly Ile Pro Gly Phe Val
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Ser Leu Arg Ser Ser Thr Gly Thr Thr Pro Leu Gly Ser Pro Arg Gly
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Arg Tyr Ala Ser Trp Thr Ser Gln Val Leu Gly Ile Ser Thr His Asp
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Ile Leu Ser Ser Ile Ser Thr Asp Ser Gly Gly Lys Ile Tyr Cys Leu
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Glu Cys Ser Val Cys His Ala Gln Thr Gly Val Thr Asp His Val Arg
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Asp Phe Leu Asp Gly Ala Pro Cys Phe Ser Pro Ser Cys Gly Gly Val
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Leu His Ile Glu Glu Val Glu Asp Asn Tyr Tyr Arg Arg Leu Tyr Ser
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Ala Ile Glu Pro Arg Thr Val Ile Ala Arg Glu His Thr Ser Met Leu
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Lys Lys Lys Asp Arg Leu Ala Leu Glu Gln Ser Phe Arg Gly Gly Glu
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Gly Ser Ala Lys Gln Ser Pro Asp Ala Pro Asn Val Leu Val Ala Thr
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Pro Thr Leu Glu Met Gly Ile Asp Ile Gly Asp Leu Ser Thr Val Met
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Arg Ala Gly Arg Leu Ser Gly Asn Ser Leu Val Leu Ala Val Val Arg
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Gly Arg Gly Val Thr Leu Pro Arg Leu Asn Gln Pro Leu Ser Met Ile
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Lys Gly Ala Ile Thr Pro Pro Val Ala Tyr Leu Ser Ala Ser Glu Ile
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Leu His Arg Gln Phe Leu Ala Tyr Val Ile Asp Cys Leu Asp Thr Arg
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Ala Glu Leu Pro Lys Leu Glu Thr Ala Ile Asp Val Phe Asp Asn Ala
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Ala Gly Lys Thr Pro Leu Val Ala Leu Leu Lys Ala Gln Ile His Ala
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Gly Leu Asp Pro Leu Leu Glu Glu Phe Val Arg Thr Leu Asn Met Gln
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Ile Ser Ile Asp Asn Ile Phe Glu Leu Arg Thr Trp Ala Ser Gly Asn
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Ser Thr Asp Ser Leu Leu Ala Leu Leu Glu Thr Ser Gln Lys Glu Trp
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Met Glu Glu Arg Arg Ser Leu Thr Ala Arg Arg Gly Glu Leu Glu Lys
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Lys Glu Glu Lys Arg Lys Thr Ala Ala Ser Leu Lys Ala Val Lys Leu
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Gln Ile Arg Asp Leu Leu Gly Glu Phe Trp Ile Ala Ala Leu Glu Arg
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Tyr Gly Leu Leu Pro Asn Phe Thr Leu Val Asp Asp Ser Val Glu Leu
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Asn Val Ala Val Thr Ser Phe Asn Pro Gln Glu Val Glu Phe Asp Thr
1330 1335 1340

Lys Asn His Ala Tyr Ser Arg Gly Ile Ser Ala Ala Leu Phe Glu Leu
1345 1350 1355 1360

Ala Pro Gly Ala Thr Phe Tyr Ala Gln Gly Ile Ala Ala Lys Val Asp
1365 1370 1375

Ser Ile Glu Ile Gly Glu His Gly Ser Ala Ile Glu Gln Trp Arg Leu
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Cys Pro Val Cys Ser His Ser Glu Ile Leu Gln Pro Gly Val Ser Thr
1395 1400 1405

Pro Gly Ser Cys Pro Thr Cys Gly Ser Pro Ala Phe Ala Asp Lys Gly
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Gln Ile Leu Glu Val Val Gln Met Arg Lys Val Ser Ser Ala Val Glu
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Lys Thr Arg Ala Ala Ile Ser Asp Asp Arg Glu Asp Arg Phe Ser Thr
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Lys Ser Trp Tyr Leu Asn Asp Gly Phe Gly Ile Glu His Leu Pro Lys
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His Cys Gly His Leu Asp Ser Glu Ala Gly Ala Asn Ser Arg Trp Asp
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His Arg Pro Trp Cys Pro His Arg Tyr Glu Gln Lys Glu Asp Thr Val
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Leu Pro Glu Tyr Phe Gly Ser Glu Ala Asp Ser Met Val Val Thr Ser
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Leu Ile Ala Ala Ile Lys Leu Gly Phe Arg Glu Val Leu Gly Gly Asp
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Pro Asp His Leu Asp Val Thr Ser Val Gln Val Pro Arg Thr Ser Gly
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Asp Gly Ala Leu Asp Ala Leu Leu Leu His Asp Gln Val Pro Gly Gly
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Thr Gly Tyr Leu Asn Gln Phe Ala Asp Pro Thr Lys Val Pro Glu Leu
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Ile Ser Arg Ala Trp Glu Arg Val Ser Arg Cys Gln Cys Gln Tyr Asp
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Glu Thr Leu Ala Cys Pro Glu Cys Leu Leu Pro Tyr Thr Arg Thr Asp
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Thr Leu Leu His Thr Phe Arg Ala Thr Ala Glu Lys Ser Leu Arg Ala
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Ile Leu Leu Asn Ser Ser Arg Pro Glu Glu Ile Thr Asp Leu Ser Ala
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Val Pro Asp Trp Thr Phe Leu Glu Lys Arg Pro Glu Asn Thr Leu Gly
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Ser Gln Leu Glu Leu Arg Phe Arg Val Met Leu Arg Arg Ala Leu Lys
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Asn Arg His Ala Lys Leu Val Asp Arg Val Asn Gly Ser Asn Ser Tyr

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Val Asp Arg Gly Tyr Thr Arg Pro Asp Phe Trp Phe Glu Pro Leu Asn			
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Gly Asn Tyr Pro Thr Val Ala Val Phe Thr Asp Gly Ala Ala Phe His			
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Ile Ser Ser Ala Asn Tyr Arg Leu Asp Gly Asp Ile Gln Lys Arg Met			
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Lys Leu Ala Leu Asp Pro Asp Asn Ile Leu Pro Trp Asn Ile Thr Ser			
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Leu Asp Leu Asp Arg Phe Ser Asn Pro Ala Ala Gln Gly Glu Glu Pro			
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Ala Trp Phe Ser Pro Ile Gly Arg Gln Leu Ser Lys Ala Asn Leu Ile			
1860	1865	1870	
Leu Asp Pro Gln Ser Thr Ala Leu Leu Ala Ala Thr Pro Met Asp Gln			
1875	1880	1885	
Leu Leu Ala Phe Leu Asp Asn Pro Ala Ala Ser Ser Trp Lys Glu Phe			
1890	1895	1900	
Ala His Ile Ala Ala Ala His Met Leu Gly His Asn Pro Gln Lys Asn			
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Gly Asp Gly Ile Val Gly Thr Phe Arg Asn Lys Ile Ser Leu Arg Ala			
1925	1930	1935	
Thr Met Val Asn Arg Glu Leu Arg Ala Arg Gln Leu Trp Leu Ala Pro			
1940	1945	1950	
Thr Thr Pro Glu Glu Leu Glu Val Asp Thr Trp Thr Ala Phe Leu Asn			
1955	1960	1965	
Leu Ala Asn Leu Met Trp Leu Ala Pro Glu Ser Val Tyr Val Ser Thr			
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Asn Gly Ser Pro His Lys Ile Asp Ile Val Pro Ala Pro Ala Ala Pro			
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Leu Val Val Glu Val Pro Glu Leu Trp Ala Pro Ile Leu Asp Gly Phe			
2005	2010	2015	
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Ile Pro Thr Ile Ala Thr Trp Pro Ser Val Lys Ile Ala Leu Leu Tyr			
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 Pro Val His Ala Ala Gly Ser Ile Gln Glu Gly Ile Thr Glu Tyr Leu
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 Ser Trp Leu Pro Glu Asn Phe Val Pro Tyr His His Gln Lys Ala Ala
 70 75 80 85

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 Phe Gln Arg Leu Ser Ser Leu Asp Asn Arg Gly Lys Asp Arg Arg Pro
 90 95 100

gat ccc acc ttg gtg gta act gga acg ggt tcc ggt aag acg gaa tct 451
 Asp Pro Thr Leu Val Val Thr Gly Thr Gly Ser Gly Lys Thr Glu Ser
 105 110 115

ttc ctc tac ccg att ctg gat cat gcc ctg cgc ctg cgg aaa cgt ggc 499
 Phe Leu Tyr Pro Ile Leu Asp His Ala Leu Arg Leu Arg Lys Arg Gly
 120 125 130

caa caa ggc atc aag gcg ctg ttg ctt tat ccc atg aac gcc ttg gcc 547
 Gln Gln Gly Ile Lys Ala Leu Leu Leu Tyr Pro Met Asn Ala Leu Ala
 135 140 145

aat gac cag gca gat cgt ttg gcg cgg ctc att cac aat aac cca gca 595
Asn Asp Gln Ala Asp Arg Leu Ala Arg Leu Ile His Asn Asn Pro Ala
150 155 160 165

ctt aaa ggt gtt acc gcc ggt att tat acc ggt gaa gcc aag ggc aat 643
Leu Lys Gly Val Thr Ala Gly Ile Tyr Thr Gly Glu Ala Lys Gly Asn
170 175 180

cgc acg cag atg ggc gaa agg gag ctt att aat gat ccc caa gcc atg 691
Arg Thr Gln Met Gly Glu Arg Glu Leu Ile Asn Asp Pro Gln Ala Met
185 190 195

cgg gtt agt ccc cca gat att ttg ctc acc aac tac aaa atg ttg gat 739
Arg Val Ser Pro Pro Asp Ile Leu Leu Thr Asn Tyr Lys Met Leu Asp
200 205 210

cag ctc ttg ctg cgc agc gtc gac cgc gaa atg tgg caa aaa tcc gcc 787
Gln Leu Leu Leu Arg Ser Val Asp Arg Glu Met Trp Gln Lys Ser Ala
215 220 225

acc tct ttg cag 799
Thr Ser Leu Gln
230

<210> 100

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

Met Ser Ser Leu Ile Pro Val His Ala Ala Gly Ser Ile Gln Glu Gly
1 5 10 15

Ile Thr Glu Tyr Leu Thr Thr Ser Phe Ser Leu Ala Asp Lys Gln Val
20 25 30

Ala Thr Glu Leu Lys Arg Phe Leu Gly His Gly Asp Ser Gly Met Phe
35 40 45

His Gly Pro Tyr Val Arg Ala Arg Leu Pro Tyr Ala Gln Ala Gln Glu
50 55 60

Trp Glu Asn Val Leu Ser Trp Leu Pro Glu Asn Phe Val Pro Tyr His
65 70 75 80

His Gln Lys Ala Ala Phe Gln Arg Leu Ser Ser Leu Asp Asn Arg Gly
85 90 95

Lys Asp Arg Arg Pro Asp Pro Thr Leu Val Val Thr Gly Thr Gly Ser
100 105 110

Gly Lys Thr Glu Ser Phe Leu Tyr Pro Ile Leu Asp His Ala Leu Arg
115 120 125

Leu Arg Lys Arg Gly Gln Gln Gly Ile Lys Ala Leu Leu Leu Tyr Pro
130 135 140

Met Asn Ala Leu Ala Asn Asp Gln Ala Asp Arg Leu Ala Arg Leu Ile
145 150 155 160

His Asn Asn Pro Ala Leu Lys Gly Val Thr Ala Gly Ile Tyr Thr Gly
 165 170 175

Glu Ala Lys Gly Asn Arg Thr Gln Met Gly Glu Arg Glu Leu Ile Asn
 180 185 190

Asp Pro Gln Ala Met Arg Val Ser Pro Pro Asp Ile Leu Leu Thr Asn
 195 200 205

Tyr Lys Met Leu Asp Gln Leu Leu Leu Arg Ser Val Asp Arg Glu Met
 210 215 220

Trp Gln Lys Ser Ala Thr Ser Leu Gln
 225 230

<210> 101
 <211> 1226
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 <222> (1)..(1203)
 <223> FRXA02357

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 Asn Ser Ser Arg Pro Glu Glu Ile Thr Asp Leu Ser Ala Val Pro Asp
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tgg act ttc ttg gaa aag cgc cca gag aac act ctt ggc tct cag ttg 96
 Trp Thr Phe Leu Glu Lys Arg Pro Glu Asn Thr Leu Gly Ser Gln Leu
 20 25 30

gaa ctg cgt ttc cgc gtg atg ctg cga cgc gcc tta aaa aat cgc cat 144
 Glu Leu Arg Phe Arg Val Met Leu Arg Arg Ala Leu Lys Asn Arg His
 35 40 45

gcc aaa ctt gtg gac cgc gtc aac ggc tca aac tct tat gtg gat att 192
 Ala Lys Leu Val Asp Arg Val Asn Gly Ser Asn Ser Tyr Val Asp Ile
 50 55 60

gag atg agc tcc ggt gtg cgc tgg cgg atg agc gaa caa gtt gat cgt 240
 Glu Met Ser Ser Gly Val Arg Trp Arg Met Ser Glu Gln Val Asp Arg
 65 70 75 80

gga tat aca cgc cct gat ttc tgg ttt gaa ccg ctc aac ggc aac tat 288
 Gly Tyr Thr Arg Pro Asp Phe Trp Phe Glu Pro Leu Asn Gly Asn Tyr
 85 90 95

ccc acc gtg gct gtt ttt acc gat ggc gct gcg ttc cat atc tct tca 336
 Pro Thr Val Ala Val Phe Thr Asp Gly Ala Ala Phe His Ile Ser Ser
 100 105 110

gct aac tac cgt ctt gat ggc gat att cag aaa cgg atg aaa cta gcg 384
 Ala Asn Tyr Arg Leu Asp Gly Asp Ile Gln Lys Arg Met Lys Leu Ala
 115 120 125

ctc gat cca gac aat att ttg ccg tgg aat atc act agc tta gac ctc 432
 Leu Asp Pro Asp Asn Ile Leu Pro Trp Asn Ile Thr Ser Leu Asp Leu

130	135	140	
gac cgc ttt agt aat ccc gct gca caa ggt gag gaa cca gca tgg ttt Asp Arg Phe Ser Asn Pro Ala Ala Gln Gly Glu Glu Pro Ala Trp Phe 145 150 155 160			480
agc ccc atc ggc agg cag ctc agc aaa gca aat ttg att ctt gat cca Ser Pro Ile Gly Arg Gln Leu Ser Lys Ala Asn Leu Ile Leu Asp Pro 165 170 175			528
caa tca act gca ctc ctg gca gca acg cct atg gat caa ctc ttg gca Gln Ser Thr Ala Leu Leu Ala Ala Thr Pro Met Asp Gln Leu Leu Ala 180 185 190			576
ttt tta gat aat ccc gcg gca tcc tcg tgg aag gag ttt gct cat atc Phe Leu Asp Asn Pro Ala Ala Ser Ser Trp Lys Glu Phe Ala His Ile 195 200 205			624
gct gct gct cac atg ctt ggg cat aat cca caa aaa aat ggc gac gga Ala Ala Ala His Met Leu Gly His Asn Pro Gln Lys Asn Gly Asp Gly 210 215 220			672
att gtt ggt acc ttc cgc aat aag att tcc ttg cgg gcc acc atg gtt Ile Val Gly Thr Phe Arg Asn Lys Ile Ser Leu Arg Ala Thr Met Val 225 230 235 240			720
aat cgg gaa ctg cgc gcc cgc caa ttg tgg ctt gct ccc acc act cca Asn Arg Glu Leu Arg Ala Arg Gln Leu Trp Leu Ala Pro Thr Thr Pro 245 250 255			768
gaa gag ctg gaa gtg gat acc tgg act gcc ttc ctc aat ttg gcc aac Glu Glu Leu Glu Val Asp Thr Trp Thr Ala Phe Leu Asn Leu Ala Asn 260 265 270			816
ctc atg tgg ctg gca ccg gaa tcc gta tac gta agc act aat ggt tca Leu Met Trp Leu Ala Pro Glu Ser Val Tyr Val Ser Thr Asn Gly Ser 275 280 285			864
ccg cat aaa att gat att gtg cct gct cca gca gct ccg ctt gtt gtt Pro His Lys Ile Asp Ile Val Pro Ala Pro Ala Ala Pro Leu Val Val 290 295 300			912
gaa gtt cct gaa ttg tgg gct ccc atc ttg gat ggc ttt acc gcc gat Glu Val Pro Glu Leu Trp Ala Pro Ile Leu Asp Gly Phe Thr Ala Asp 305 310 315 320			960
gaa gat gaa gaa gcc gaa ggc gct ttg cag atc ttg gct aag gaa cat Glu Asp Glu Glu Ala Glu Gly Ala Leu Gln Ile Leu Ala Lys Glu His 325 330 335			1008
gcc ctg gtt cca gag acc acc ggt gat gag ctc tcg agt att cct acg Ala Leu Val Pro Glu Thr Thr Gly Asp Glu Leu Ser Ser Ile Pro Thr 340 345 350			1056
att gct acg tgg ccg agt gtc aag atc gct ttg ctc tat gaa tct gat Ile Ala Thr Trp Pro Ser Val Lys Ile Ala Leu Leu Tyr Glu Ser Asp 355 360 365			1104
ccc gat gag cct ttg gag gat gat ctc aaa gct gaa ggt tgg acg ctg Pro Asp Glu Pro Leu Glu Asp Asp Leu Lys Ala Glu Gly Trp Thr Leu 370 375 380			1152

ctt ttt gca aat gac ctc gag acc tcc gat att ccc gct gcc ctt cgt 1200
 Leu Phe Ala Asn Asp Leu Glu Thr Ser Asp Ile Pro Ala Ala Leu Arg
 385 390 395 400

ccc tagtacaccc aaagtttatg aaa 1226
 Pro

<210> 102

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

Asn Ser Ser Arg Pro Glu Glu Ile Thr Asp Leu Ser Ala Val Pro Asp
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Trp Thr Phe Leu Glu Lys Arg Pro Glu Asn Thr Leu Gly Ser Gln Leu
 20 25 30

Glu Leu Arg Phe Arg Val Met Leu Arg Arg Ala Leu Lys Asn Arg His
 35 40 45

Ala Lys Leu Val Asp Arg Val Asn Gly Ser Asn Ser Tyr Val Asp Ile
 50 55 60

Glu Met Ser Ser Gly Val Arg Trp Arg Met Ser Glu Gln Val Asp Arg
 65 70 75 80

Gly Tyr Thr Arg Pro Asp Phe Trp Phe Glu Pro Leu Asn Gly Asn Tyr
 85 90 95

Pro Thr Val Ala Val Phe Thr Asp Gly Ala Ala Phe His Ile Ser Ser
 100 105 110

Ala Asn Tyr Arg Leu Asp Gly Asp Ile Gln Lys Arg Met Lys Leu Ala
 115 120 125

Leu Asp Pro Asp Asn Ile Leu Pro Trp Asn Ile Thr Ser Leu Asp Leu
 130 135 140

Asp Arg Phe Ser Asn Pro Ala Ala Gln Gly Glu Glu Pro Ala Trp Phe
 145 150 155 160

Ser Pro Ile Gly Arg Gln Leu Ser Lys Ala Asn Leu Ile Leu Asp Pro
 165 170 175

Gln Ser Thr Ala Leu Leu Ala Ala Thr Pro Met Asp Gln Leu Leu Ala
 180 185 190

Phe Leu Asp Asn Pro Ala Ala Ser Ser Trp Lys Glu Phe Ala His Ile
 195 200 205

Ala Ala Ala His Met Leu Gly His Asn Pro Gln Lys Asn Gly Asp Gly
 210 215 220

Ile Val Gly Thr Phe Arg Asn Lys Ile Ser Leu Arg Ala Thr Met Val
 225 230 235 240

<400> 103																	
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Pro	Val	Ser	Tyr	Pro	Leu	Val	Glu	Asp	Ile	Glu	Val	Val	Leu	Asp	Thr		
1				5					10					15			
atc	gcc	aca	gct	caa	cat	gag	gac	gat	tat	gca	cag	ctc	tgc	ttc	cgc	96	
Ile	Ala	Thr	Ala	Gln	His	Glu	Asp	Asp	Tyr	Ala	Gln	Leu	Cys	Phe	Arg		
			20					25					30				
gtt	ttt	tgt	gag	aaa	gtg	tgg	ctg	tgt	gag	gct	gat	ctg	cac	gca	gcg	144	
Val	Phe	Cys	Glu	Lys	Val	Trp	Leu	Cys	Glu	Ala	Asp	Leu	His	Ala	Ala		
		35					40					45					
atc	agt	gct	tat	gcg	gct	cat	gat	tta	act	gct	gcg	att	ttg	cag	cat	192	
Ile	Ser	Ala	Tyr	Ala	Ala	His	Asp	Leu	Thr	Ala	Ala	Ile	Leu	Gln	His		
	50					55					60						

gct gct gat tcc acc ccg ctt agc agg cgt gat caa gat gag gtc act	240
Ala Ala Asp Ser Thr Pro Leu Ser Arg Arg Asp Gln Asp Glu Val Thr	
65 70 75 80	
gcc ctt ccg gag ctg gta ttg ggg gct acc gcc cgc atc tta ggt gag	288
Ala Leu Pro Glu Leu Val Leu Gly Ala Thr Ala Arg Ile Leu Gly Glu	
85 90 95	
gtt aaa gct gcg gaa ttt atc agc cat gca ctg gct gcc atg gca ttt	336
Val Lys Ala Ala Glu Phe Ile Ser His Ala Leu Ala Ala Met Ala Phe	
100 105 110	
gtg cgc gcg gaa tac ggc aaa gtt gcc gcc tgg ggt gcc aag cgc cta	384
Val Arg Ala Glu Tyr Gly Lys Val Ala Ala Trp Gly Ala Lys Arg Leu	
115 120 125	
cct ggc gtc gaa acg cat ctt tgg gtg cgc gag gtc tcc cgc att gac	432
Pro Gly Val Glu Thr His Leu Trp Val Arg Glu Val Ser Arg Ile Asp	
130 135 140	
cgc gcc ctg ggg gtt ggg gat gaa caa tcc atg ttt cgc tgg tcc gat	480
Arg Ala Leu Gly Val Gly Asp Glu Gln Ser Met Phe Arg Trp Ser Asp	
145 150 155 160	
gat ggc ccg gca gaa gat gcc aat acc caa caa tgg ttg ccg gcg tgt	528
Asp Gly Pro Ala Glu Asp Ala Asn Thr Gln Gln Trp Leu Pro Ala Cys	
165 170 175	
tat tgc cgc agt tgt ggc cgt tcc ggc tgg atg gtc agc ctg gaa caa	576
Tyr Cys Arg Ser Cys Gly Arg Ser Gly Trp Met Val Ser Leu Glu Gln	
180 185 190	
ggc acc aat atc ccg gtg ttg gaa gaa caa aaa att cgc ctc aac tcc	624
Gly Thr Asn Ile Pro Val Leu Glu Glu Gln Lys Ile Arg Leu Asn Ser	
195 200 205	
ttt gaa caa ccc cat aaa caa aga gcg ctt ctc gac gcc acc tct gag	672
Phe Glu Gln Pro His Lys Gln Arg Ala Leu Leu Asp Ala Thr Ser Glu	
210 215 220	
cag cgc gca gcc att gag cag ggg cgc agc gtt gct ggg ccg cga gga	720
Gln Arg Ala Ala Ile Glu Gln Gly Arg Ser Val Ala Gly Pro Arg Gly	
225 230 235 240	
gtt gat ggc acc tca gca gtg ctg tgg ttc cat agc gcc agc aat gaa	768
Val Asp Gly Thr Ser Ala Val Leu Trp Phe His Ser Ala Ser Asn Glu	
245 250 255	
ctc agc acg cgc caa ccc agc cca gaa gaa gaa caa tca ggt tct tct	816
Leu Ser Thr Arg Gln Pro Ser Pro Glu Glu Glu Gln Ser Gly Ser Ser	
260 265 270	
atc gca gtg ctc acc cac ttt ggc cct gag gca gac gat ctc tcc gcc	864
Ile Ala Val Leu Thr His Phe Gly Pro Glu Ala Asp Asp Leu Ser Ala	
275 280 285	
aaa cag acc tgc cct tcc tgt ggt gat gtt gat tcc atc cgt tat atc	912
Lys Gln Thr Cys Pro Ser Cys Gly Asp Val Asp Ser Ile Arg Tyr Ile	
290 295 300	
gga tcg gga atc tct acc ctg ctc tct gtc tca ctc tcc aat ctt ttt	960

Gly 305	Ser	Gly	Ile	Ser	Thr 310	Leu	Leu	Ser	Val	Ser 315	Leu	Ser	Asn	Leu	Phe 320	
ggt	atg	gcc	gat	ttg	gat	agc	gct	gag	aaa	aag	acg	ctg	gtc	ttt	gcc	1008
Gly	Met	Ala	Asp	Leu	Asp	Ser	Ala	Glu	Lys	Lys	Thr	Leu	Val	Phe	Ala	
				325					330					335		
gat	tcc	gtg	caa	gat	gcc	gcg	cac	cgc	gcc	ggg	tac	gtc	caa	gca	cgt	1056
Asp	Ser	Val	Gln	Asp	Ala	Ala	His	Arg	Ala	Gly	Tyr	Val	Gln	Ala	Arg	
			340					345					350			
tcc	cgc	gct	ttt	gcc	ctt	cgt	acc	tat	acc	cgg	cgc	gca	gtg	ggg	gat	1104
Ser	Arg	Ala	Phe	Ala	Leu	Arg	Thr	Tyr	Thr	Arg	Arg	Ala	Val	Gly	Asp	
		355					360					365				
aat	gaa	gtc	acc	ttg	cca	tca	atc	tcc	cgg	gcg	ctg	atg	gat	aac	gcc	1152
Asn	Glu	Val	Thr	Leu	Pro	Ser	Ile	Ser	Arg	Ala	Leu	Met	Asp	Asn	Ala	
	370					375					380					
acc	tct	ggg	cgc	acc	cgt	tat	gag	ctc	cta	ccc	cct	gac	ctg	acc	gat	1200
Thr	Ser	Gly	Arg	Thr	Arg	Tyr	Glu	Leu	Leu	Pro	Pro	Asp	Leu	Thr	Asp	
385					390					395					400	
ctt	gat	att	tac	aaa	cct	tat	tgg	cac	ccc	gat	gcc	agc	aag	gct	gag	1248
Leu	Asp	Ile	Tyr	Lys	Pro	Tyr	Trp	His	Pro	Asp	Ala	Ser	Lys	Ala	Glu	
				405					410					415		
cgc	cgt	gag	gcc	tcc	cgc	aat	gtg	cat	aaa	cgt	tta	agt	ttt	gat	ctc	1296
Arg	Arg	Glu	Ala	Ser	Arg	Asn	Val	His	Lys	Arg	Leu	Ser	Phe	Asp	Leu	
			420					425					430			
gcc	ctc	gag	ttt	gga	caa	cgc	gct	gat	cta	ccc	cgt	tcc	ctt	gcg	ctg	1344
Ala	Leu	Glu	Phe	Gly	Gln	Arg	Ala	Asp	Leu	Pro	Arg	Ser	Leu	Ala	Leu	
		435					440					445				
acc	ggc	gct	ttg	agt	gct	ttt	gtg	gat	ttg	ccc	aaa	ggg	gtt	gca	ttg	1392
Thr	Gly	Ala	Leu	Ser	Ala	Phe	Val	Asp	Leu	Pro	Lys	Gly	Val	Ala	Leu	
	450					455					460					
tcc	gcg	gct	gcc	gaa	gca	ctt	tat	gcc	atc	gaa	gtt	ccc	acc	tta	gat	1440
Ser	Ala	Ala	Ala	Glu	Ala	Leu	Tyr	Ala	Ile	Glu	Val	Pro	Thr	Leu	Asp	
465					470					475					480	
att	gag	gat	gag	aac	ctg	cga	ctg	cgc	tgg	gtg	caa	ggg	gcc	ctg	gaa	1488
Ile	Glu	Asp	Glu	Asn	Leu	Arg	Leu	Arg	Trp	Val	Gln	Gly	Ala	Leu	Glu	
				485					490					495		
ctt	ttg	cgc	gcc	cgc	ggg	ggc	atc	aac	cat	gag	tgg	ttt	ggc	gcc	tac	1536
Leu	Leu	Arg	Ala	Arg	Gly	Gly	Ile	Asn	His	Glu	Trp	Phe	Gly	Ala	Tyr	
		500						505					510			
ctg	cgc	acc	gat	ggc	aac	ccc	tat	atg	ctt	aac	cgc	cgc	caa	gcc	cgc	1584
Leu	Arg	Thr	Asp	Gly	Asn	Pro	Tyr	Met	Leu	Asn	Arg	Arg	Gln	Ala	Arg	
		515					520					525				
gct	gag	ggc	att	ccc	ggg	ttt	gtc	cgc	ggg	ggg	gca	cct	gaa	ttc	cca	1632
Ala	Glu	Gly	Ile	Pro	Gly	Phe	Val	Arg	Gly	Gly	Ala	Pro	Glu	Phe	Pro	
	530					535					540					
cgt	gta	ggg	tcc	gca	ctt	tcc	gga	tcc	ctg	cgt	tcc	agc	acc	ggc	acc	1680
Arg	Val	Gly	Ser	Ala	Leu	Ser	Gly	Ser	Leu	Arg	Ser	Ser	Thr	Gly	Thr	

545	550	555	560	
acc ccg ctt ggt agc ccg cgc gga cgt tat gcg tcc tgg acc tcg cag				1728
Thr Pro Leu Gly Ser Pro Arg Gly Arg Tyr Ala Ser Trp Thr Ser Gln	565	570	575	
gtg ctt ggc atc agc acc cac gat gcc gcc acc gcc atc aca aag ctt				1776
Val Leu Gly Ile Ser Thr His Asp Ala Ala Thr Ala Ile Thr Lys Leu	580	585	590	
ttc gac gct tta agc aac cgc agc att ctc tcc tca ata tct acc gac				1824
Phe Asp Ala Leu Ser Asn Arg Ser Ile Leu Ser Ser Ile Ser Thr Asp	595	600	605	
agc ggc gga aaa atc tac tgc ctc gag gcc gaa cgc atc cgt att ttt				1872
Ser Gly Gly Lys Ile Tyr Cys Leu Glu Ala Glu Arg Ile Arg Ile Phe	610	615	620	
agc gaa gac cat ccc gaa gtt ctg gaa tgc agc gtg tgc cat gcc caa				1920
Ser Glu Asp His Pro Glu Val Leu Glu Cys Ser Val Cys His Ala Gln	625	630	635	640
act ggt gta act gat cat gtg cgt gac ttc ctt gat ggc gct ccg tgt				1968
Thr Gly Val Thr Asp His Val Arg Asp Phe Leu Asp Gly Ala Pro Cys	645	650	655	
ttt agc cct agt tgt ggg ggc gtt ctc cat atc gag gaa gta gaa gac				2016
Phe Ser Pro Ser Cys Gly Gly Val Leu His Ile Glu Glu Val Glu Asp	660	665	670	
aac tac tac cgc agg ctt tat tcc gca att gaa ccg cgc act gtc att				2064
Asn Tyr Tyr Arg Arg Leu Tyr Ser Ala Ile Glu Pro Arg Thr Val Ile	675	680	685	
gcc cgc gag cac acc agc atg ctc aag aaa aaa gac cgc ctc gca ctc				2112
Ala Arg Glu His Thr Ser Met Leu Lys Lys Lys Asp Arg Leu Ala Leu	690	695	700	
gaa caa tcc ttt aga ggt gga gaa ggc tcg gcc aaa caa tcc ccc gat				2160
Glu Gln Ser Phe Arg Gly Gly Glu Gly Ser Ala Lys Gln Ser Pro Asp	705	710	715	720
gcg ccc aat gtg ttg gta gct acg cca acg ctg gaa atg ggt att gac				2208
Ala Pro Asn Val Leu Val Ala Thr Pro Thr Leu Glu Met Gly Ile Asp	725	730	735	
atc ggc gat ctc tcc acc gtg atg ctt gcg tct ttg cca aca tca gtg				2256
Ile Gly Asp Leu Ser Thr Val Met Leu Ala Ser Leu Pro Thr Ser Val	740	745	750	
gcc agt tat gta cag cgt gtt ggt cgt gcc ggg cgc ctc agc gga aac				2304
Ala Ser Tyr Val Gln Arg Val Gly Arg Ala Gly Arg Leu Ser Gly Asn	755	760	765	
tcg ttg gta ctc gcc gtg gtg cgt ggc cgc ggt gtc aca ttg cct cgt				2352
Ser Leu Val Leu Ala Val Val Arg Gly Arg Gly Val Thr Leu Pro Arg	770	775	780	
ctt aac caa ccg ctc tcc atg atc aag gga gct att acc cca cca gtt				2400
Leu Asn Gln Pro Leu Ser Met Ile Lys Gly Ala Ile Thr Pro Pro Val	785	790	795	800

gcg tat ctt tcc gcc agt gaa atc ttg cac cgc caa ttc ttg gca tat	2448
Ala Tyr Leu Ser Ala Ser Glu Ile Leu His Arg Gln Phe Leu Ala Tyr	
805 810 815	
gtg atc gac tgc tta gat act cgc gcc gaa ctg cca aaa ctc gaa aca	2496
Val Ile Asp Cys Leu Asp Thr Arg Ala Glu Leu Pro Lys Leu Glu Thr	
820 825 830	
gca att gat gtt ttt gat aat gcc gcc gga aaa aca cct ttg gtt gca	2544
Ala Ile Asp Val Phe Asp Asn Ala Ala Gly Lys Thr Pro Leu Val Ala	
835 840 845	
tta ctc aaa gcg cag att cac gca ggc cta gat cct ttg ctg gag gaa	2592
Leu Leu Lys Ala Gln Ile His Ala Gly Leu Asp Pro Leu Leu Glu Glu	
850 855 860	
ttt gta cgc acc ctc aac atg caa atc agc att gat aat att ttc gaa	2640
Phe Val Arg Thr Leu Asn Met Gln Ile Ser Ile Asp Asn Ile Phe Glu	
865 870 875 880	
ctg cgc act tgg gca tct gga aat agc aca gac tcc ctc ctc gcg ctg	2688
Leu Arg Thr Trp Ala Ser Gly Asn Ser Thr Asp Ser Leu Leu Ala Leu	
885 890 895	
ctg gaa acc tcc caa aaa gag tgg atg gaa gaa cgc cgc agc ctt acc	2736
Leu Glu Thr Ser Gln Lys Glu Trp Met Glu Glu Arg Arg Ser Leu Thr	
900 905 910	
gcg cgg cgg gga gaa ctc gaa aaa atc ttt gac aaa cta gat gcg cgc	2784
Ala Arg Arg Gly Glu Leu Glu Lys Ile Phe Asp Lys Leu Asp Ala Arg	
915 920 925	
aat gat gca cat gat gaa gag cta aag gaa gaa aaa cgt aaa acc gca	2832
Asn Asp Ala His Asp Glu Glu Leu Lys Glu Glu Lys Arg Lys Thr Ala	
930 935 940	
gct tcc ctt aaa gcc gtc aaa ctt caa atc cgt gat cta ctt ggt gaa	2880
Ala Ser Leu Lys Ala Val Lys Leu Gln Ile Arg Asp Leu Leu Gly Glu	
945 950 955 960	
ttc tgg atc gct gct ttg gag cgt tat ggt ctc ctg ccc aac ttc acc	2928
Phe Trp Ile Ala Ala Leu Glu Arg Tyr Gly Leu Leu Pro Asn Phe Thr	
965 970 975	
ctg gtt gat gat tcc gta gaa ctt aat gtg gcg gtt act tcg ttc aac	2976
Leu Val Asp Asp Ser Val Glu Leu Asn Val Ala Val Thr Ser Phe Asn	
980 985 990	
ccc cag gaa gtg gaa ttt gat acc aag aat cat gcc tac tcg cgt ggg	3024
Pro Gln Glu Val Glu Phe Asp Thr Lys Asn His Ala Tyr Ser Arg Gly	
995 1000 1005	
atc tct gca gcg ctt ttt gag ctc gct ccc ggt gcg acc ttt tat gcc	3072
Ile Ser Ala Ala Leu Phe Glu Leu Ala Pro Gly Ala Thr Phe Tyr Ala	
1010 1015 1020	
caa gga att gct gcc aaa gtt gat tcc att gag att ggt gaa cat gcc	3120
Gln Gly Ile Ala Ala Lys Val Asp Ser Ile Glu Ile Gly Glu His Gly	
1025 1030 1035 1040	

tct gcc att gag caa tgg cgg ttg tgc ccc gtg tgc tcg cac tcc gaa	3168
Ser Ala Ile Glu Gln Trp Arg Leu Cys Pro Val Cys Ser His Ser Glu	
1045 1050 1055	
atc ctc cag ccg ggt gtc tct aca ccg gga tcg tgt cct acc tgt ggc	3216
Ile Leu Gln Pro Gly Val Ser Thr Pro Gly Ser Cys Pro Thr Cys Gly	
1060 1065 1070	
tcc ccc gcc ttt gcc gat aag gga caa atc cta gag gta gtg caa atg	3264
Ser Pro Ala Phe Ala Asp Lys Gly Gln Ile Leu Glu Val Val Gln Met	
1075 1080 1085	
cgt aag gtt tcc tcc gca gtg gag aaa act cgc gct gcc att agc gat	3312
Arg Lys Val Ser Ser Ala Val Glu Lys Thr Arg Ala Ala Ile Ser Asp	
1090 1095 1100	
gac cgt gaa gat cgc ttt agc acc cgc ttt aac cag cac gtc agc ttt	3360
Asp Arg Glu Asp Arg Phe Ser Thr Arg Phe Asn Gln His Val Ser Phe	
1105 1110 1115 1120	
gtc gtt cca cca gat ggc cat gga aaa tcc tgg tat ttg aat gat ggt	3408
Val Val Pro Pro Asp Gly His Gly Lys Ser Trp Tyr Leu Asn Asp Gly	
1125 1130 1135	
ttt ggc att gag cat ctg ccc aag gtg gaa tta cgc tgg ctg aac tta	3456
Phe Gly Ile Glu His Leu Pro Lys Val Glu Leu Arg Trp Leu Asn Leu	
1140 1145 1150	
gga att ggc aat ggc caa aag cgt cgg ctc ggt ggc ttt gaa gtc acc	3504
Gly Ile Gly Asn Gly Gln Lys Arg Arg Leu Gly Gly Phe Glu Val Thr	
1155 1160 1165	
agc cca cta ttt aat gtg tgc cgc cac tgt gga cat tta gat tcc gag	3552
Ser Pro Leu Phe Asn Val Cys Arg His Cys Gly His Leu Asp Ser Glu	
1170 1175 1180	
gca gga gct aac tca cgc tgg gat cac cga ccc tgg tgc cca cac cgt	3600
Ala Gly Ala Asn Ser Arg Trp Asp His Arg Pro Trp Cys Pro His Arg	
1185 1190 1195 1200	
tat gag caa aaa gaa gat acc gta tct ttc gct ttg ggt cgt act ctt	3648
Tyr Glu Gln Lys Glu Asp Thr Val Ser Phe Ala Leu Gly Arg Thr Leu	
1205 1210 1215	
aaa acc caa ggc gtg ctc atg ctg ctg ccc gaa tat ttt ggc agt gaa	3696
Lys Thr Gln Gly Val Leu Met Leu Leu Pro Glu Tyr Phe Gly Ser Glu	
1220 1225 1230	
gcc gat tct atg gtg gta acc agc ctc att gct gct atc aaa tta gga	3744
Ala Asp Ser Met Val Val Thr Ser Leu Ile Ala Ala Ile Lys Leu Gly	
1235 1240 1245	
ttt cgt gag gtg ttg ggt ggc gat cct gac cac ctg gat gtc acc agt	3792
Phe Arg Glu Val Leu Gly Gly Asp Pro Asp His Leu Asp Val Thr Ser	
1250 1255 1260	
gtg cag gtc ccc cgt act tct ggc gat ggt gca ctt gat gcc ctt ttg	3840
Val Gln Val Pro Arg Thr Ser Gly Asp Gly Ala Leu Asp Ala Leu Leu	
1265 1270 1275 1280	
ctg cac gat cag gtt	3855

Leu His Asp Gln Val
1285

<210> 104

<211> 1285

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

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20 25 30

Val Phe Cys Glu Lys Val Trp Leu Cys Glu Ala Asp Leu His Ala Ala
35 40 45

Ile Ser Ala Tyr Ala Ala His Asp Leu Thr Ala Ala Ile Leu Gln His
50 55 60

Ala Ala Asp Ser Thr Pro Leu Ser Arg Arg Asp Gln Asp Glu Val Thr
65 70 75 80

Ala Leu Pro Glu Leu Val Leu Gly Ala Thr Ala Arg Ile Leu Gly Glu
85 90 95

Val Lys Ala Ala Glu Phe Ile Ser His Ala Leu Ala Ala Met Ala Phe
100 105 110

Val Arg Ala Glu Tyr Gly Lys Val Ala Ala Trp Gly Ala Lys Arg Leu
115 120 125

Pro Gly Val Glu Thr His Leu Trp Val Arg Glu Val Ser Arg Ile Asp
130 135 140

Arg Ala Leu Gly Val Gly Asp Glu Gln Ser Met Phe Arg Trp Ser Asp
145 150 155 160

Asp Gly Pro Ala Glu Asp Ala Asn Thr Gln Gln Trp Leu Pro Ala Cys
165 170 175

Tyr Cys Arg Ser Cys Gly Arg Ser Gly Trp Met Val Ser Leu Glu Gln
180 185 190

Gly Thr Asn Ile Pro Val Leu Glu Glu Gln Lys Ile Arg Leu Asn Ser
195 200 205

Phe Glu Gln Pro His Lys Gln Arg Ala Leu Leu Asp Ala Thr Ser Glu
210 215 220

Gln Arg Ala Ala Ile Glu Gln Gly Arg Ser Val Ala Gly Pro Arg Gly
225 230 235 240

Val Asp Gly Thr Ser Ala Val Leu Trp Phe His Ser Ala Ser Asn Glu
245 250 255

Leu Ser Thr Arg Gln Pro Ser Pro Glu Glu Glu Gln Ser Gly Ser Ser
260 265 270

Ile Ala Val Leu Thr His Phe Gly Pro Glu Ala Asp Asp Leu Ser Ala
275 280 285

Lys Gln Thr Cys Pro Ser Cys Gly Asp Val Asp Ser Ile Arg Tyr Ile
290 295 300

Gly Ser Gly Ile Ser Thr Leu Leu Ser Val Ser Leu Ser Asn Leu Phe
305 310 315 320

Gly Met Ala Asp Leu Asp Ser Ala Glu Lys Lys Thr Leu Val Phe Ala
325 330 335

Asp Ser Val Gln Asp Ala Ala His Arg Ala Gly Tyr Val Gln Ala Arg
340 345 350

Ser Arg Ala Phe Ala Leu Arg Thr Tyr Thr Arg Arg Ala Val Gly Asp
355 360 365

Asn Glu Val Thr Leu Pro Ser Ile Ser Arg Ala Leu Met Asp Asn Ala
370 375 380

Thr Ser Gly Arg Thr Arg Tyr Glu Leu Leu Pro Pro Asp Leu Thr Asp
385 390 395 400

Leu Asp Ile Tyr Lys Pro Tyr Trp His Pro Asp Ala Ser Lys Ala Glu
405 410 415

Arg Arg Glu Ala Ser Arg Asn Val His Lys Arg Leu Ser Phe Asp Leu
420 425 430

Ala Leu Glu Phe Gly Gln Arg Ala Asp Leu Pro Arg Ser Leu Ala Leu
435 440 445

Thr Gly Ala Leu Ser Ala Phe Val Asp Leu Pro Lys Gly Val Ala Leu
450 455 460

Ser Ala Ala Ala Glu Ala Leu Tyr Ala Ile Glu Val Pro Thr Leu Asp
465 470 475 480

Ile Glu Asp Glu Asn Leu Arg Leu Arg Trp Val Gln Gly Ala Leu Glu
485 490 495

Leu Leu Arg Ala Arg Gly Gly Ile Asn His Glu Trp Phe Gly Ala Tyr
500 505 510

Leu Arg Thr Asp Gly Asn Pro Tyr Met Leu Asn Arg Arg Gln Ala Arg
515 520 525

Ala Glu Gly Ile Pro Gly Phe Val Arg Gly Gly Ala Pro Glu Phe Pro
530 535 540

Arg Val Gly Ser Ala Leu Ser Gly Ser Leu Arg Ser Ser Thr Gly Thr
545 550 555 560

Thr Pro Leu Gly Ser Pro Arg Gly Arg Tyr Ala Ser Trp Thr Ser Gln
565 570 575

Val Leu Gly Ile Ser Thr His Asp Ala Ala Thr Ala Ile Thr Lys Leu
580 585 590

Phe Asp Ala Leu Ser Asn Arg Ser Ile Leu Ser Ser Ile Ser Thr Asp

595					600					605					
Ser	Gly	Gly	Lys	Ile	Tyr	Cys	Leu	Glu	Ala	Glu	Arg	Ile	Arg	Ile	Phe
610						615					620				
Ser	Glu	Asp	His	Pro	Glu	Val	Leu	Glu	Cys	Ser	Val	Cys	His	Ala	Gln
625					630					635					640
Thr	Gly	Val	Thr	Asp	His	Val	Arg	Asp	Phe	Leu	Asp	Gly	Ala	Pro	Cys
				645					650					655	
Phe	Ser	Pro	Ser	Cys	Gly	Gly	Val	Leu	His	Ile	Glu	Glu	Val	Glu	Asp
			660					665					670		
Asn	Tyr	Tyr	Arg	Arg	Leu	Tyr	Ser	Ala	Ile	Glu	Pro	Arg	Thr	Val	Ile
		675					680					685			
Ala	Arg	Glu	His	Thr	Ser	Met	Leu	Lys	Lys	Lys	Asp	Arg	Leu	Ala	Leu
	690					695					700				
Glu	Gln	Ser	Phe	Arg	Gly	Gly	Glu	Gly	Ser	Ala	Lys	Gln	Ser	Pro	Asp
705					710					715					720
Ala	Pro	Asn	Val	Leu	Val	Ala	Thr	Pro	Thr	Leu	Glu	Met	Gly	Ile	Asp
			725						730					735	
Ile	Gly	Asp	Leu	Ser	Thr	Val	Met	Leu	Ala	Ser	Leu	Pro	Thr	Ser	Val
			740					745					750		
Ala	Ser	Tyr	Val	Gln	Arg	Val	Gly	Arg	Ala	Gly	Arg	Leu	Ser	Gly	Asn
		755					760					765			
Ser	Leu	Val	Leu	Ala	Val	Val	Arg	Gly	Arg	Gly	Val	Thr	Leu	Pro	Arg
	770					775					780				
Leu	Asn	Gln	Pro	Leu	Ser	Met	Ile	Lys	Gly	Ala	Ile	Thr	Pro	Pro	Val
785					790					795					800
Ala	Tyr	Leu	Ser	Ala	Ser	Glu	Ile	Leu	His	Arg	Gln	Phe	Leu	Ala	Tyr
				805					810					815	
Val	Ile	Asp	Cys	Leu	Asp	Thr	Arg	Ala	Glu	Leu	Pro	Lys	Leu	Glu	Thr
			820					825					830		
Ala	Ile	Asp	Val	Phe	Asp	Asn	Ala	Ala	Gly	Lys	Thr	Pro	Leu	Val	Ala
		835					840					845			
Leu	Leu	Lys	Ala	Gln	Ile	His	Ala	Gly	Leu	Asp	Pro	Leu	Leu	Glu	Glu
	850					855					860				
Phe	Val	Arg	Thr	Leu	Asn	Met	Gln	Ile	Ser	Ile	Asp	Asn	Ile	Phe	Glu
865					870					875					880
Leu	Arg	Thr	Trp	Ala	Ser	Gly	Asn	Ser	Thr	Asp	Ser	Leu	Leu	Ala	Leu
				885					890					895	
Leu	Glu	Thr	Ser	Gln	Lys	Glu	Trp	Met	Glu	Glu	Arg	Arg	Ser	Leu	Thr
			900					905					910		
Ala	Arg	Arg	Gly	Glu	Leu	Glu	Lys	Ile	Phe	Asp	Lys	Leu	Asp	Ala	Arg
		915					920					925			

Asn Asp Ala His Asp Glu Glu Leu Lys Glu Glu Lys Arg Lys Thr Ala
930 935 940

Ala Ser Leu Lys Ala Val Lys Leu Gln Ile Arg Asp Leu Leu Gly Glu
945 950 955 960

Phe Trp Ile Ala Ala Leu Glu Arg Tyr Gly Leu Leu Pro Asn Phe Thr
965 970 975

Leu Val Asp Asp Ser Val Glu Leu Asn Val Ala Val Thr Ser Phe Asn
980 985 990

Pro Gln Glu Val Glu Phe Asp Thr Lys Asn His Ala Tyr Ser Arg Gly
995 1000 1005

Ile Ser Ala Ala Leu Phe Glu Leu Ala Pro Gly Ala Thr Phe Tyr Ala
1010 1015 1020

Gln Gly Ile Ala Ala Lys Val Asp Ser Ile Glu Ile Gly Glu His Gly
1025 1030 1035 1040

Ser Ala Ile Glu Gln Trp Arg Leu Cys Pro Val Cys Ser His Ser Glu
1045 1050 1055

Ile Leu Gln Pro Gly Val Ser Thr Pro Gly Ser Cys Pro Thr Cys Gly
1060 1065 1070

Ser Pro Ala Phe Ala Asp Lys Gly Gln Ile Leu Glu Val Val Gln Met
1075 1080 1085

Arg Lys Val Ser Ser Ala Val Glu Lys Thr Arg Ala Ala Ile Ser Asp
1090 1095 1100

Asp Arg Glu Asp Arg Phe Ser Thr Arg Phe Asn Gln His Val Ser Phe
1105 1110 1115 1120

Val Val Pro Pro Asp Gly His Gly Lys Ser Trp Tyr Leu Asn Asp Gly
1125 1130 1135

Phe Gly Ile Glu His Leu Pro Lys Val Glu Leu Arg Trp Leu Asn Leu
1140 1145 1150

Gly Ile Gly Asn Gly Gln Lys Arg Arg Leu Gly Gly Phe Glu Val Thr
1155 1160 1165

Ser Pro Leu Phe Asn Val Cys Arg His Cys Gly His Leu Asp Ser Glu
1170 1175 1180

Ala Gly Ala Asn Ser Arg Trp Asp His Arg Pro Trp Cys Pro His Arg
1185 1190 1195 1200

Tyr Glu Gln Lys Glu Asp Thr Val Ser Phe Ala Leu Gly Arg Thr Leu
1205 1210 1215

Lys Thr Gln Gly Val Leu Met Leu Leu Pro Glu Tyr Phe Gly Ser Glu
1220 1225 1230

Ala Asp Ser Met Val Val Thr Ser Leu Ile Ala Ala Ile Lys Leu Gly
1235 1240 1245

Phe Arg Glu Val Leu Gly Gly Asp Pro Asp His Leu Asp Val Thr Ser
 1250 1255 1260

Val Gln Val Pro Arg Thr Ser Gly Asp Gly Ala Leu Asp Ala Leu Leu
 1265 1270 1275 1280

Leu His Asp Gln Val
 1285

<210> 105

<211> 1545

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1522)

<223> RXA01740

<400> 105

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gttgcttcac accgccgggg cggtgtagaa ttccccggcg gtg gcg gag gag ttc 115
 Val Ala Glu Glu Phe
 1 5

cgc cag cag tat cgc agc ttt gtg gtc gat gag tat cag gat gtg acg 163
 Arg Gln Gln Tyr Arg Ser Phe Val Val Asp Glu Tyr Gln Asp Val Thr
 10 15 20

cct ctg cag cag cgg gtg ctc gat gcg tgg ctc ggc gat cgc gat gac 211
 Pro Leu Gln Gln Arg Val Leu Asp Ala Trp Leu Gly Asp Arg Asp Asp
 25 30 35

ctg acg gtt gtc ggc gat gct aac cag aca att tat tcg ttc acg ggg 259
 Leu Thr Val Val Gly Asp Ala Asn Gln Thr Ile Tyr Ser Phe Thr Gly
 40 45 50

gca aca cct gaa ttt ttg ctt aat ttc tcg agg aaa tat ccg gag gca 307
 Ala Thr Pro Glu Phe Leu Leu Asn Phe Ser Arg Lys Tyr Pro Glu Ala
 55 60 65

acc gtc gtc aag ctg cag cgc gac tac cgc tca acg ccg cag gtc acc 355
 Thr Val Val Lys Leu Gln Arg Asp Tyr Arg Ser Thr Pro Gln Val Thr
 70 75 80 85

gcg ctg gcc aat acc gtc atc ggc cag gcg cgg ggg cgc gtt gct ggc 403
 Ala Leu Ala Asn Thr Val Ile Gly Gln Ala Arg Gly Arg Val Ala Gly
 90 95 100

acg cgc ctg gag ctt cag gga atg cgg atc gcc ggg ccg gag ccc gaa 451
 Thr Arg Leu Glu Leu Gln Gly Met Arg Ile Ala Gly Pro Glu Pro Glu
 105 110 115

ttt tcg gct ttc gac gac gaa ccc acc gaa gcc cgc gaa gtt gcg ggc 499
 Phe Ser Ala Phe Asp Asp Glu Pro Thr Glu Ala Arg Glu Val Ala Gly
 120 125 130

cgc att ttg acg ctg ctt aaa aac ggc gtt cag gcc tca gaa atc gcc 547
 Arg Ile Leu Thr Leu Leu Lys Asn Gly Val Gln Ala Ser Glu Ile Ala

135	140	145	
gtt ttg tac cgc atc aac gcg cag tcg gcg gtt ttc gag caa gcg ctt			595
Val Leu Tyr Arg Ile Asn Ala Gln Ser Ala Val Phe Glu Gln Ala Leu			
150	155	160	165
gcc gac gcc ggc atc gta tat cag gtg cgc ggc ggc gaa ggc ttt ttc			643
Ala Asp Ala Gly Ile Val Tyr Gln Val Arg Gly Gly Glu Gly Phe Phe			
	170	175	180
acc cgc cca gaa att cgc caa gcc ctg agt caa ctg atc cgc act tcc			691
Thr Arg Pro Glu Ile Arg Gln Ala Leu Ser Gln Leu Ile Arg Thr Ser			
	185	190	195
caa cgc gac gtc gat gaa agc gat ctg gtg cgt ctg acg caa cgc aca			739
Gln Arg Asp Val Asp Glu Ser Asp Leu Val Arg Leu Thr Gln Arg Thr			
	200	205	210
ctc gtg cca ctt ggg ttg agt tcg gaa gag ccc agc ggt gcc caa gag			787
Leu Val Pro Leu Gly Leu Ser Ser Glu Glu Pro Ser Gly Ala Gln Glu			
	215	220	225
cgg gaa cgc tgg caa tcg ctc aac gct tta gtc gat ctg gtg aaa gac			835
Arg Glu Arg Trp Gln Ser Leu Asn Ala Leu Val Asp Leu Val Lys Asp			
	230	235	240
ctt gtt aaa gcc aca cca gat ttg gat ctc aca ggc ttg ctg ctg aaa			883
Leu Val Lys Ala Thr Pro Asp Leu Asp Leu Thr Gly Leu Leu Leu Lys			
	250	255	260
ctt cgg gaa cgc caa gag gcg aag cat ccg ccg acc gtc gaa ggt gtc			931
Leu Arg Glu Arg Gln Glu Ala Lys His Pro Pro Thr Val Glu Gly Val			
	265	270	275
acc ttg gca tcg cta cac gcg gcg aaa ggc ctc gaa tgg gat gcg gtg			979
Thr Leu Ala Ser Leu His Ala Ala Lys Gly Leu Glu Trp Asp Ala Val			
	280	285	290
ttt ctt gtc gga ctt gtc gat tcc acg tta ccg atc agc cac gcc att			1027
Phe Leu Val Gly Leu Val Asp Ser Thr Leu Pro Ile Ser His Ala Ile			
	295	300	305
aaa tct ggc gat gaa gca atc gaa gag gaa cgt cgc ctg ttc tat gtc			1075
Lys Ser Gly Asp Glu Ala Ile Glu Glu Glu Arg Leu Phe Tyr Val			
	310	315	320
ggt gtg acc cgt gcc cgc gaa cac ctc cac tgc agt tgg gca ctc gcg			1123
Gly Val Thr Arg Ala Arg Glu His Leu His Cys Ser Trp Ala Leu Ala			
	330	335	340
agg caa gaa ggc gga cgg aaa tcg aga aag cgg agt cga ttc ctc gat			1171
Arg Gln Glu Gly Gly Arg Lys Ser Arg Lys Arg Ser Arg Phe Leu Asp			
	345	350	355
ggc ata gtc gtg gag atg gcc tcc gaa tcg ggc aca cct cgc agc aat			1219
Gly Ile Val Val Glu Met Ala Ser Glu Ser Gly Thr Pro Arg Ser Asn			
	360	365	370
cgt ccg aaa aac tgc cga gtg tgc gga tcg gtt ctt tca agc cct gcc			1267
Arg Pro Lys Asn Cys Arg Val Cys Gly Ser Val Leu Ser Ser Pro Ala			
	375	380	385

gaa aaa gct gtc ggt cgg tgt gcg agt tgc ccg atc caa gcg gat gaa 1315
 Glu Lys Ala Val Gly Arg Cys Ala Ser Cys Pro Ile Gln Ala Asp Glu
 390 395 400 405

cga gtc ttc gaa cag ctg cga acg tgg cgc aat gac acc gcg aag cgc 1363
 Arg Val Phe Glu Gln Leu Arg Thr Trp Arg Asn Asp Thr Ala Lys Arg
 410 415 420

gaa aac aaa gcg gcg tac atg gtg ttc agc aat gca acg ttg atg gcg 1411
 Glu Asn Lys Ala Ala Tyr Met Val Phe Ser Asn Ala Thr Leu Met Ala
 425 430 435

atc gct gaa atg aac ccc acc aac gaa aac gaa ttg ctc agc gtg ccg 1459
 Ile Ala Glu Met Asn Pro Thr Asn Glu Asn Glu Leu Leu Ser Val Pro
 440 445 450

ggt gtg ggg ccg atg aag atc gag aac tat ggc gat gac gtg ctc gcg 1507
 Gly Val Gly Pro Met Lys Ile Glu Asn Tyr Gly Asp Asp Val Leu Ala
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<210> 106

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

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Gly Asp Arg Asp Asp Leu Thr Val Val Gly Asp Ala Asn Gln Thr Ile
 35 40 45

Tyr Ser Phe Thr Gly Ala Thr Pro Glu Phe Leu Leu Asn Phe Ser Arg
 50 55 60

Lys Tyr Pro Glu Ala Thr Val Val Lys Leu Gln Arg Asp Tyr Arg Ser
 65 70 75 80

Thr Pro Gln Val Thr Ala Leu Ala Asn Thr Val Ile Gly Gln Ala Arg
 85 90 95

Gly Arg Val Ala Gly Thr Arg Leu Glu Leu Gln Gly Met Arg Ile Ala
 100 105 110

Gly Pro Glu Pro Glu Phe Ser Ala Phe Asp Asp Glu Pro Thr Glu Ala
 115 120 125

Arg Glu Val Ala Gly Arg Ile Leu Thr Leu Leu Lys Asn Gly Val Gln
 130 135 140

Ala Ser Glu Ile Ala Val Leu Tyr Arg Ile Asn Ala Gln Ser Ala Val
 145 150 155 160

Phe Glu Gln Ala Leu Ala Asp Ala Gly Ile Val Tyr Gln Val Arg Gly
165 170 175

Gly Glu Gly Phe Phe Thr Arg Pro Glu Ile Arg Gln Ala Leu Ser Gln
180 185 190

Leu Ile Arg Thr Ser Gln Arg Asp Val Asp Glu Ser Asp Leu Val Arg
195 200 205

Leu Thr Gln Arg Thr Leu Val Pro Leu Gly Leu Ser Ser Glu Glu Pro
210 215 220

Ser Gly Ala Gln Glu Arg Glu Arg Trp Gln Ser Leu Asn Ala Leu Val
225 230 235 240

Asp Leu Val Lys Asp Leu Val Lys Ala Thr Pro Asp Leu Asp Leu Thr
245 250 255

Gly Leu Leu Leu Lys Leu Arg Glu Arg Gln Glu Ala Lys His Pro Pro
260 265 270

Thr Val Glu Gly Val Thr Leu Ala Ser Leu His Ala Ala Lys Gly Leu
275 280 285

Glu Trp Asp Ala Val Phe Leu Val Gly Leu Val Asp Ser Thr Leu Pro
290 295 300

Ile Ser His Ala Ile Lys Ser Gly Asp Glu Ala Ile Glu Glu Glu Arg
305 310 315 320

Arg Leu Phe Tyr Val Gly Val Thr Arg Ala Arg Glu His Leu His Cys
325 330 335

Ser Trp Ala Leu Ala Arg Gln Glu Gly Gly Arg Lys Ser Arg Lys Arg
340 345 350

Ser Arg Phe Leu Asp Gly Ile Val Val Glu Met Ala Ser Glu Ser Gly
355 360 365

Thr Pro Arg Ser Asn Arg Pro Lys Asn Cys Arg Val Cys Gly Ser Val
370 375 380

Leu Ser Ser Pro Ala Glu Lys Ala Val Gly Arg Cys Ala Ser Cys Pro
385 390 395 400

Ile Gln Ala Asp Glu Arg Val Phe Glu Gln Leu Arg Thr Trp Arg Asn
405 410 415

Asp Thr Ala Lys Arg Glu Asn Lys Ala Ala Tyr Met Val Phe Ser Asn
420 425 430

Ala Thr Leu Met Ala Ile Ala Glu Met Asn Pro Thr Asn Glu Asn Glu
435 440 445

Leu Leu Ser Val Pro Gly Val Gly Pro Met Lys Ile Glu Asn Tyr Gly
450 455 460

Asp Asp Val Leu Ala Ile Leu Gly Ala Leu
465 470

cgc gtt cca aac ttg ttg atg aac ggt tgc ggc ggc att gcg gtc ggc 643
Arg Val Pro Asn Leu Leu Met Asn Gly Ser Gly Gly Ile Ala Val Gly
170 175 180

atg gcc acc aac atc cca ccg cac aac ctc aac gag ctt gcc gac gcc	691
Met Ala Thr Asn Ile Pro Pro His Asn Leu Asn Glu Leu Ala Asp Ala	
185 190 195	
atc ttc tgg ctc ctg gaa aac cca gac gcc gaa gaa tcc gaa gct ctc	739
Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu Glu Ser Glu Ala Leu	
200 205 210	
gaa gcc tgc atg aag ttt gtg aag ggc cca gac ttc cca acc gct ggc	787
Glu Ala Cys Met Lys Phe Val Lys Gly Pro Asp Phe Pro Thr Ala Gly	
215 220 225	
ctc atc atc ggt gac aag ggc atc cac gat gcc tac acc acc ggc cgc	835
Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala Tyr Thr Thr Gly Arg	
230 235 240 245	
ggc tcc atc cgc atg cgc ggt gtc acc tcc atc gag gag gaa ggc aac	883
Gly Ser Ile Arg Met Arg Gly Val Thr Ser Ile Glu Glu Glu Gly Asn	
250 255 260	
cgc acc gtc atc gtt atc acc gag ctg cca tac cag gtc aac ccg gat	931
Arg Thr Val Ile Val Ile Thr Glu Leu Pro Tyr Gln Val Asn Pro Asp	
265 270 275	
aac ctg atc tct aat atc gcg gag cag gtg cgc gac ggc aag ctc gtg	979
Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg Asp Gly Lys Leu Val	
280 285 290	
ggc atc tcc aag att gaa gat gaa tcc tcc gac cgc gtc ggc atg cgc	1027
Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp Arg Val Gly Met Arg	
295 300 305	
att gtg gtc acc ctc aag cgc gac gca gtt gcc cgc gtg gtg ctg aac	1075
Ile Val Val Thr Leu Lys Arg Asp Ala Val Ala Arg Val Val Leu Asn	
310 315 320 325	
aac ctg ttc aag cac tcc cag ctg caa gcc aac ttt ggt gcg aac atg	1123
Asn Leu Phe Lys His Ser Gln Leu Gln Ala Asn Phe Gly Ala Asn Met	
330 335 340	
ctc tcc atc gtc gat ggc gtg cca cgc acc ctt cgc ctg gac cag atg	1171
Leu Ser Ile Val Asp Gly Val Pro Arg Thr Leu Arg Leu Asp Gln Met	
345 350 355	
ctg cgc tac tac gtg gca cac cag atc gaa gtc atc gtg cgc cgc acc	1219
Leu Arg Tyr Tyr Val Ala His Gln Ile Glu Val Ile Val Arg Arg Thr	
360 365 370	
caa tac cgc ctc gac aag gct gaa gag cgc gcc cac ctc ctc cgc ggc	1267
Gln Tyr Arg Leu Asp Lys Ala Glu Glu Arg Ala His Leu Leu Arg Gly	
375 380 385	
ctg gtc aag gcc ctg gac atg ctg gac gag gtc atc gcg ctc atc cgc	1315
Leu Val Lys Ala Leu Asp Met Leu Asp Glu Val Ile Ala Leu Ile Arg	
390 395 400 405	
cgc agc cca acc cca gat gaa gcc cgc acc ggc ctc atg tcg ctt ctc	1363
Arg Ser Pro Thr Pro Asp Glu Ala Arg Thr Gly Leu Met Ser Leu Leu	
410 415 420	

gac gtc gac gag gcg cag gct gac gca att ctg gca atg cag ctg cgt	1411
Asp Val Asp Glu Ala Gln Ala Asp Ala Ile Leu Ala Met Gln Leu Arg	
425 430 435	
cgc ctg gcg gca ctg gaa cgc caa aag atc atc gat gag ctc gct gaa	1459
Arg Leu Ala Ala Leu Glu Arg Gln Lys Ile Ile Asp Glu Leu Ala Glu	
440 445 450	
atc gag ctg gaa atc gct gac ctg aag gcc atc ctg gca agc cca gaa	1507
Ile Glu Leu Glu Ile Ala Asp Leu Lys Ala Ile Leu Ala Ser Pro Glu	
455 460 465	
cgt cag cgc acc atc gtt cgc gat gag ctg acc gaa atc gtg gaa aag	1555
Arg Gln Arg Thr Ile Val Arg Asp Glu Leu Thr Glu Ile Val Glu Lys	
470 475 480 485	
tac ggc gac gag cgt cgt tcc cag atc atc gct gcc acc ggc gac gtg	1603
Tyr Gly Asp Glu Arg Ser Gln Ile Ile Ala Ala Thr Gly Asp Val	
490 495 500	
tct gaa gaa gac ctc att gcg cgt gaa aac gtt gtc atc acc att acc	1651
Ser Glu Glu Asp Leu Ile Ala Arg Glu Asn Val Val Ile Thr Ile Thr	
505 510 515	
tcc acc ggt tac gca aag cgc acc aag gtc gat gcc tac aag tcg caa	1699
Ser Thr Gly Tyr Ala Lys Arg Thr Lys Val Asp Ala Tyr Lys Ser Gln	
520 525 530	
aag cgt ggc ggc aag ggt gtt cgt ggc gca gag ctc aag caa gat gac	1747
Lys Arg Gly Gly Lys Gly Val Arg Gly Ala Glu Leu Lys Gln Asp Asp	
535 540 545	
att gtt cgt cac ttc ttc gtc agc tcc acc cac gac tgg att ttg ttc	1795
Ile Val Arg His Phe Phe Val Ser Ser Thr His Asp Trp Ile Leu Phe	
550 555 560 565	
ttc acc aac tac ggt cgc gtg tac cgc ctc aag gca ttc gaa ctt cca	1843
Phe Thr Asn Tyr Gly Arg Val Tyr Arg Leu Lys Ala Phe Glu Leu Pro	
570 575 580	
gag gca tcc cgc acc gca cgt gga cag cac gtg gcc aac ctt ctg gaa	1891
Glu Ala Ser Arg Thr Ala Arg Gly Gln His Val Ala Asn Leu Leu Glu	
585 590 595	
ttc caa cct ggt gag caa atc gcc cag gtc atc cag ttg gaa agc tac	1939
Phe Gln Pro Gly Glu Gln Ile Ala Gln Val Ile Gln Leu Glu Ser Tyr	
600 605 610	
aac gac ttc cca tac ctg gtg ctc gca acc gca cac ggt cgc gtg aag	1987
Asn Asp Phe Pro Tyr Leu Val Leu Ala Thr Ala His Gly Arg Val Lys	
615 620 625	
aag tcc cgc ctg ctc gac tac gaa tca gca cgt tcc ggt ggc ctc atc	2035
Lys Ser Arg Leu Leu Asp Tyr Glu Ser Ala Arg Ser Gly Gly Leu Ile	
630 635 640 645	
gcc atc aac ctg aac gag gac gat cgc ctc atc ggc gcc gca ctt tgc	2083
Ala Ile Asn Leu Asn Glu Asp Asp Arg Leu Ile Gly Ala Ala Leu Cys	
650 655 660	
ggt gaa gaa gac gat ctg ctg ctg gtc tct gaa ttc gga cag tcc atc	2131

Gly	Glu	Glu	Asp	Asp	Leu	Leu	Leu	Val	Ser	Glu	Phe	Gly	Gln	Ser	Ile		
			665					670					675				
cgc	ttc	acc	gcc	gac	gat	gag	cag	ctc	cgc	ccc	atg	ggc	cgc	gcc	acc	2179	
Arg	Phe	Thr	Ala	Asp	Asp	Glu	Gln	Leu	Arg	Pro	Met	Gly	Arg	Ala	Thr		
		680					685					690					
gcc	ggt	gtc	aag	ggc	atg	cgc	ttc	cgc	gac	aac	gac	caa	ctg	ctg	tcc	2227	
Ala	Gly	Val	Lys	Gly	Met	Arg	Phe	Arg	Asp	Asn	Asp	Gln	Leu	Leu	Ser		
		695				700					705						
atg	tcc	gtg	gtc	cgc	gac	ggc	gaa	ttc	ctc	ctc	gtt	gcc	acc	tcc	ggc	2275	
Met	Ser	Val	Val	Arg	Asp	Gly	Glu	Phe	Leu	Leu	Val	Ala	Thr	Ser	Gly		
710					715					720					725		
ggc	tac	ggc	aag	cgc	acc	cca	ctt	gag	gat	tac	tcc	acc	cag	ggc	cgt	2323	
Gly	Tyr	Gly	Lys	Arg	Thr	Pro	Leu	Glu	Asp	Tyr	Ser	Thr	Gln	Gly	Arg		
				730					735					740			
ggt	ggc	ctc	ggc	gtg	gtg	acc	ttc	aag	tac	acc	ccg	aag	cgc	ggt	cgc	2371	
Gly	Gly	Leu	Gly	Val	Val	Thr	Phe	Lys	Tyr	Thr	Pro	Lys	Arg	Gly	Arg		
			745					750					755				
ctc	gtc	agc	gcc	atc	gca	gtt	gag	gaa	gat	gac	gag	atc	ttc	gcc	atc	2419	
Leu	Val	Ser	Ala	Ile	Ala	Val	Glu	Glu	Asp	Asp	Glu	Ile	Phe	Ala	Ile		
		760					765					770					
acc	tcc	gcc	ggc	ggc	gtt	gtt	cgc	acc	gaa	gtc	aag	cag	atc	cga	cca	2467	
Thr	Ser	Ala	Gly	Gly	Val	Val	Arg	Thr	Glu	Val	Lys	Gln	Ile	Arg	Pro		
		775				780					785						
tcc	tcc	cgt	gca	aca	atg	ggt	gtt	cga	ctg	gtc	aac	ttg	gaa	gaa	ggt	2515	
Ser	Ser	Arg	Ala	Thr	Met	Gly	Val	Arg	Leu	Val	Asn	Leu	Glu	Glu	Gly		
790					795					800					805		
gta	gaa	ctg	ctt	gcc	atc	gac	aag	aac	gtc	gaa	gac	cag	ggc	gaa	gca	2563	
Val	Glu	Leu	Leu	Ala	Ile	Asp	Lys	Asn	Val	Glu	Asp	Gln	Gly	Glu	Ala		
				810					815					820			
tcc	gca	gaa	gca	gta	gca	aag	ggt	gca	gtc	gaa	gga	cca	gca	tcc	aag	2611	
Ser	Ala	Glu	Ala	Val	Ala	Lys	Gly	Ala	Val	Glu	Gly	Pro	Ala	Ser	Lys		
			825					830					835				
act	gct	gcc	gaa	gaa	acc	gac	tcc	gtt	gac	aac	gga	tcc	gac	gaa	aac	2659	
Thr	Ala	Ala	Glu	Glu	Thr	Asp	Ser	Val	Asp	Asn	Gly	Ser	Asp	Glu	Asn		
		840					845					850					
ggc	gag	gaa	taatttatgg	catccc	gaga	agt										2691	
Gly	Glu	Glu															
		855															

<210> 108

<211> 856

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

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Ile Asn Glu Glu Met Gln Ser Ser Tyr Ile Asp Tyr Ala Met Ser Val
 20 25 30
 Ile Val Gly Arg Ala Leu Pro Glu Val Arg Asp Gly Leu Lys Pro Val
 35 40 45
 His Arg Arg Val Leu Tyr Ala Met Phe Asp Asn Gly Tyr Arg Pro Asp
 50 55 60
 Arg Ser Tyr Val Lys Ser Ala Lys Pro Val Ala Asp Thr Met Gly Asn
 65 70 75 80
 Phe His Pro His Gly Asp Thr Ala Ile Tyr Asp Thr Leu Val Arg Met
 85 90 95
 Ala Gln Pro Trp Ser Met Arg Tyr Pro Leu Val Asp Gly Gln Gly Asn
 100 105 110
 Phe Gly Ser Arg Gly Asn Asp Gly Pro Ala Ala Met Arg Tyr Thr Glu
 115 120 125
 Cys Arg Met Thr Pro Leu Ala Met Glu Met Val Arg Asp Ile Arg Glu
 130 135 140
 Asn Thr Val Asn Phe Ser Pro Asn Tyr Asp Gly Lys Thr Leu Glu Pro
 145 150 155 160
 Asp Val Leu Pro Ser Arg Val Pro Asn Leu Leu Met Asn Gly Ser Gly
 165 170 175
 Gly Ile Ala Val Gly Met Ala Thr Asn Ile Pro Pro His Asn Leu Asn
 180 185 190
 Glu Leu Ala Asp Ala Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu
 195 200 205
 Glu Ser Glu Ala Leu Glu Ala Cys Met Lys Phe Val Lys Gly Pro Asp
 210 215 220
 Phe Pro Thr Ala Gly Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala
 225 230 235 240
 Tyr Thr Thr Gly Arg Gly Ser Ile Arg Met Arg Gly Val Thr Ser Ile
 245 250 255
 Glu Glu Glu Gly Asn Arg Thr Val Ile Val Ile Thr Glu Leu Pro Tyr
 260 265 270
 Gln Val Asn Pro Asp Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg
 275 280 285
 Asp Gly Lys Leu Val Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp
 290 295 300
 Arg Val Gly Met Arg Ile Val Val Thr Leu Lys Arg Asp Ala Val Ala
 305 310 315 320
 Arg Val Val Leu Asn Asn Leu Phe Lys His Ser Gln Leu Gln Ala Asn
 325 330 335
 Phe Gly Ala Asn Met Leu Ser Ile Val Asp Gly Val Pro Arg Thr Leu

340					345					350					
Arg	Leu	Asp	Gln	Met	Leu	Arg	Tyr	Tyr	Val	Ala	His	Gln	Ile	Glu	Val
		355					360					365			
Ile	Val	Arg	Arg	Thr	Gln	Tyr	Arg	Leu	Asp	Lys	Ala	Glu	Glu	Arg	Ala
	370					375					380				
His	Leu	Leu	Arg	Gly	Leu	Val	Lys	Ala	Leu	Asp	Met	Leu	Asp	Glu	Val
	385					390					395				400
Ile	Ala	Leu	Ile	Arg	Arg	Ser	Pro	Thr	Pro	Asp	Glu	Ala	Arg	Thr	Gly
				405					410					415	
Leu	Met	Ser	Leu	Leu	Asp	Val	Asp	Glu	Ala	Gln	Ala	Asp	Ala	Ile	Leu
				420					425					430	
Ala	Met	Gln	Leu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Arg	Gln	Lys	Ile	Ile
		435					440							445	
Asp	Glu	Leu	Ala	Glu	Ile	Glu	Leu	Glu	Ile	Ala	Asp	Leu	Lys	Ala	Ile
	450					455					460				
Leu	Ala	Ser	Pro	Glu	Arg	Gln	Arg	Thr	Ile	Val	Arg	Asp	Glu	Leu	Thr
	465					470					475				480
Glu	Ile	Val	Glu	Lys	Tyr	Gly	Asp	Glu	Arg	Arg	Ser	Gln	Ile	Ile	Ala
				485					490						495
Ala	Thr	Gly	Asp	Val	Ser	Glu	Glu	Asp	Leu	Ile	Ala	Arg	Glu	Asn	Val
			500						505					510	
Val	Ile	Thr	Ile	Thr	Ser	Thr	Gly	Tyr	Ala	Lys	Arg	Thr	Lys	Val	Asp
		515						520						525	
Ala	Tyr	Lys	Ser	Gln	Lys	Arg	Gly	Gly	Lys	Gly	Val	Arg	Gly	Ala	Glu
	530					535					540				
Leu	Lys	Gln	Asp	Asp	Ile	Val	Arg	His	Phe	Phe	Val	Ser	Ser	Thr	His
	545					550					555				560
Asp	Trp	Ile	Leu	Phe	Phe	Thr	Asn	Tyr	Gly	Arg	Val	Tyr	Arg	Leu	Lys
				565					570					575	
Ala	Phe	Glu	Leu	Pro	Glu	Ala	Ser	Arg	Thr	Ala	Arg	Gly	Gln	His	Val
				580					585					590	
Ala	Asn	Leu	Leu	Glu	Phe	Gln	Pro	Gly	Glu	Gln	Ile	Ala	Gln	Val	Ile
		595						600						605	
Gln	Leu	Glu	Ser	Tyr	Asn	Asp	Phe	Pro	Tyr	Leu	Val	Leu	Ala	Thr	Ala
		610				615					620				
His	Gly	Arg	Val	Lys	Lys	Ser	Arg	Leu	Leu	Asp	Tyr	Glu	Ser	Ala	Arg
	625					630					635				640
Ser	Gly	Gly	Leu	Ile	Ala	Ile	Asn	Leu	Asn	Glu	Asp	Asp	Arg	Leu	Ile
				645					650					655	
Gly	Ala	Ala	Leu	Cys	Gly	Glu	Glu	Asp	Asp	Leu	Leu	Leu	Val	Ser	Glu
			660					665						670	

Phe Gly Gln Ser Ile Arg Phe Thr Ala Asp Asp Glu Gln Leu Arg Pro
 675 680 685
 Met Gly Arg Ala Thr Ala Gly Val Lys Gly Met Arg Phe Arg Asp Asn
 690 695 700
 Asp Gln Leu Leu Ser Met Ser Val Val Arg Asp Gly Glu Phe Leu Leu
 705 710 715 720
 Val Ala Thr Ser Gly Gly Tyr Gly Lys Arg Thr Pro Leu Glu Asp Tyr
 725 730 735
 Ser Thr Gln Gly Arg Gly Gly Leu Gly Val Val Thr Phe Lys Tyr Thr
 740 745 750
 Pro Lys Arg Gly Arg Leu Val Ser Ala Ile Ala Val Glu Glu Asp Asp
 755 760 765
 Glu Ile Phe Ala Ile Thr Ser Ala Gly Gly Val Val Arg Thr Glu Val
 770 775 780
 Lys Gln Ile Arg Pro Ser Ser Arg Ala Thr Met Gly Val Arg Leu Val
 785 790 795 800
 Asn Leu Glu Glu Gly Val Glu Leu Leu Ala Ile Asp Lys Asn Val Glu
 805 810 815
 Asp Gln Gly Glu Ala Ser Ala Glu Ala Val Ala Lys Gly Ala Val Glu
 820 825 830
 Gly Pro Ala Ser Lys Thr Ala Ala Glu Glu Thr Asp Ser Val Asp Asn
 835 840 845
 Gly Ser Asp Glu Asn Gly Glu Glu
 850 855

<210> 109

<211> 257

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(234)

<223> FRXA01682

<400> 109

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 Arg Thr Lys Val Asp Ala Tyr Lys Ser Gln Lys Arg Gly Gly Lys Gly
 1 5 10 15

gtt tgt ggc gca gag ctc aag caa gat gac att gtt cgt cac ttc ttc 96
 Val Cys Gly Ala Glu Leu Lys Gln Asp Asp Ile Val Arg His Phe Phe
 20 25 30

gtc agc tcc acc cac gac tgg att ttg ttt ctt cac caa cta cgg tcg 144
 Val Ser Ser Thr His Asp Trp Ile Leu Phe Leu His Gln Leu Arg Ser
 35 40 45

cag ttg gaa agc tac aac gac ttc cca tac ctg gtg ctc gca acc gca 259
Gln Leu Glu Ser Tyr Asn Asp Phe Pro Tyr Leu Val Leu Ala Thr Ala
40 45 50

cac ggt cgc gtg aag aag tcc cgc ctg ctc gac tac gaa tca gca cgt	307
His Gly Arg Val Lys Lys Ser Arg Leu Leu Asp Tyr Glu Ser Ala Arg	
55 60 65	
tcc ggt ggc ctc atc gcc atc aac ctg aac gag gac gat cgc ctc atc	355
Ser Gly Gly Leu Ile Ala Ile Asn Leu Asn Glu Asp Asp Arg Leu Ile	
70 75 80 85	
ggc gcc gca ctt tgc ggt gaa gaa gac gat ctg ctg ctg gtc tct gaa	403
Gly Ala Ala Leu Cys Gly Glu Glu Asp Asp Leu Leu Leu Val Ser Glu	
90 95 100	
ttc gga cag tcc atc cgc ttc acc gcc gac gat gag cag ctc cgc ccc	451
Phe Gly Gln Ser Ile Arg Phe Thr Ala Asp Asp Glu Gln Leu Arg Pro	
105 110 115	
atg ggc cgc gcc acc gcc ggt gtc aag ggc atg cgc ttc cgc gac aac	499
Met Gly Arg Ala Thr Ala Gly Val Lys Gly Met Arg Phe Arg Asp Asn	
120 125 130	
gac caa ctg ctg tcc atg tcc gtg gtc cgc gac ggc gaa ttc ctc ctc	547
Asp Gln Leu Leu Ser Met Ser Val Val Arg Asp Gly Glu Phe Leu Leu	
135 140 145	
gtt gcc acc tcc ggc ggc tac ggc aag cgc acc cca ctt gag gat tac	595
Val Ala Thr Ser Gly Gly Tyr Gly Lys Arg Thr Pro Leu Glu Asp Tyr	
150 155 160 165	
tcc acc cag ggc cgt ggt ggc ctc ggc gtg gtg acc ttc aag tac acc	643
Ser Thr Gln Gly Arg Gly Gly Leu Gly Val Val Thr Phe Lys Tyr Thr	
170 175 180	
ccg aag cgc ggt cgc ctc gtc agc gcc atc gca gtt gag gaa gat gac	691
Pro Lys Arg Gly Arg Leu Val Ser Ala Ile Ala Val Glu Glu Asp Asp	
185 190 195	
gag atc ttc gcc atc acc tcc gcc ggc ggc gtt gtt cgc acc gaa gtc	739
Glu Ile Phe Ala Ile Thr Ser Ala Gly Gly Val Val Arg Thr Glu Val	
200 205 210	
aag cag atc cga cca tcc tcc cgt gca aca atg ggt gtt cga ctg gtc	787
Lys Gln Ile Arg Pro Ser Ser Arg Ala Thr Met Gly Val Arg Leu Val	
215 220 225	
aac ttg gaa gaa ggt gta gaa ctg ctt gcc atc gac aag aac gtc gaa	835
Asn Leu Glu Glu Gly Val Glu Leu Leu Ala Ile Asp Lys Asn Val Glu	
230 235 240 245	
gac cag ggc gaa gca	850
Asp Gln Gly Glu Ala	
250	

<210> 112

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

Val Tyr Arg Leu Lys Ala Phe Glu Leu Pro Glu Ala Ser Arg Thr Ala

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 Arg Gly Gln His Val Ala Asn Leu Leu Glu Phe Gln Pro Gly Glu Gln
 20 25 30
 Ile Ala Gln Val Ile Gln Leu Glu Ser Tyr Asn Asp Phe Pro Tyr Leu
 35 40 45
 Val Leu Ala Thr Ala His Gly Arg Val Lys Lys Ser Arg Leu Leu Asp
 50 55 60
 Tyr Glu Ser Ala Arg Ser Gly Gly Leu Ile Ala Ile Asn Leu Asn Glu
 65 70 75 80
 Asp Asp Arg Leu Ile Gly Ala Ala Leu Cys Gly Glu Glu Asp Asp Leu
 85 90 95
 Leu Leu Val Ser Glu Phe Gly Gln Ser Ile Arg Phe Thr Ala Asp Asp
 100 105 110
 Glu Gln Leu Arg Pro Met Gly Arg Ala Thr Ala Gly Val Lys Gly Met
 115 120 125
 Arg Phe Arg Asp Asn Asp Gln Leu Leu Ser Met Ser Val Val Arg Asp
 130 135 140
 Gly Glu Phe Leu Leu Val Ala Thr Ser Gly Gly Tyr Gly Lys Arg Thr
 145 150 155 160
 Pro Leu Glu Asp Tyr Ser Thr Gln Gly Arg Gly Gly Leu Gly Val Val
 165 170 175
 Thr Phe Lys Tyr Thr Pro Lys Arg Gly Arg Leu Val Ser Ala Ile Ala
 180 185 190
 Val Glu Glu Asp Asp Glu Ile Phe Ala Ile Thr Ser Ala Gly Gly Val
 195 200 205
 Val Arg Thr Glu Val Lys Gln Ile Arg Pro Ser Ser Arg Ala Thr Met
 210 215 220
 Gly Val Arg Leu Val Asn Leu Glu Glu Gly Val Glu Leu Leu Ala Ile
 225 230 235 240
 Asp Lys Asn Val Glu Asp Gln Gly Glu Ala
 245 250

<210> 113
 <211> 873
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(873)
 <223> FRXA01684

<400> 113
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 Gly Asp Thr Ala Ile Tyr Asp Thr Leu Val Arg Met Ala Gln Pro Trp

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tcc atg cga tac	ccg ctg gta gac	ggc cag ggt aac ttc	ggt tcc cgc	96
Ser Met Arg Tyr	Pro Leu Val Asp	Gly Gln Gly Asn Phe	Gly Ser Arg	
20		25	30	
ggc aac gac ggc	cct gca gca atg	cgt tac acc gag	tgc cgc atg acc	144
Gly Asn Asp Gly	Pro Ala Ala Met	Arg Tyr Thr Glu	Cys Arg Met Thr	
35	40	45		
cca ctg gcc atg	gag atg gtg cgc	gac atc cgc gaa	aac acc gtc aac	192
Pro Leu Ala Met	Glu Met Val Arg	Asp Ile Arg Glu	Asn Thr Val Asn	
50	55	60		
ttc tca cca aac	tac gac ggt aaa	acc ctc gaa cca	gac gtt ttg cca	240
Phe Ser Pro Asn	Tyr Asp Gly Lys	Thr Leu Glu Pro	Asp Val Leu Pro	
65	70	75	80	
tcg cgc gtt cca	aac ttg ttg atg	aac ggt tcg ggc	ggc att gcg gtc	288
Ser Arg Val Pro	Asn Leu Leu Met	Asn Gly Ser Gly	Gly Ile Ala Val	
85		90	95	
ggc atg gcc acc	aac atc cca ccg	cac aac ctc aac	gag ctt gcc gac	336
Gly Met Ala Thr	Asn Ile Pro Pro	His Asn Leu Asn	Glu Leu Ala Asp	
100		105	110	
gcc atc ttc tgg	ctc ctg gaa aac	cca gac gcc gaa	gaa tcc gaa gct	384
Ala Ile Phe Trp	Leu Leu Glu Asn	Pro Asp Ala Glu	Glu Glu Ser Glu	
115	120	125		
ctc gaa gcc tgc	atg aag ttt gtg	aag ggc cca gac	ttc cca acc gct	432
Leu Glu Ala Cys	Met Lys Phe Val	Lys Gly Pro Asp	Phe Pro Thr Ala	
130	135	140		
ggc ctc atc atc	ggt gac aag ggc	atc cac gat gcc	tac acc acc ggc	480
Gly Leu Ile Ile	Gly Asp Lys Gly	Ile His Asp Ala	Tyr Thr Thr Gly	
145	150	155	160	
cgc ggc tcc atc	cgc atg cgc ggt	gtc acc tcc atc	gag gag gaa ggc	528
Arg Gly Ser Ile	Arg Met Arg Gly	Val Thr Ser Ile	Glu Glu Glu Gly	
165		170	175	
aac cgc acc gtc	atc gtt atc acc	gag ctg cca tac	cag gtc aac ccg	576
Asn Arg Thr Val	Ile Val Ile Thr	Glu Leu Pro Tyr	Gln Val Asn Pro	
180		185	190	
gat aac ctg atc	tct aat atc gcg	gag cag gtg cgc	gac ggc aag ctc	624
Asp Asn Leu Ile	Ser Asn Ile Ala	Glu Gln Val Arg	Asp Gly Lys Leu	
195	200	205		
gtg ggc atc tcc	aag att gaa gat	gaa tcc tcc gac	cgc gtc ggc atg	672
Val Gly Ile Ser	Lys Ile Glu Asp	Glu Ser Ser Asp	Arg Val Gly Met	
210	215	220		
cgc att gtg gtc	acc ctc aag cgc	gac gca gtt gcc	cgc gtg gtg ctg	720
Arg Ile Val Val	Thr Leu Lys Arg	Asp Ala Val Ala	Arg Val Val Leu	
225	230	235	240	
aac aac ctg ttc	aag cac tcc cag	ctg caa gcc aac	ttt ggt gcg aac	768
Asn Asn Leu Phe	Lys His Ser Gln	Leu Gln Ala Asn	Phe Gly Ala Asn	
245		250	255	

atg ctc tcc atc gtc gat ggc gtg cca cgc acc ctt cgc ctg gac cag 816
 Met Leu Ser Ile Val Asp Gly Val Pro Arg Thr Leu Arg Leu Asp Gln
 260 265 270

atg ctg cgc tac tac gtg gca cac cag atc gaa gtc atc gtg cgc cgc 864
 Met Leu Arg Tyr Tyr Val Ala His Gln Ile Glu Val Ile Val Arg Arg
 275 280 285

acc caa tac 873
 Thr Gln Tyr
 290

<210> 114

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 114

Gly Asp Thr Ala Ile Tyr Asp Thr Leu Val Arg Met Ala Gln Pro Trp
 1 5 10 15

Ser Met Arg Tyr Pro Leu Val Asp Gly Gln Gly Asn Phe Gly Ser Arg
 20 25 30

Gly Asn Asp Gly Pro Ala Ala Met Arg Tyr Thr Glu Cys Arg Met Thr
 35 40 45

Pro Leu Ala Met Glu Met Val Arg Asp Ile Arg Glu Asn Thr Val Asn
 50 55 60

Phe Ser Pro Asn Tyr Asp Gly Lys Thr Leu Glu Pro Asp Val Leu Pro
 65 70 75 80

Ser Arg Val Pro Asn Leu Leu Met Asn Gly Ser Gly Gly Ile Ala Val
 85 90 95

Gly Met Ala Thr Asn Ile Pro Pro His Asn Leu Asn Glu Leu Ala Asp
 100 105 110

Ala Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu Glu Ser Glu Ala
 115 120 125

Leu Glu Ala Cys Met Lys Phe Val Lys Gly Pro Asp Phe Pro Thr Ala
 130 135 140

Gly Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala Tyr Thr Thr Gly
 145 150 155 160

Arg Gly Ser Ile Arg Met Arg Gly Val Thr Ser Ile Glu Glu Glu Gly
 165 170 175

Asn Arg Thr Val Ile Val Ile Thr Glu Leu Pro Tyr Gln Val Asn Pro
 180 185 190

Asp Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg Asp Gly Lys Leu
 195 200 205

Val Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp Arg Val Gly Met
 210 215 220

Arg Ile Val Val Thr Leu Lys Arg Asp Ala Val Ala Arg Val Val Leu
225 230 235 240

Asn Asn Leu Phe Lys His Ser Gln Leu Gln Ala Asn Phe Gly Ala Asn
245 250 255

Met Leu Ser Ile Val Asp Gly Val Pro Arg Thr Leu Arg Leu Asp Gln
260 265 270

Met Leu Arg Tyr Tyr Val Ala His Gln Ile Glu Val Ile Val Arg Arg
275 280 285

Thr Gln Tyr
290

<210> 115

<211> 953

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(930)

<223> RXN01688

<400> 115

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Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Ile Lys
1 5 10 15

tcc ttc gtg cag cgc atg gcc aac gag cac atc ggc cac tgg ttg gaa 96
Ser Phe Val Gln Arg Met Ala Asn Glu His Ile Gly His Trp Leu Glu
20 25 30

gca aac cct gct gaa gcc aag gtc atc atc aac aag gct gtc ggt tcc 144
Ala Asn Pro Ala Glu Ala Lys Val Ile Ile Asn Lys Ala Val Gly Ser
35 40 45

gcg cag gca cgc ctt gct gct cga aaa gcc cgt gac ctg gtc cga cgg 192
Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Asp Leu Val Arg Arg
50 55 60

aag tca gca acc gat ctg ggt gga ctg ccc ggt aag ctt gcc gac tgc 240
Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys
65 70 75 80

cgt tcc aag gat cca gaa aag tcc gaa ctt tac atc gtg gag ggc gac 288
Arg Ser Lys Asp Pro Glu Lys Ser Glu Leu Tyr Ile Val Glu Gly Asp
85 90 95

tcc gca ggt ggt tct gcg aag tcc ggc cgt gac tcc atg ttc cag gca 336
Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala
100 105 110

atc ctt cca ctg cga ggc aag atc ctc aac gtg gaa aag gcc cgc cta 384
Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Arg Leu
115 120 125

gac aag gtt ctg aag aac gcc gaa gtc caa gcg atc atc acc gca ctg 432

Asp Lys Val Leu Lys Asn Ala Glu Val Gln Ala Ile Ile Thr Ala Leu
 130 135 140
 ggt acc ggc atc cac gac gag ttc gac atc aac aag ctg cgc tac cac 480
 Gly Thr Gly Ile His Asp Glu Phe Asp Ile Asn Lys Leu Arg Tyr His
 145 150 155 160
 aag atc gtg ctg atg gcc gac gcc gat gtt gac ggc cag cac atc gca 528
 Lys Ile Val Leu Met Ala Asp Ala Asp Val Asp Gly Gln His Ile Ala
 165 170 175
 acg ctg ctg ctc acc ctg ctt ttc cgc ttc atg cca gac ctc gtc gcc 576
 Thr Leu Leu Leu Thr Leu Leu Phe Arg Phe Met Pro Asp Leu Val Ala
 180 185 190
 gaa ggc cac gtc tac ttg gca cag cca cct ttg tac aaa ctg aag tgg 624
 Glu Gly His Val Tyr Leu Ala Gln Pro Pro Leu Tyr Lys Leu Lys Trp
 195 200 205
 cag cgc gga gag cca gga ttc gca tac tcc gat gag gag cgc gat gag 672
 Gln Arg Gly Glu Pro Gly Phe Ala Tyr Ser Asp Glu Glu Arg Asp Glu
 210 215 220
 cag ctc aac gaa ggc ctt gcc gct gga cgc aag atc aac aag gac gac 720
 Gln Leu Asn Glu Gly Leu Ala Ala Gly Arg Lys Ile Asn Lys Asp Asp
 225 230 235 240
 ggc atc cag cgc tac aag ggt ctc ggc gag atg aac gcc agc gag ctg 768
 Gly Ile Gln Arg Tyr Lys Gly Leu Gly Glu Met Asn Ala Ser Glu Leu
 245 250 255
 tgg gaa acc acc atg gac cca act gtt cgt att ctg cgc cgc gtg gac 816
 Trp Glu Thr Thr Met Asp Pro Thr Val Arg Ile Leu Arg Arg Val Asp
 260 265 270
 atc acc gat gct cag cgt gct gat gaa ctg ttc tcc atc ttg atg ggt 864
 Ile Thr Asp Ala Gln Arg Ala Asp Glu Leu Phe Ser Ile Leu Met Gly
 275 280 285
 gac gac gtt gtg gct cgc cgc agc ttc atc acc cga aat gcc aag gat 912
 Asp Asp Val Val Ala Arg Arg Ser Phe Ile Thr Arg Asn Ala Lys Asp
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 gtt cgt ttc ctc gat atc taaagcgct tacttaaccc gcc 953
 Val Arg Phe Leu Asp Ile
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<210> 116

<211> 310

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

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Ser Phe Val Gln Arg Met Ala Asn Glu His Ile Gly His Trp Leu Glu
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Ala Asn Pro Ala Glu Ala Lys Val Ile Ile Asn Lys Ala Val Gly Ser

35					40					45						
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Lys	Ser	Ala	Thr	Asp	Leu	Gly	Gly	Leu	Pro	Gly	Lys	Leu	Ala	Asp	Cys	
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Arg	Ser	Lys	Asp	Pro	Glu	Lys	Ser	Glu	Leu	Tyr	Ile	Val	Glu	Gly	Asp	
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Ser	Ala	Gly	Gly	Ser	Ala	Lys	Ser	Gly	Arg	Asp	Ser	Met	Phe	Gln	Ala	
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Ile	Leu	Pro	Leu	Arg	Gly	Lys	Ile	Leu	Asn	Val	Glu	Lys	Ala	Arg	Leu	
115					120					125						
Asp	Lys	Val	Leu	Lys	Asn	Ala	Glu	Val	Gln	Ala	Ile	Ile	Thr	Ala	Leu	
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Gly	Thr	Gly	Ile	His	Asp	Glu	Phe	Asp	Ile	Asn	Lys	Leu	Arg	Tyr	His	
145					150					155					160	
Lys	Ile	Val	Leu	Met	Ala	Asp	Ala	Asp	Val	Asp	Gly	Gln	His	Ile	Ala	
165					170					175						
Thr	Leu	Leu	Leu	Thr	Leu	Leu	Phe	Arg	Phe	Met	Pro	Asp	Leu	Val	Ala	
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Glu	Gly	His	Val	Tyr	Leu	Ala	Gln	Pro	Pro	Leu	Tyr	Lys	Leu	Lys	Trp	
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Gln	Arg	Gly	Glu	Pro	Gly	Phe	Ala	Tyr	Ser	Asp	Glu	Glu	Arg	Asp	Glu	
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Gln	Leu	Asn	Glu	Gly	Leu	Ala	Ala	Gly	Arg	Lys	Ile	Asn	Lys	Asp	Asp	
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Gly	Ile	Gln	Arg	Tyr	Lys	Gly	Leu	Gly	Glu	Met	Asn	Ala	Ser	Glu	Leu	
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Trp	Glu	Thr	Thr	Met	Asp	Pro	Thr	Val	Arg	Ile	Leu	Arg	Arg	Val	Asp	
260					265					270						
Ile	Thr	Asp	Ala	Gln	Arg	Ala	Asp	Glu	Leu	Phe	Ser	Ile	Leu	Met	Gly	
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Asp	Asp	Val	Val	Ala	Arg	Arg	Ser	Phe	Ile	Thr	Arg	Asn	Ala	Lys	Asp	
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<211> 564

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(564)

<223> FRXA01688

<400> 117

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tcc ttc gtg cag cgc atg gcc aac gag cac atc ggc cac tgg ttg gaa	96
Ser Phe Val Gln Arg Met Ala Asn Glu His Ile Gly His Trp Leu Glu	
20 25 30	
gca aac cct gct gaa gcc aag gtc atc atc aac aag gct gtc ggt tcc	144
Ala Asn Pro Ala Glu Ala Lys Val Ile Ile Asn Lys Ala Val Gly Ser	
35 40 45	
gcg cag gca cgc ctt gct gct cga aaa gcc cgt gac ctg gtc cga cgg	192
Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Asp Leu Val Arg Arg	
50 55 60	
aag tca gca acc gat ctg ggt gga ctg ccc ggt aag ctt gcc gac tgc	240
Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys	
65 70 75 80	
cgt tcc aag gat cca gaa aag tcc gaa ctt tac atc gtg gag ggc gac	288
Arg Ser Lys Asp Pro Glu Lys Ser Glu Leu Tyr Ile Val Glu Gly Asp	
85 90 95	
tcc gca ggt ggt tct gcg aag tcc ggc cgt gac tcc atg ttc cag gca	336
Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala	
100 105 110	
atc ctt cca ctg cga ggc aag atc ctc aac gtg gaa aag gcc cgc cta	384
Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Arg Leu	
115 120 125	
gac aag gtt ctg aag aac gcc gaa gtc caa gcg atc atc acc gca ctg	432
Asp Lys Val Leu Lys Asn Ala Glu Val Gln Ala Ile Ile Thr Ala Leu	
130 135 140	
ggt acc ggc atc cac gac gag ttc gac atc aac aag ctg cgc tac cac	480
Gly Thr Gly Ile His Asp Glu Phe Asp Ile Asn Lys Leu Arg Tyr His	
145 150 155 160	
aag atc gtg ctg atg gcc gac gcc gat gtt gac ggc cag cac atc gca	528
Lys Ile Val Leu Met Ala Asp Ala Asp Val Asp Gly Gln His Ile Ala	
165 170 175	
acg ctg ctg ctc acc ctg ctt ttc cgc ttc atg cca	564
Thr Leu Leu Leu Thr Leu Leu Phe Arg Phe Met Pro	
180 185	

<210> 118

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 118

Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Ile Lys	
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acgtctgtat cggataagta gcgaggagtg ttcgttaaaa gtg gca aac act gaa 115
                               Val Ala Asn Thr Glu
                               1                               5

cac aat tat gac gct tca tcg atc acc atc ctt gaa ggt ctt gag gcg 163
His Asn Tyr Asp Ala Ser Ser Ile Thr Ile Leu Glu Gly Leu Glu Ala
                               10                               15                               20

gta cgt aag cgc ccg ggc atg tac atc ggt tca act gga ccg cgt gga 211
Val Arg Lys Arg Pro Gly Met Tyr Ile Gly Ser Thr Gly Pro Arg Gly
                               25                               30                               35

ctg cac cac ctg att tgg gaa gtc gtt gac aac tca gtg gat gag gcc 259

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Leu	His	His	Leu	Ile	Trp	Glu	Val	Val	Asp	Asn	Ser	Val	Asp	Glu	Ala		
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atg	gct	ggc	cac	gcc	acc	aag	gtt	gaa	gtg	acc	ctt	ctg	gaa	gat	ggc	307	
Met	Ala	Gly	His	Ala	Thr	Lys	Val	Glu	Val	Thr	Leu	Leu	Glu	Asp	Gly		
	55					60					65						
ggc	gtt	caa	gtt	gtc	gat	gac	ggc	cga	gga	att	ccc	gtc	gat	atg	cac	355	
Gly	Val	Gln	Val	Val	Asp	Asp	Gly	Arg	Gly	Ile	Pro	Val	Asp	Met	His		
70					75					80					85		
cca	tcc	ggc	gca	cca	acc	gtg	cag	gtt	gtt	atg	acc	cag	ctg	cac	gcc	403	
Pro	Ser	Gly	Ala	Pro	Thr	Val	Gln	Val	Val	Met	Thr	Gln	Leu	His	Ala		
				90					95					100			
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Gly	Gly	Lys	Phe	Asp	Ser	Asp	Ser	Tyr	Ala	Val	Ser	Gly	Gly	Leu	His		
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ggc	gtt	ggc	att	tct	gtg	gtg	aac	gcc	ctg	tcc	acc	cgc	gtg	gaa	gcc	499	
Gly	Val	Gly	Ile	Ser	Val	Val	Asn	Ala	Leu	Ser	Thr	Arg	Val	Glu	Ala		
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gac	atc	aag	ttg	cac	ggc	aag	cac	tgg	tac	caa	aac	ttt	gaa	aag	tct	547	
Asp	Ile	Lys	Leu	His	Gly	Lys	His	Trp	Tyr	Gln	Asn	Phe	Glu	Lys	Ser		
	135					140					145						
gtt	cca	gac	gag	ttg	atc	gaa	ggc	ggc	aac	gct	cgc	ggc	acc	ggc	acc	595	
Val	Pro	Asp	Glu	Leu	Ile	Glu	Gly	Gly	Asn	Ala	Arg	Gly	Thr	Gly	Thr		
150					155				160						165		
acc	att	cgt	ttt	tgg	cca	gac	gct	gaa	att	ttc	gaa	acc	acc	gag	ttt	643	
Thr	Ile	Arg	Phe	Trp	Pro	Asp	Ala	Glu	Ile	Phe	Glu	Thr	Thr	Glu	Phe		
				170					175					180			
gat	ttc	gaa	acg	att	tct	cga	cgt	ctg	cag	gaa	atg	gca	ttc	ctt	aac	691	
Asp	Phe	Glu	Thr	Ile	Ser	Arg	Arg	Leu	Gln	Glu	Met	Ala	Phe	Leu	Asn		
			185					190					195				
aag	ggc	ctg	acc	atc	acc	ttg	acg	gac	aac	cgc	gcc	acc	gac	gag	gaa	739	
Lys	Gly	Leu	Thr	Ile	Thr	Leu	Thr	Asp	Asn	Arg	Ala	Thr	Asp	Glu	Glu		
	200						205					210					
ctc	gag	ctc	gaa	gca	ctc	gct	gag	cag	ggc	gaa	acc	gca	acg	gaa	cta	787	
Leu	Glu	Leu	Glu	Ala	Leu	Ala	Glu	Gln	Gly	Glu	Thr	Ala	Thr	Glu	Leu		
	215					220					225						
tcc	ctc	gat	gag	atc	gac	aac	gaa	acc	gaa	ctc	gtt	gaa	gag	acc	acc	835	
Ser	Leu	Asp	Glu	Ile	Asp	Asn	Glu	Thr	Glu	Leu	Val	Glu	Glu	Thr	Thr		
230					235					240				245			
gat	gct	cca	aag	aag	cca	aaa	aag	cgt	gag	aag	aag	aaa	atc	ttc	cac	883	
Asp	Ala	Pro	Lys	Lys	Pro	Lys	Lys	Arg	Glu	Lys	Lys	Lys	Ile	Phe	His		
				250				255						260			
tac	ccc	aat	ggc	ctc	gag	gac	tac	gtt	cac	tac	ctc	aac	cgc	agc	aag	931	
Tyr	Pro	Asn	Gly	Leu	Glu	Asp	Tyr	Val	His	Tyr	Leu	Asn	Arg	Ser	Lys		
			265					270					275				
acc	aac	atc	cac	cct	tca	atc	gtg	tca	ttc	gag	gca	aag	gga	gat	gac	979	
Thr	Asn	Ile	His	Pro	Ser	Ile	Val	Ser	Phe	Glu	Ala	Lys	Gly	Asp	Asp		

280	285	290	
cac gag gtt gag gtg gca atg cag tgg aac tcc tcc tac aag gaa tcc			1027
His Glu Val Glu Val Ala Met Gln Trp Asn Ser Ser Tyr Lys Glu Ser			
295	300	305	
gtc cac acc ttc gcc aac acc att aac acc cgc gaa ggc ggc acc cac			1075
Val His Thr Phe Ala Asn Thr Ile Asn Thr Arg Glu Gly Gly Thr His			
310	315	320	325
gag gaa ggt ttc cgc tct gcg ctg acc tcc ctg atg aac cgc tac gca			1123
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Leu Met Asn Arg Tyr Ala			
	330	335	340
cgt gag cac aag ctt ctg aaa gaa aag gaa gca aac ctt acc ggt gac			1171
Arg Glu His Lys Leu Leu Lys Glu Lys Glu Ala Asn Leu Thr Gly Asp			
	345	350	355
gac tgt cgt gaa ggc ctg tcc gcg gtt att ttc cgt gcg cgt tgg			1216
Asp Cys Arg Glu Gly Leu Ser Ala Val Ile Phe Arg Ala Arg Trp			
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tgacccacag ttcgaaggcc aga			1239

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<211> 372

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

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		20						25					30		

Thr	Gly	Pro	Arg	Gly	Leu	His	His	Leu	Ile	Trp	Glu	Val	Val	Asp	Asn
		35					40					45			

Ser	Val	Asp	Glu	Ala	Met	Ala	Gly	His	Ala	Thr	Lys	Val	Glu	Val	Thr
	50					55					60				

Leu	Leu	Glu	Asp	Gly	Gly	Val	Gln	Val	Val	Asp	Asp	Gly	Arg	Gly	Ile
65					70					75					80

Pro	Val	Asp	Met	His	Pro	Ser	Gly	Ala	Pro	Thr	Val	Gln	Val	Val	Met
				85					90					95	

Thr	Gln	Leu	His	Ala	Gly	Gly	Lys	Phe	Asp	Ser	Asp	Ser	Tyr	Ala	Val
		100						105					110		

Ser	Gly	Gly	Leu	His	Gly	Val	Gly	Ile	Ser	Val	Val	Asn	Ala	Leu	Ser
	115						120					125			

Thr	Arg	Val	Glu	Ala	Asp	Ile	Lys	Leu	His	Gly	Lys	His	Trp	Tyr	Gln
	130					135					140				

Asn	Phe	Glu	Lys	Ser	Val	Pro	Asp	Glu	Leu	Ile	Glu	Gly	Gly	Asn	Ala
145					150					155					160

Arg Gly Thr Gly Thr Thr Ile Arg Phe Trp Pro Asp Ala Glu Ile Phe
 165 170 175
 Glu Thr Thr Glu Phe Asp Phe Glu Thr Ile Ser Arg Arg Leu Gln Glu
 180 185 190
 Met Ala Phe Leu Asn Lys Gly Leu Thr Ile Thr Leu Thr Asp Asn Arg
 195 200 205
 Ala Thr Asp Glu Glu Leu Glu Leu Glu Ala Leu Ala Glu Gln Gly Glu
 210 215 220
 Thr Ala Thr Glu Leu Ser Leu Asp Glu Ile Asp Asn Glu Thr Glu Leu
 225 230 235 240
 Val Glu Glu Thr Thr Asp Ala Pro Lys Lys Pro Lys Lys Arg Glu Lys
 245 250 255
 Lys Lys Ile Phe His Tyr Pro Asn Gly Leu Glu Asp Tyr Val His Tyr
 260 265 270
 Leu Asn Arg Ser Lys Thr Asn Ile His Pro Ser Ile Val Ser Phe Glu
 275 280 285
 Ala Lys Gly Asp Asp His Glu Val Glu Val Ala Met Gln Trp Asn Ser
 290 295 300
 Ser Tyr Lys Glu Ser Val His Thr Phe Ala Asn Thr Ile Asn Thr Arg
 305 310 315 320
 Glu Gly Gly Thr His Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Leu
 325 330 335
 Met Asn Arg Tyr Ala Arg Glu His Lys Leu Leu Lys Glu Lys Glu Ala
 340 345 350
 Asn Leu Thr Gly Asp Asp Cys Arg Glu Gly Leu Ser Ala Val Ile Phe
 355 360 365
 Arg Ala Arg Trp
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<210> 121

<211> 726

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(726)

<223> FRXA01689

<400> 121

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 1 5 10 15

att tct gtg gtg aac gcc ctg tcc acc cgc gtg gaa gcc gac atc aag 96
 Ile Ser Val Val Asn Ala Leu Ser Thr Arg Val Glu Ala Asp Ile Lys
 20 25 30

ttg cac ggc aag cac tgg tac caa aac ttt gaa aag tct gtt cca gac	144
Leu His Gly Lys His Trp Tyr Gln Asn Phe Glu Lys Ser Val Pro Asp	
35 40 45	
gag ttg atc gaa ggc ggc aac gct cgc ggc acc ggt acc acc att cgt	192
Glu Leu Ile Glu Gly Gly Asn Ala Arg Gly Thr Gly Thr Thr Ile Arg	
50 55 60	
ttt tgg cca gac gct gaa att ttc gaa acc acc gag ttt gat ttc gaa	240
Phe Trp Pro Asp Ala Glu Ile Phe Glu Thr Thr Glu Phe Asp Phe Glu	
65 70 75 80	
acg att tct cga cgt ctg cag gaa atg gca ttc ctt aac aag ggt ctg	288
Thr Ile Ser Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu	
85 90 95	
acc atc acc ttg acg gac aac cgc gcc acc gac gag gaa ctc gag ctc	336
Thr Ile Thr Leu Thr Asp Asn Arg Ala Thr Asp Glu Glu Leu Glu Leu	
100 105 110	
gaa gca ctc gct gag cag ggc gaa acc gca acg gaa cta tcc ctc gat	384
Glu Ala Leu Ala Glu Gln Gly Glu Thr Ala Thr Glu Leu Ser Leu Asp	
115 120 125	
gag atc gac aac gaa acc gaa ctc gtt gaa gag acc acc gat gct cca	432
Glu Ile Asp Asn Glu Thr Glu Leu Val Glu Glu Thr Thr Asp Ala Pro	
130 135 140	
aag aag cca aaa aag cgt gag aag aag aaa atc ttc cac tac ccc aat	480
Lys Lys Pro Lys Lys Arg Glu Lys Lys Lys Ile Phe His Tyr Pro Asn	
145 150 155 160	
ggc ctc gag gac tac gtt cac tac ctc aac cgc agc aag acc aac atc	528
Gly Leu Glu Asp Tyr Val His Tyr Leu Asn Arg Ser Lys Thr Asn Ile	
165 170 175	
cac cct tca atc gtg tca ttc gag gca aag gga gat gac cac gag gtt	576
His Pro Ser Ile Val Ser Phe Glu Ala Lys Gly Asp Asp His Glu Val	
180 185 190	
gag gtg gca atg cag tgg aac tcc tcc tac aag gaa tcc gtc cac acc	624
Glu Val Ala Met Gln Trp Asn Ser Ser Tyr Lys Glu Ser Val His Thr	
195 200 205	
ttc gcc aac acc att aac acc cgc gaa ggc ggc acc cac gag gaa ggt	672
Phe Ala Asn Thr Ile Asn Thr Arg Glu Gly Gly Thr His Glu Glu Gly	
210 215 220	
ttc cgc tct gcg ctg acc tcc ctg atg aac cgc tac gca cgt gag cac	720
Phe Arg Ser Ala Leu Thr Ser Leu Met Asn Arg Tyr Ala Arg Glu His	
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Lys Leu	

<210> 122

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

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Ile Ser Val Val Asn Ala Leu Ser Thr Arg Val Glu Ala Asp Ile Lys
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Leu His Gly Lys His Trp Tyr Gln Asn Phe Glu Lys Ser Val Pro Asp
35 40 45

Glu Leu Ile Glu Gly Gly Asn Ala Arg Gly Thr Gly Thr Thr Ile Arg
50 55 60

Phe Trp Pro Asp Ala Glu Ile Phe Glu Thr Thr Glu Phe Asp Phe Glu
65 70 75 80

Thr Ile Ser Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95

Thr Ile Thr Leu Thr Asp Asn Arg Ala Thr Asp Glu Glu Leu Glu Leu
100 105 110

Glu Ala Leu Ala Glu Gln Gly Glu Thr Ala Thr Glu Leu Ser Leu Asp
115 120 125

Glu Ile Asp Asn Glu Thr Glu Leu Val Glu Glu Thr Thr Asp Ala Pro
130 135 140

Lys Lys Pro Lys Lys Arg Glu Lys Lys Lys Ile Phe His Tyr Pro Asn
145 150 155 160

Gly Leu Glu Asp Tyr Val His Tyr Leu Asn Arg Ser Lys Thr Asn Ile
165 170 175

His Pro Ser Ile Val Ser Phe Glu Ala Lys Gly Asp Asp His Glu Val
180 185 190

Glu Val Ala Met Gln Trp Asn Ser Ser Tyr Lys Glu Ser Val His Thr
195 200 205

Phe Ala Asn Thr Ile Asn Thr Arg Glu Gly Gly Thr His Glu Glu Gly
210 215 220

Phe Arg Ser Ala Leu Thr Ser Leu Met Asn Arg Tyr Ala Arg Glu His
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Lys Leu

<210> 123

<211> 382

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(382)

<223> FRXA01735

<400> 123

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                               Val Ala Asn Thr Glu
                               1                               5

cac aat tat gac gct tca tcg atc acc atc ctt gaa ggt ctt gag gcg 163
His Asn Tyr Asp Ala Ser Ser Ile Thr Ile Leu Glu Gly Leu Glu Ala
                               10                               15                               20

gta cgt aag cgc ccg ggc atg tac atc ggt tca act gga ccg cgt gga 211
Val Arg Lys Arg Pro Gly Met Tyr Ile Gly Ser Thr Gly Pro Arg Gly
                               25                               30                               35

ctg cac cac ctg att tgg gaa gtc gtt gac aac tca gtg gat gag gcc 259
Leu His His Leu Ile Trp Glu Val Val Asp Asn Ser Val Asp Glu Ala
                               40                               45                               50

atg gct ggc cac gcc acc aag gtt gaa gtg acc ctt ctg gaa gat ggt 307
Met Ala Gly His Ala Thr Lys Val Glu Val Thr Leu Leu Glu Asp Gly
                               55                               60                               65

ggc gtt caa gtt gtc gat gac ggt cga gga att ccc gtc gat atg cac 355
Gly Val Gln Val Val Asp Asp Gly Arg Gly Ile Pro Val Asp Met His
70                               75                               80                               85

cca tcc ggt gca cca acc gtg cag gtt 382
Pro Ser Gly Ala Pro Thr Val Gln Val
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<210> 124

<211> 94

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

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Thr Gly Pro Arg Gly Leu His His Leu Ile Trp Glu Val Val Asp Asn
35                               40                               45

Ser Val Asp Glu Ala Met Ala Gly His Ala Thr Lys Val Glu Val Thr
50                               55                               60

Leu Leu Glu Asp Gly Gly Val Gln Val Val Asp Asp Gly Arg Gly Ile
65                               70                               75                               80

Pro Val Asp Met His Pro Ser Gly Ala Pro Thr Val Gln Val
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<210> 125

<211> 1962

<212> DNA

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<221> CDS

<222> (101) .. (1939)

<223> RXN03093

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Val Ala Asp Thr Ala
1 5

ggc acc aca gga tgc aaa aag aag tac ttg gtg atc gtc gag tgc gcg 163
Gly Thr Thr Gly Ser Lys Lys Lys Tyr Leu Val Ile Val Glu Ser Ala
10 15 20

acc aag gct aaa aag att cag cct tac ctt ggc aac gac tac atc gtc 211
Thr Lys Ala Lys Lys Ile Gln Pro Tyr Leu Gly Asn Asp Tyr Ile Val
25 30 35

gag gcc tcc gtt ggt cat att cgt gat ctg cca cgt ggc gct gct gac 259
Glu Ala Ser Val Gly His Ile Arg Asp Leu Pro Arg Gly Ala Ala Asp
40 45 50

atc cct gca aag tac aag aag gag cct tgg gct cgt ctt ggt gtg gac 307
Ile Pro Ala Lys Tyr Lys Lys Glu Pro Trp Ala Arg Leu Gly Val Asp
55 60 65

acc gat cgc ggt ttc gcg ccg ctt tat gtg gtg agc ccc gat aaa aag 355
Thr Asp Arg Gly Phe Ala Pro Leu Tyr Val Val Ser Pro Asp Lys Lys
70 75 80 85

aag aag gtc gct gac ctc aag gcg aag ctc aag ctc gtt gat gag ttg 403
Lys Lys Val Ala Asp Leu Lys Ala Lys Leu Lys Leu Val Asp Glu Leu
90 95 100

ctg	ctg	gca	aca	gac	ccc	gac	cgt	gag	ggc	gag	gcg	att	gcg	tgg	cat	451
Leu	Leu	Ala	Thr	Asp	Pro	Asp	Arg	Glu	Gly	Glu	Ala	Ile	Ala	Trp	His	
			105					110					115			

ttg	ctt	gag	gtg	ttg	aag	ccg	act	gtt	cct	gtg	cgt	cgc	atg	gtg	ttc	499
Leu	Leu	Glu	Val	Leu	Lys	Pro	Thr	Val	Pro	Val	Arg	Arg	Met	Val	Phe	
		120					125					130				

aat gag atc acg aag cct gcc att ttg gct gcg gcg gaa aac act cgt 547
Asn Glu Ile Thr Lys Pro Ala Ile Leu Ala Ala Ala Glu Asn Thr Arg
135 140 145

gag ctg gat gag aac ctg gtg gat gcg cag gaa act cgt cgt att ctg 595
Glu Leu Asp Glu Asn Leu Val Asp Ala Gln Glu Thr Arg Arg Ile Leu
150 155 160 165

gac cgt ttg tac ggc tat gaa gtc tct cct gtg ctg tgg aaa aag gtc 643
Asp Arg Leu Tyr Gly Tyr Glu Val Ser Pro Val Leu Trp Lys Lys Val
170 175 180

atg ccg agg ttg tcg gcg ggc cgt gtg cag tcg gtg gca acc cgt gtg 691
Met Pro Arg Leu Ser Ala Gly Arg Val Gln Ser Val Ala Thr Arg Val
185 190 195

att gtt gag cgg gag cgc gag cgc atg gcg ttc gtg tcg gcg gat tat	739
Ile Val Glu Arg Glu Arg Glu Arg Met Ala Phe Val Ser Ala Asp Tyr	
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tgg gat ctg tcg gcg gag ttt aat gcg cgt gaa aac ggc aag gcg gat	787
Trp Asp Leu Ser Ala Glu Phe Asn Ala Arg Glu Asn Gly Lys Ala Asp	
215 220 225	
tcg gat aac ccg tcg tcg ttt act gcg cgt ttg tcc acg att gat gga	835
Ser Asp Asn Pro Ser Ser Phe Thr Ala Arg Leu Ser Thr Ile Asp Gly	
230 235 240 245	
aac cgt gtt gct caa ggc cgt gat ttt aat gat cgg gga gag ctg acc	883
Asn Arg Val Ala Gln Gly Arg Asp Phe Asn Asp Arg Gly Glu Leu Thr	
250 255 260	
tcg gag gct gtc gtc gtc gat aag cag cgt gct gag gcg tta gcc gag	931
Ser Glu Ala Val Val Val Asp Lys Gln Arg Ala Glu Ala Leu Ala Glu	
265 270 275	
gct ttg gaa ggc cag gaa atg gcc gtc gtt ggg gtc gag gaa aag ccg	979
Ala Leu Glu Gly Gln Glu Met Ala Val Val Gly Val Glu Glu Lys Pro	
280 285 290	
tac acc cgt cgc cct tat gcg ccg ttt atg acc tct acg ctg cag caa	1027
Tyr Thr Arg Arg Pro Tyr Ala Pro Phe Met Thr Ser Thr Leu Gln Gln	
295 300 305	
gag tct ggc cgc aag ctg cat tac act tct gag cgc acg atg cgt att	1075
Glu Ser Gly Arg Lys Leu His Tyr Thr Ser Glu Arg Thr Met Arg Ile	
310 315 320 325	
gcg cag cgc ttg tat gaa aac ggc cat atc act tat atg cgt act gac	1123
Ala Gln Arg Leu Tyr Glu Asn Gly His Ile Thr Tyr Met Arg Thr Asp	
330 335 340	
tcg acc tcg ttg tcg gag cag ggc atg aag gct gcg cgc gat cag gcg	1171
Ser Thr Ser Leu Ser Glu Gln Gly Met Lys Ala Ala Arg Asp Gln Ala	
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ttg gag ctg tac ggt gcg gaa tat gtt tcg ccg agc cca cgt acc tat	1219
Leu Glu Leu Tyr Gly Ala Glu Tyr Val Ser Pro Ser Pro Arg Thr Tyr	
360 365 370	
gac cgc aag gtg aag aac tcc cag gag gcc cac gag gcg att cgc cca	1267
Asp Arg Lys Val Lys Asn Ser Gln Glu Ala His Glu Ala Ile Arg Pro	
375 380 385	
gct ggt gaa act ttt gcg acc ccg ggc cag ctg cat ggc cag ttg gat	1315
Ala Gly Glu Thr Phe Ala Thr Pro Gly Gln Leu His Gly Gln Leu Asp	
390 395 400 405	
gcg gaa gaa ttt aag ctc tat gag ctg att tgg cag cgc act gtg gcc	1363
Ala Glu Glu Phe Lys Leu Tyr Glu Leu Ile Trp Gln Arg Thr Val Ala	
410 415 420	
tcc cag atg gcc gat gcc aag ggc acg tcc atg aag gtc acc atc ggt	1411
Ser Gln Met Ala Asp Ala Lys Gly Thr Ser Met Lys Val Thr Ile Gly	
425 430 435	

ggc acc gcg aag acc ggc gag aag act gag ttc aac gcg acc ggc cgc 1459
 Gly Thr Ala Lys Thr Gly Glu Lys Thr Glu Phe Asn Ala Thr Gly Arg
 440 445 450

acg ctg act ttc cct ggc ttc ctg cgc gct tac gtg gaa acc acc cgc 1507
 Thr Leu Thr Phe Pro Gly Phe Leu Arg Ala Tyr Val Glu Thr Thr Arg
 455 460 465

acc gcc gat ggc cgc gac gta gct gac aac gcc gaa aag cgt ctg cca 1555
 Thr Ala Asp Gly Arg Asp Val Ala Asp Asn Ala Glu Lys Arg Leu Pro
 470 475 480 485

ctg ctg tct gag ggc gat ctg ctc aag gtt ttg agc atc gaa gcc gat 1603
 Leu Leu Ser Glu Gly Asp Leu Leu Lys Val Leu Ser Ile Glu Ala Asp
 490 495 500

ggt cac agc acc aat cca cct gcg cgc tac aca gag gcg tcg ctg gtg 1651
 Gly His Ser Thr Asn Pro Pro Ala Arg Tyr Thr Glu Ala Ser Leu Val
 505 510 515

aag aag atg gaa gat ctg ggc atc ggc cgt cct tcc act tat gca tcg 1699
 Lys Lys Met Glu Asp Leu Gly Ile Gly Arg Pro Ser Thr Tyr Ala Ser
 520 525 530

atc att aag acg att cag gat cga ggc tac gtt tat tcg cgt ggc aat 1747
 Ile Ile Lys Thr Ile Gln Asp Arg Gly Tyr Val Tyr Ser Arg Gly Asn
 535 540 545

gcg ctg gtg ccg tcc tgg gtc gcg ttc gcc gtg gtc gga ttg ctt gaa 1795
 Ala Leu Val Pro Ser Trp Val Ala Phe Ala Val Val Gly Leu Leu Glu
 550 555 560 565

gcc aac ttc acc tcg ctg gtg gat tac gat ttc acc tcc tcc atg gaa 1843
 Ala Asn Phe Thr Ser Leu Val Asp Tyr Asp Phe Thr Ser Ser Met Glu
 570 575 580

gat gag ctg gac aac atc gcc gca ggt cgc gag ggc cgc acg gag tgg 1891
 Asp Glu Leu Asp Asn Ile Ala Ala Gly Arg Glu Gly Arg Thr Glu Trp
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ctc aac ggt ttc tac ttc ggg cga tgc cga agc gga tca gtc cat ggc 1939
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<210> 126

<211> 613

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

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 20 25 30

Asn Asp Tyr Ile Val Glu Ala Ser Val Gly His Ile Arg Asp Leu Pro
 35 40 45

Arg Gly Ala Ala Asp Ile Pro Ala Lys Tyr Lys Lys Glu Pro Trp Ala
 50 55 60
 Arg Leu Gly Val Asp Thr Asp Arg Gly Phe Ala Pro Leu Tyr Val Val
 65 70 75 80
 Ser Pro Asp Lys Lys Lys Lys Val Ala Asp Leu Lys Ala Lys Leu Lys
 85 90 95
 Leu Val Asp Glu Leu Leu Leu Ala Thr Asp Pro Asp Arg Glu Gly Glu
 100 105 110
 Ala Ile Ala Trp His Leu Leu Glu Val Leu Lys Pro Thr Val Pro Val
 115 120 125
 Arg Arg Met Val Phe Asn Glu Ile Thr Lys Pro Ala Ile Leu Ala Ala
 130 135 140
 Ala Glu Asn Thr Arg Glu Leu Asp Glu Asn Leu Val Asp Ala Gln Glu
 145 150 155 160
 Thr Arg Arg Ile Leu Asp Arg Leu Tyr Gly Tyr Glu Val Ser Pro Val
 165 170 175
 Leu Trp Lys Lys Val Met Pro Arg Leu Ser Ala Gly Arg Val Gln Ser
 180 185 190
 Val Ala Thr Arg Val Ile Val Glu Arg Glu Arg Glu Arg Met Ala Phe
 195 200 205
 Val Ser Ala Asp Tyr Trp Asp Leu Ser Ala Glu Phe Asn Ala Arg Glu
 210 215 220
 Asn Gly Lys Ala Asp Ser Asp Asn Pro Ser Ser Phe Thr Ala Arg Leu
 225 230 235 240
 Ser Thr Ile Asp Gly Asn Arg Val Ala Gln Gly Arg Asp Phe Asn Asp
 245 250 255
 Arg Gly Glu Leu Thr Ser Glu Ala Val Val Val Asp Lys Gln Arg Ala
 260 265 270
 Glu Ala Leu Ala Glu Ala Leu Glu Gly Gln Glu Met Ala Val Val Gly
 275 280 285
 Val Glu Glu Lys Pro Tyr Thr Arg Arg Pro Tyr Ala Pro Phe Met Thr
 290 295 300
 Ser Thr Leu Gln Gln Glu Ser Gly Arg Lys Leu His Tyr Thr Ser Glu
 305 310 315 320
 Arg Thr Met Arg Ile Ala Gln Arg Leu Tyr Glu Asn Gly His Ile Thr
 325 330 335
 Tyr Met Arg Thr Asp Ser Thr Ser Leu Ser Glu Gln Gly Met Lys Ala
 340 345 350
 Ala Arg Asp Gln Ala Leu Glu Leu Tyr Gly Ala Glu Tyr Val Ser Pro
 355 360 365

Ser Pro Arg Thr Tyr Asp Arg Lys Val Lys Asn Ser Gln Glu Ala His
 370 375 380
 Glu Ala Ile Arg Pro Ala Gly Glu Thr Phe Ala Thr Pro Gly Gln Leu
 385 390 395 400
 His Gly Gln Leu Asp Ala Glu Glu Phe Lys Leu Tyr Glu Leu Ile Trp
 405 410 415
 Gln Arg Thr Val Ala Ser Gln Met Ala Asp Ala Lys Gly Thr Ser Met
 420 425 430
 Lys Val Thr Ile Gly Gly Thr Ala Lys Thr Gly Glu Lys Thr Glu Phe
 435 440 445
 Asn Ala Thr Gly Arg Thr Leu Thr Phe Pro Gly Phe Leu Arg Ala Tyr
 450 455 460
 Val Glu Thr Thr Arg Thr Ala Asp Gly Arg Asp Val Ala Asp Asn Ala
 465 470 475 480
 Glu Lys Arg Leu Pro Leu Leu Ser Glu Gly Asp Leu Leu Lys Val Leu
 485 490 495
 Ser Ile Glu Ala Asp Gly His Ser Thr Asn Pro Pro Ala Arg Tyr Thr
 500 505 510
 Glu Ala Ser Leu Val Lys Lys Met Glu Asp Leu Gly Ile Gly Arg Pro
 515 520 525
 Ser Thr Tyr Ala Ser Ile Ile Lys Thr Ile Gln Asp Arg Gly Tyr Val
 530 535 540
 Tyr Ser Arg Gly Asn Ala Leu Val Pro Ser Trp Val Ala Phe Ala Val
 545 550 555 560
 Val Gly Leu Leu Glu Ala Asn Phe Thr Ser Leu Val Asp Tyr Asp Phe
 565 570 575
 Thr Ser Ser Met Glu Asp Glu Leu Asp Asn Ile Ala Ala Gly Arg Glu
 580 585 590
 Gly Arg Thr Glu Trp Leu Asn Gly Phe Tyr Phe Gly Arg Cys Arg Ser
 595 600 605
 Gly Ser Val His Gly
 610

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<211> 2378

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2355)

<223> FRXA00798

<400> 127

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1				5					10					15		
gcg	gat	tcg	gat	aac	ccg	tcg	tcg	ttt	act	gcg	cgt	ttg	tcc	acg	att	96
Ala	Asp	Ser	Asp	Asn	Pro	Ser	Ser	Phe	Thr	Ala	Arg	Leu	Ser	Thr	Ile	
			20					25					30			
gat	gga	aac	cgt	gtt	gct	caa	ggc	cgt	gat	ttt	aat	gat	cgg	gga	gag	144
Asp	Gly	Asn	Arg	Val	Ala	Gln	Gly	Arg	Asp	Phe	Asn	Asp	Arg	Gly	Glu	
		35					40					45				
ctg	acc	tcg	gag	gct	gtc	gtc	gtc	gat	aag	cag	cgt	gct	gag	gcg	tta	192
Leu	Thr	Ser	Glu	Ala	Val	Val	Val	Asp	Lys	Gln	Arg	Ala	Glu	Ala	Leu	
	50					55					60					
gcc	gag	gct	ttg	gaa	ggc	cag	gaa	atg	gcc	gtc	gtt	ggg	gtc	gag	gaa	240
Ala	Glu	Ala	Leu	Glu	Gly	Gln	Glu	Met	Ala	Val	Val	Gly	Val	Glu	Glu	
65					70					75					80	
aag	ccg	tac	acc	cgt	cgc	cct	tat	gcg	ccg	ttt	atg	acc	tct	acg	ctg	288
Lys	Pro	Tyr	Thr	Arg	Arg	Pro	Tyr	Ala	Pro	Phe	Met	Thr	Ser	Thr	Leu	
				85					90					95		
cag	caa	gag	tct	ggc	cgc	aag	ctg	cat	tac	act	tct	gag	cgc	acg	atg	336
Gln	Gln	Glu	Ser	Gly	Arg	Lys	Leu	His	Tyr	Thr	Ser	Glu	Arg	Thr	Met	
			100				105						110			
cgt	att	gcg	cag	cgc	ttg	tat	gaa	aac	ggc	cat	atc	act	tat	atg	cgt	384
Arg	Ile	Ala	Gln	Arg	Leu	Tyr	Glu	Asn	Gly	His	Ile	Thr	Tyr	Met	Arg	
	115						120					125				
act	gac	tcg	acc	tcg	ttg	tcg	gag	cag	ggc	atg	aag	gct	gcg	cgc	gat	432
Thr	Asp	Ser	Thr	Ser	Leu	Ser	Glu	Gln	Gly	Met	Lys	Ala	Ala	Arg	Asp	
	130					135					140					
cag	gcg	ttg	gag	ctg	tac	ggt	gcg	gaa	tat	gtt	tcg	ccg	agc	cca	cgt	480
Gln	Ala	Leu	Glu	Leu	Tyr	Gly	Ala	Glu	Tyr	Val	Ser	Pro	Ser	Pro	Arg	
145					150					155					160	
acc	tat	gac	cgc	aag	gtg	aag	aac	tcc	cag	gag	gcc	cac	gag	gcg	att	528
Thr	Tyr	Asp	Arg	Lys	Val	Lys	Asn	Ser	Gln	Glu	Ala	His	Glu	Ala	Ile	
				165					170					175		
cgc	cca	gct	ggt	gaa	act	ttt	gcg	acc	ccg	ggc	cag	ctg	cat	ggc	cag	576
Arg	Pro	Ala	Gly	Glu	Thr	Phe	Ala	Thr	Pro	Gly	Gln	Leu	His	Gly	Gln	
			180					185					190			
ttg	gat	gcg	gaa	gaa	ttt	aag	ctc	tat	gag	ctg	att	tgg	cag	cgc	act	624
Leu	Asp	Ala	Glu	Glu	Phe	Lys	Leu	Tyr	Glu	Leu	Ile	Trp	Gln	Arg	Thr	
		195					200					205				
gtg	gcc	tcc	cag	atg	gcc	gat	gcc	aag	ggc	acg	tcc	atg	aag	gtc	acc	672
Val	Ala	Ser	Gln	Met	Ala	Asp	Ala	Lys	Gly	Thr	Ser	Met	Lys	Val	Thr	
	210					215					220					
atc	ggt	ggc	acc	gcg	aag	acc	ggc	gag	aag	act	gag	ttc	aac	gcg	acc	720
Ile	Gly	Gly	Thr	Ala	Lys	Thr	Gly	Glu	Lys	Thr	Glu	Phe	Asn	Ala	Thr	
225					230					235				240		
ggc	cgc	acg	ctg	act	ttc	cct	ggc	ttc	ctg	cgc	gct	tac	gtg	gaa	acc	768
Gly	Arg	Thr	Leu	Thr	Phe	Pro	Gly	Phe	Leu	Arg	Ala	Tyr	Val	Glu	Thr	

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acc cgc acc gcc gat ggc cgc gac gta gct gac aac gcc gaa aag cgt Thr Arg Thr Ala Asp Gly Arg Asp Val Ala Asp Asn Ala Glu Lys Arg 260 265 270			816
ctg cca ctg ctg tct gag ggc gat ctg ctc aag gtt ttg agc atc gaa Leu Pro Leu Leu Ser Glu Gly Asp Leu Leu Lys Val Leu Ser Ile Glu 275 280 285			864
gcc gat ggt cac agc acc aat cca cct gcg cgc tac aca gag gcg tcg Ala Asp Gly His Ser Thr Asn Pro Pro Ala Arg Tyr Thr Glu Ala Ser 290 295 300			912
ctg gtg aag aag atg gaa gat ctg ggc atc ggc cgt cct tcc act tat Leu Val Lys Lys Met Glu Asp Leu Gly Ile Gly Arg Pro Ser Thr Tyr 305 310 315 320			960
gca tcg atc att aag acg att cag gat cga ggc tac gtt tat tcg cgt Ala Ser Ile Ile Lys Thr Ile Gln Asp Arg Gly Tyr Val Tyr Ser Arg 325 330 335			1008
ggc aat gcg ctg gtg ccg tcc tgg gtc gcg ttc gcc gtg gtc gga ttg Gly Asn Ala Leu Val Pro Ser Trp Val Ala Phe Ala Val Val Gly Leu 340 345 350			1056
ctt gaa gcc aac ttc acc tcg ctg gtg gat tac gat ttc acc tcc tcc Leu Glu Ala Asn Phe Thr Ser Leu Val Asp Tyr Asp Phe Thr Ser Ser 355 360 365			1104
atg gaa gat gag ctg gac aac atc gcc gca ggt cgc gag gcc cgc acg Met Glu Asp Glu Leu Asp Asn Ile Ala Ala Gly Arg Glu Gly Arg Thr 370 375 380			1152
gag tgg ctc aac ggt ttc tac ttc ggc gat gcc gaa gcg gat cag tcc Glu Trp Leu Asn Gly Phe Tyr Phe Gly Asp Ala Glu Ala Asp Gln Ser 385 390 395 400			1200
atg gct gaa tca gtt gcc cgc cag ggc ggt ttg aag gcg ctt gtc gac Met Ala Glu Ser Val Ala Arg Gln Gly Gly Leu Lys Ala Leu Val Asp 405 410 415			1248
gcg aac ctg gag cac atc gac gcg cgt tca gta aac tca ctc aag ctt Ala Asn Leu Glu His Ile Asp Ala Arg Ser Val Asn Ser Leu Lys Leu 420 425 430			1296
ttc gac gac gcc gaa ggc cgt gcc gtg aac gtt cga gtc gga cgc tac Phe Asp Asp Ala Glu Gly Arg Ala Val Asn Val Arg Val Gly Arg Tyr 435 440 445			1344
ggt ccg tac atc gag cgc atc gtg ggc acc acc gcg gaa ggc gag cca Gly Pro Tyr Ile Glu Arg Ile Val Gly Thr Thr Ala Glu Gly Glu Pro 450 455 460			1392
gaa ttt cag cgc gcc aac cta cct gag gaa acc acg cct gat gag ctg Glu Phe Gln Arg Ala Asn Leu Pro Glu Glu Thr Thr Pro Asp Glu Leu 465 470 475 480			1440
acc ctc gag gtc gct gag aag ctt ttc gct acc cca caa ggt gga cgt Thr Leu Glu Val Ala Glu Lys Leu Phe Ala Thr Pro Gln Gly Gly Arg 485 490 495			1488

gaa ctg ggc att aac cca gca aac ggt cgc atg gtg gtg gct aag gaa	1536
Glu Leu Gly Ile Asn Pro Ala Asn Gly Arg Met Val Val Ala Lys Glu	
500 505 510	
ggc cgc ttt ggt cca tac gtg atc gag cag gtc acg gac tca gag cgc	1584
Gly Arg Phe Gly Pro Tyr Val Ile Glu Gln Val Thr Asp Ser Glu Arg	
515 520 525	
gct ggc gcc gaa gcc caa gca gaa gaa gtc gtt gca gcg gaa cga aaa	1632
Ala Gly Ala Glu Ala Gln Ala Glu Glu Val Val Ala Ala Glu Arg Lys	
530 535 540	
gct gaa gac gaa caa cgt gcc acc gat gga atg cga ccc aag aac tgg	1680
Ala Glu Asp Glu Gln Arg Ala Thr Asp Gly Met Arg Pro Lys Asn Trp	
545 550 555 560	
gaa acc aag act gcc gca aac cag aag gaa aag cgc atc aac cag ctg	1728
Glu Thr Lys Thr Ala Ala Asn Gln Lys Glu Lys Arg Ile Asn Gln Leu	
565 570 575	
gtt gag gaa aac ctc aag cca gcg acc gca tcc ctg ttc agc ggc atg	1776
Val Glu Glu Asn Leu Lys Pro Ala Thr Ala Ser Leu Phe Ser Gly Met	
580 585 590	
gaa cct gca gcc gtg acc ctg gaa gaa gcc ctc aag ctg ctg tcc ctg	1824
Glu Pro Ala Ala Val Thr Leu Glu Glu Ala Leu Lys Leu Leu Ser Leu	
595 600 605	
cca cgc gaa gta ggt gtc gat cct tcc gac aac gaa gtg atc acc gct	1872
Pro Arg Glu Val Gly Val Asp Pro Ser Asp Asn Glu Val Ile Thr Ala	
610 615 620	
caa aac gga cga tac ggc cct tat ctg aag aag ggt agc gac tcc cgt	1920
Gln Asn Gly Arg Tyr Gly Pro Tyr Leu Lys Lys Gly Ser Asp Ser Arg	
625 630 635 640	
tcc ctc aac agc gaa gag cag atc ttc acc gtc act ttg gat gag gct	1968
Ser Leu Asn Ser Glu Glu Gln Ile Phe Thr Val Thr Leu Asp Glu Ala	
645 650 655	
cgc cgc atc tac gcc gaa cca aag cgt cgt gga cgc gcc gct gct cag	2016
Arg Arg Ile Tyr Ala Glu Pro Lys Arg Arg Gly Arg Ala Ala Gln	
660 665 670	
cca cca ctg aag caa ctt ggc gac aat gac gtt tcc ggc aaa cca atg	2064
Pro Pro Leu Lys Gln Leu Gly Asp Asn Asp Val Ser Gly Lys Pro Met	
675 680 685	
acc gtc aag gac gga cgt ttc ggc cca tac gtc acc gac ggc acc acc	2112
Thr Val Lys Asp Gly Arg Phe Gly Pro Tyr Val Thr Asp Gly Thr Thr	
690 695 700	
aac gcg tca ctg cgc aag ggc gat gtt cca gag tcc ctg acc gat gcg	2160
Asn Ala Ser Leu Arg Lys Gly Asp Val Pro Glu Ser Leu Thr Asp Ala	
705 710 715 720	
cgt gcc aac gag tta ctt tcc gag cgt cgt gcc aag gaa gca gca gat	2208
Arg Ala Asn Glu Leu Leu Ser Glu Arg Arg Ala Lys Glu Ala Ala Asp	
725 730 735	

ggc gga gct cct gcg aag aag acg tcc act aaa aag act gca gcc aag 2256
 Gly Gly Ala Pro Ala Lys Lys Thr Ser Thr Lys Lys Thr Ala Ala Lys
 740 745 750

aag acc acg gct aaa aag aca aca gct aag aaa acc gtg agg aag gct 2304
 Lys Thr Thr Ala Lys Lys Thr Thr Ala Lys Lys Thr Val Arg Lys Ala
 755 760 765

ccg ccg aaa acc acc aaa aac gtg gtg aag gcc ggc gct aag aag aag 2352
 Pro Pro Lys Thr Thr Lys Asn Val Val Lys Ala Gly Ala Lys Lys Lys
 770 775 780

tcc taaaacatgc tgaacgggtt cgt 2378
 Ser
 785

<210> 128

<211> 785

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

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 20 25 30

Asp Gly Asn Arg Val Ala Gln Gly Arg Asp Phe Asn Asp Arg Gly Glu
 35 40 45

Leu Thr Ser Glu Ala Val Val Val Asp Lys Gln Arg Ala Glu Ala Leu
 50 55 60

Ala Glu Ala Leu Glu Gly Gln Glu Met Ala Val Val Gly Val Glu Glu
 65 70 75 80

Lys Pro Tyr Thr Arg Arg Pro Tyr Ala Pro Phe Met Thr Ser Thr Leu
 85 90 95

Gln Gln Glu Ser Gly Arg Lys Leu His Tyr Thr Ser Glu Arg Thr Met
 100 105 110

Arg Ile Ala Gln Arg Leu Tyr Glu Asn Gly His Ile Thr Tyr Met Arg
 115 120 125

Thr Asp Ser Thr Ser Leu Ser Glu Gln Gly Met Lys Ala Ala Arg Asp
 130 135 140

Gln Ala Leu Glu Leu Tyr Gly Ala Glu Tyr Val Ser Pro Ser Pro Arg
 145 150 155 160

Thr Tyr Asp Arg Lys Val Lys Asn Ser Gln Glu Ala His Glu Ala Ile
 165 170 175

Arg Pro Ala Gly Glu Thr Phe Ala Thr Pro Gly Gln Leu His Gly Gln
 180 185 190

Leu Asp Ala Glu Glu Phe Lys Leu Tyr Glu Leu Ile Trp Gln Arg Thr
 195 200 205

Val Ala Ser Gln Met Ala Asp Ala Lys Gly Thr Ser Met Lys Val Thr
210 215 220

Ile Gly Gly Thr Ala Lys Thr Gly Glu Lys Thr Glu Phe Asn Ala Thr
225 230 235 240

Gly Arg Thr Leu Thr Phe Pro Gly Phe Leu Arg Ala Tyr Val Glu Thr
245 250 255

Thr Arg Thr Ala Asp Gly Arg Asp Val Ala Asp Asn Ala Glu Lys Arg
260 265 270

Leu Pro Leu Leu Ser Glu Gly Asp Leu Leu Lys Val Leu Ser Ile Glu
275 280 285

Ala Asp Gly His Ser Thr Asn Pro Pro Ala Arg Tyr Thr Glu Ala Ser
290 295 300

Leu Val Lys Lys Met Glu Asp Leu Gly Ile Gly Arg Pro Ser Thr Tyr
305 310 315 320

Ala Ser Ile Ile Lys Thr Ile Gln Asp Arg Gly Tyr Val Tyr Ser Arg
325 330 335

Gly Asn Ala Leu Val Pro Ser Trp Val Ala Phe Ala Val Val Gly Leu
340 345 350

Leu Glu Ala Asn Phe Thr Ser Leu Val Asp Tyr Asp Phe Thr Ser Ser
355 360 365

Met Glu Asp Glu Leu Asp Asn Ile Ala Ala Gly Arg Glu Gly Arg Thr
370 375 380

Glu Trp Leu Asn Gly Phe Tyr Phe Gly Asp Ala Glu Ala Asp Gln Ser
385 390 395 400

Met Ala Glu Ser Val Ala Arg Gln Gly Gly Leu Lys Ala Leu Val Asp
405 410 415

Ala Asn Leu Glu His Ile Asp Ala Arg Ser Val Asn Ser Leu Lys Leu
420 425 430

Phe Asp Asp Ala Glu Gly Arg Ala Val Asn Val Arg Val Gly Arg Tyr
435 440 445

Gly Pro Tyr Ile Glu Arg Ile Val Gly Thr Thr Ala Glu Gly Glu Pro
450 455 460

Glu Phe Gln Arg Ala Asn Leu Pro Glu Glu Thr Thr Pro Asp Glu Leu
465 470 475 480

Thr Leu Glu Val Ala Glu Lys Leu Phe Ala Thr Pro Gln Gly Gly Arg
485 490 495

Glu Leu Gly Ile Asn Pro Ala Asn Gly Arg Met Val Val Ala Lys Glu
500 505 510

Gly Arg Phe Gly Pro Tyr Val Ile Glu Gln Val Thr Asp Ser Glu Arg
515 520 525

Ala Gly Ala Glu Ala Gln Ala Glu Glu Val Val Ala Ala Glu Arg Lys
530 535 540

Ala Glu Asp Glu Gln Arg Ala Thr Asp Gly Met Arg Pro Lys Asn Trp
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Glu Thr Lys Thr Ala Ala Asn Gln Lys Glu Lys Arg Ile Asn Gln Leu
565 570 575

Val Glu Glu Asn Leu Lys Pro Ala Thr Ala Ser Leu Phe Ser Gly Met
580 585 590

Glu Pro Ala Ala Val Thr Leu Glu Glu Ala Leu Lys Leu Leu Ser Leu
595 600 605

Pro Arg Glu Val Gly Val Asp Pro Ser Asp Asn Glu Val Ile Thr Ala
610 615 620

Gln Asn Gly Arg Tyr Gly Pro Tyr Leu Lys Lys Gly Ser Asp Ser Arg
625 630 635 640

Ser Leu Asn Ser Glu Glu Gln Ile Phe Thr Val Thr Leu Asp Glu Ala
645 650 655

Arg Arg Ile Tyr Ala Glu Pro Lys Arg Arg Gly Arg Ala Ala Ala Gln
660 665 670

Pro Pro Leu Lys Gln Leu Gly Asp Asn Asp Val Ser Gly Lys Pro Met
675 680 685

Thr Val Lys Asp Gly Arg Phe Gly Pro Tyr Val Thr Asp Gly Thr Thr
690 695 700

Asn Ala Ser Leu Arg Lys Gly Asp Val Pro Glu Ser Leu Thr Asp Ala
705 710 715 720

Arg Ala Asn Glu Leu Leu Ser Glu Arg Arg Ala Lys Glu Ala Ala Asp
725 730 735

Gly Gly Ala Pro Ala Lys Lys Thr Ser Thr Lys Lys Thr Ala Ala Lys
740 745 750

Lys Thr Thr Ala Lys Lys Thr Thr Ala Lys Lys Thr Val Arg Lys Ala
755 760 765

Pro Pro Lys Thr Thr Lys Asn Val Val Lys Ala Gly Ala Lys Lys Lys
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Ser
785

<210> 129

<211> 488

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(465)

<223> RXN00990

<400> 129

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 Asp Asp Val Ser Leu Val Val His Val Asp Pro Pro Ala Glu His Lys
 20 25 30

gcg tat ttg cac cgc gct ggt cgt act gca cga gcc gga act tcc ggt 144
 Ala Tyr Leu His Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly
 35 40 45

aca gtt gtg act cta gta atg gac gaa caa atc aag gaa gtc cgt gaa 192
 Thr Val Val Thr Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu
 50 55 60

ctt ttc caa aaa gca ggc gtg aca gcc gct gag gta aaa gtc aac gaa 240
 Leu Phe Gln Lys Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu
 65 70 75 80

aac tca cct gaa ttg gct aaa att act ggt gca cga cgc ccg tca ggc 288
 Asn Ser Pro Glu Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly
 85 90 95

gtt gct ctt cca gca cct gga cag cag cag cca aag cgg gaa caa aaa 336
 Val Ala Leu Pro Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys
 100 105 110

aat acc cat aat cgt tct gat tcc aga ggt tcc agc cgg aat cca cgc 384
 Asn Thr His Asn Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg
 115 120 125

agg cgc gga caa agc gga tcc aga tca acg ggc cgc tcc aac ccg agg 432
 Arg Arg Gly Gln Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg
 130 135 140

cgt cag act tca agg aaa gac ggt ccc aag agc taaaactccc ccacggcacg 485
 Arg Gln Thr Ser Arg Lys Asp Gly Pro Lys Ser
 145 150 155

cga 488

<210> 130

<211> 155

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

Ile Pro Val Leu Val Ala Thr Asp Ile Ala Ala Arg Gly Ile Asp Val
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Asp Asp Val Ser Leu Val Val His Val Asp Pro Pro Ala Glu His Lys
 20 25 30

Ala Tyr Leu His Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly
 35 40 45

Thr Val Val Thr Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu

50 55 60
 Leu Phe Gln Lys Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu
 65 70 75 80
 Asn Ser Pro Glu Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly
 85 90 95
 Val Ala Leu Pro Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys
 100 105 110
 Asn Thr His Asn Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg
 115 120 125
 Arg Arg Gly Gln Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg
 130 135 140
 Arg Gln Thr Ser Arg Lys Asp Gly Pro Lys Ser
 145 150 155

<210> 131
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 <223> FRXA00990

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 Leu Val Val His Val Asp Pro Pro Ala Glu His Lys Ala Tyr Leu His
 20 25 30
 cgc gct ggt cgt act gca cga gcc gga act tcc ggt aca gtt gtg act 144
 Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly Thr Val Val Thr
 35 40 45
 cta gta atg gac gaa caa atc aag gaa gtc cgt gaa ctt ttc caa aaa 192
 Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu Leu Phe Gln Lys
 50 55 60
 gca ggc gtg aca gcc gct gag gta aaa gtc aac gaa aac tca cct gaa 240
 Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu Asn Ser Pro Glu
 65 70 75 80
 ttg gct aaa att act ggt gca cga cgc ccg tca ggc gtt gct ctt cca 288
 Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly Val Ala Leu Pro
 85 90 95
 gca cct gga cag cag cag cca aag cgg gaa caa aaa aat acc cat aat 336
 Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys Asn Thr His Asn
 100 105 110
 cgt tct gat tcc aga ggt tcc agc cgg aat cca cgc agg cgc gga caa 384

Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg Arg Arg Gly Gln
115 120 125

agc gga tcc aga tca acg ggc cgc tcc aac ccg agg cgt cag act tca 432
Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg Arg Gln Thr Ser
130 135 140

agg aaa gac ggt ccc aag agc taaaactccc ccacggcacg cga 476
Arg Lys Asp Gly Pro Lys Ser
145 150

<210> 132

<211> 151

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

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Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly Thr Val Val Thr
35 40 45

Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu Leu Phe Gln Lys
50 55 60

Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu Asn Ser Pro Glu
65 70 75 80

Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly Val Ala Leu Pro
85 90 95

Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys Asn Thr His Asn
100 105 110

Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg Arg Arg Gly Gln
115 120 125

Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg Arg Gln Thr Ser
130 135 140

Arg Lys Asp Gly Pro Lys Ser
145 150

<210> 133

<211> 451

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXN00994

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Leu Arg Ser Gln Gly Ile Thr Glu Ala Phe Pro Ile Gln Glu Ala Ala
      20             25             30

Ile Pro Asp Ala Leu Ala Gly Lys Asp Val Leu Gly Arg Gly Pro Thr
      35             40             45

Gly Ser Gly Lys Thr Phe Thr Phe Gly Leu Pro Met Ile Thr Arg Leu
  50             55             60

Ala Arg Ser Gly Ala Ser Lys Pro Gly Arg Pro Arg Gly Leu Val Leu
  65             70             75             80

Val Pro Thr Arg Glu Leu Ala Ala Gln Val Arg Glu Arg Leu Asp Asp
      85             90             95

Pro Ala Arg Val Met Gly Leu Arg Val Leu Glu Val Val Gly Gly Val
      100             105             110

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Asn Ile Asn Arg Asn
115

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<223> FRXA00994

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Met Thr Thr Phe Leu
1 5
gaa ctc aag ctt ccc gac gag att gtg cgc gaa ctt cgc agt cag gga 163
Glu Leu Lys Leu Pro Asp Glu Ile Val Arg Glu Leu Arg Ser Gln Gly
10 15 20
atc acc gag gca ttc ccc atc caa gaa gca gcc atc ccc gat gcg ctc 211
Ile Thr Glu Ala Phe Pro Ile Gln Glu Ala Ala Ile Pro Asp Ala Leu
25 30 35
gct ggc aaa gat gtc ctc ggc cgt gga ccc acc ggc tct ggt aaa acc 259
Ala Gly Lys Asp Val Leu Gly Arg Gly Pro Thr Gly Ser Gly Lys Thr
40 45 50
ttc acc ttt ggg ctt ccc atg atc acc cga ctc gcg cgc tcg ggc gcc 307
Phe Thr Phe Gly Leu Pro Met Ile Thr Arg Leu Ala Arg Ser Gly Ala
55 60 65
tcc aaa cca ggt cgc ccc cgc ggg ctt gtc ctg gtt ccc acc cgt gaa 355
Ser Lys Pro Gly Arg Pro Arg Gly Leu Val Leu Val Pro Thr Arg Glu
70 75 80 85
cta gca gct cag gtg cgt gaa cgc ctc gac gat ccc gcc cgc gtt atg 403
Leu Ala Ala Gln Val Arg Glu Arg Leu Asp Asp Pro Ala Arg Val Met
90 95 100
ggt ctg cgc gtc ctc gag gtg gtc ggt ggc gtc aac atc 442
Gly Leu Arg Val Leu Glu Val Val Gly Gly Val Asn Ile
105 110

<210> 136
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 136
Met Thr Thr Phe Leu Glu Leu Lys Leu Pro Asp Glu Ile Val Arg Glu
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Asn Ile

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											gtg	gaa	atc	acc	gac	115
											Val	Glu	Ile	Thr	Asp	
											1				5	
gca	ctc	gaa	gcc	ctc	ggc	atc	aac	cga	act	ttc	gcg	atc	cag	gag	tac	163
Ala	Leu	Glu	Ala	Leu	Gly	Ile	Asn	Arg	Thr	Phe	Ala	Ile	Gln	Glu	Tyr	
				10					15					20		
aca	ctt	ccc	atc	gcg	ctc	gac	ggc	cac	gac	ttc	atc	ggc	caa	gcc	cgc	211
Thr	Leu	Pro	Ile	Ala	Leu	Asp	Gly	His	Asp	Phe	Ile	Gly	Gln	Ala	Arg	
			25					30					35			
acc	ggc	atg	ggc	aaa	acc	tac	gga	ttc	ggt	gtc	cca	ctc	ctc	gat	aga	259
Thr	Gly	Met	Gly	Lys	Thr	Tyr	Gly	Phe	Gly	Val	Pro	Leu	Leu	Asp	Arg	
		40					45					50				
gtc	ttc	gac	tca	gcc	gac	gtc	gca	gaa	acc	gac	ggt	acc	ccc	cga	gcc	307
Val	Phe	Asp	Ser	Ala	Asp	Val	Ala	Glu	Thr	Asp	Gly	Thr	Pro	Arg	Ala	
	55					60					65					
ctc	gtc	atc	gtg	ccc	acc	cga	gaa	ctc	gca	gtc	caa	gtc	ggc	gac	gac	355
Leu	Val	Ile	Val	Pro	Thr	Arg	Glu	Leu	Ala	Val	Gln	Val	Gly	Asp	Asp	
	70				75					80					85	
ctc	caa	cgc	gca	gca	acc	aac	ctg	ccg	cta	aag	atc	ttc	acc	ttc	tac	403
Leu	Gln	Arg	Ala	Ala	Thr	Asn	Leu	Pro	Leu	Lys	Ile	Phe	Thr	Phe	Tyr	
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ggc ggc acc ccc tac gaa gaa cag atc gac gca ctc aaa gtc ggc gtc	451
Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala Leu Lys Val Gly Val	
105 110 115	
gac gtt gtc gta ggc aca ccc gga cga tta ctc gac ctg cac aaa cga	499
Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu Asp Leu His Lys Arg	
120 125 130	
ggc gcg cta tcg ctc gac aaa gta gcg atc tta gtc ctc gat gaa gcc	547
Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu Val Leu Asp Glu Ala	
135 140 145	
gac gaa atg ctc gat ctg ggc ttt ctg ccc gac atc gaa aaa atc ctc	595
Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp Ile Glu Lys Ile Leu	
150 155 160 165	
cgt gcc ctc acc cac cag cat caa acc atg ctg ttc tct gcc acg atg	643
Arg Ala Leu Thr His Gln His Gln Thr Met Leu Phe Ser Ala Thr Met	
170 175 180	
ccc ggc gcg atc ctc aca ctc gca cgc agc ttc ctg aac aaa cca gtg	691
Pro Gly Ala Ile Leu Thr Leu Ala Arg Ser Phe Leu Asn Lys Pro Val	
185 190 195	
cac atc cga gcc gag aca tcg gac gcc tca gca aca cac aaa acc acc	739
His Ile Arg Ala Glu Thr Ser Asp Ala Ser Ala Thr His Lys Thr Thr	
200 205 210	
aga caa gtg gtt ttt cag gca cac aaa atg gac aag gaa gcc atc acc	787
Arg Gln Val Val Phe Gln Ala His Lys Met Asp Lys Glu Ala Ile Thr	
215 220 225	
gcg aaa att ctg cag tcg aaa gat cgc ggc aaa acg atc atc ttc gcc	835
Ala Lys Ile Leu Gln Ser Lys Asp Arg Gly Lys Thr Ile Ile Phe Ala	
230 235 240 245	
cgc acg aaa cgc acc gca gcg caa gtt gcc gaa gac cta gcc tcc aga	883
Arg Thr Lys Arg Thr Ala Ala Gln Val Ala Glu Asp Leu Ala Ser Arg	
250 255 260	
gga ttc tcc gtc gga tca gtg cac ggc gac atg ggc caa cca gcc cgc	931
Gly Phe Ser Val Gly Ser Val His Gly Asp Met Gly Gln Pro Ala Arg	
265 270 275	
gag aaa tca ctc aac gca ttc cgc aca gga aaa att gac atc ctt gta	979
Glu Lys Ser Leu Asn Ala Phe Arg Thr Gly Lys Ile Asp Ile Leu Val	
280 285 290	
gcc aca gac gta gcc gcc cga ggc atc gat gtt gat gac gtc acc cac	1027
Ala Thr Asp Val Ala Ala Arg Gly Ile Asp Val Asp Asp Val Thr His	
295 300 305	
gtg atc aac tac caa acc ccc gac gat cct atg acc tac gtc cat cgt	1075
Val Ile Asn Tyr Gln Thr Pro Asp Asp Pro Met Thr Tyr Val His Arg	
310 315 320 325	
atc gga cgc acg gga cgc gca ggg cac aac gga aca gcc gtc act ctt	1123
Ile Gly Arg Thr Gly Arg Ala Gly His Asn Gly Thr Ala Val Thr Leu	
330 335 340	
gtc ggg tac gac gaa acc ctc aaa tgg act gtc atc gac aac gaa ctc	1171

Val Gly Tyr Asp Glu Thr Leu Lys Trp Thr Val Ile Asp Asn Glu Leu
 345 350 355

gaa ctc ggc caa cca aac cca cca caa tgg ttc tcc acc tca cca gag 1219
 Glu Leu Gly Gln Pro Asn Pro Pro Gln Trp Phe Ser Thr Ser Pro Glu
 360 365 370

ctg ctt gaa aca ctg gac atc cca gaa ggt gtc acc gaa cga gtc gga 1267
 Leu Leu Glu Thr Leu Asp Ile Pro Glu Gly Val Thr Glu Arg Val Gly
 375 380 385

cca cca acc aaa gtt cta ggc gga aca gcc cca cga cca cca cgc cgc 1315
 Pro Pro Thr Lys Val Leu Gly Gly Thr Ala Pro Arg Pro Pro Arg Arg
 390 395 400 405

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 <213> Corynebacterium glutamicum

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 20 25 30

Ile Gly Gln Ala Arg Thr Gly Met Gly Lys Thr Tyr Gly Phe Gly Val
 35 40 45

Pro Leu Leu Asp Arg Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp
 50 55 60

Gly Thr Pro Arg Ala Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val
 65 70 75 80

Gln Val Gly Asp Asp Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys
 85 90 95

Ile Phe Thr Phe Tyr Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala
 100 105 110

Leu Lys Val Gly Val Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu
 115 120 125

Asp Leu His Lys Arg Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu
 130 135 140

Val Leu Asp Glu Ala Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp
 145 150 155 160

Ile Glu Lys Ile Leu Arg Ala Leu Thr His Gln His Gln Thr Met Leu
 165 170 175

Phe Ser Ala Thr Met Pro Gly Ala Ile Leu Thr Leu Ala Arg Ser Phe
 180 185 190

Leu Asn Lys Pro Val His Ile Arg Ala Glu Thr Ser Asp Ala Ser Ala
195 200 205

Thr His Lys Thr Thr Arg Gln Val Val Phe Gln Ala His Lys Met Asp
210 215 220

Lys Glu Ala Ile Thr Ala Lys Ile Leu Gln Ser Lys Asp Arg Gly Lys
225 230 235 240

Thr Ile Ile Phe Ala Arg Thr Lys Arg Thr Ala Ala Gln Val Ala Glu
245 250 255

Asp Leu Ala Ser Arg Gly Phe Ser Val Gly Ser Val His Gly Asp Met
260 265 270

Gly Gln Pro Ala Arg Glu Lys Ser Leu Asn Ala Phe Arg Thr Gly Lys
275 280 285

Ile Asp Ile Leu Val Ala Thr Asp Val Ala Ala Arg Gly Ile Asp Val
290 295 300

Asp Asp Val Thr His Val Ile Asn Tyr Gln Thr Pro Asp Asp Pro Met
305 310 315 320

Thr Tyr Val His Arg Ile Gly Arg Thr Gly Arg Ala Gly His Asn Gly
325 330 335

Thr Ala Val Thr Leu Val Gly Tyr Asp Glu Thr Leu Lys Trp Thr Val
340 345 350

Ile Asp Asn Glu Leu Glu Leu Gly Gln Pro Asn Pro Pro Gln Trp Phe
355 360 365

Ser Thr Ser Pro Glu Leu Leu Glu Thr Leu Asp Ile Pro Glu Gly Val
370 375 380

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385 390 395 400

Arg Pro Pro Arg Arg Thr Arg Lys
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<223> FRXA02463

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176,199,203, or 215
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<223> Xaa = Ile or Met

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<223> Xaa = Tyr, His, Asn, or Asp

<220>

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<222> 33

<223> Xaa = Val, Ala, Asp, or Gly

<220>

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<222> 34

<223> Xaa = Ile or Met

<400> 139

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				Met	Thr	Tyr	Val	His	
				1				5	

tgt	atn	gga	cgc	acg	gga	cgc	gca	ggg	cac	aac	gga	aca	gcc	gtc	act	163
Cys	Xaa	Gly	Arg	Thr	Gly	Arg	Ala	Gly	His	Asn	Gly	Thr	Ala	Val	Thr	
				10				15						20		

ctt	gtc	ggg	ttc	nac	gaa	acc	ctn	aaa	tgg	act	gnc	atn	gac	aac	gaa	211
Leu	Val	Gly	Phe	Xaa	Glu	Thr	Leu	Lys	Trp	Thr	Xaa	Xaa	Asp	Asn	Glu	
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ctn	naactcgggc	aaccaaacc	acc	237
Leu				

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<223> Xaa = Ile or Met

<400> 140

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Xaa Xaa Asp Asn Glu Leu
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<210> 141

<211> 631

<212> DNA

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<223> FRXA02468

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tgaaagcccc agacctacgt tcacagagct cggcggttgcg gtg gaa atc acc gac 115
 Val Glu Ile Thr Asp
 1 5

gca ctc gaa gcc ctc ggc atc aac cga act ttc gcg atc cag gag tac 163
 Ala Leu Glu Ala Leu Gly Ile Asn Arg Thr Phe Ala Ile Gln Glu Tyr
 10 15 20

aca ctt ccc atc gcg ctc gac ggc cac gac ttc atc ggc caa gcc cgc 211
 Thr Leu Pro Ile Ala Leu Asp Gly His Asp Phe Ile Gly Gln Ala Arg
 25 30 35

acc ggc atg ggc aaa acc tac gga ttc ggt gtc cca ctc ctc gat aga 259
 Thr Gly Met Gly Lys Thr Tyr Gly Phe Gly Val Pro Leu Leu Asp Arg
 40 45 50

gtc ttc gac tca gcc gac gtc gca gaa acc gac ggt acc ccc cga gcc 307
 Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp Gly Thr Pro Arg Ala
 55 60 65

ctc gtc atc gtg ccc acc cga gaa ctc gca gtc caa gtc ggc gac gac 355
 Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val Gln Val Gly Asp Asp
 70 75 80 85

ctc caa cgc gca gca acc aac ctg ccg cta aag atc ttc acc ttc tac 403
 Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys Ile Phe Thr Phe Tyr
 90 95 100

ggc ggc acc ccc tac gaa gaa cag atc gac gca ctc aaa gtc ggc gtc 451
 Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala Leu Lys Val Gly Val
 105 110 115

gac gtt gtc gta ggc aca ccc gga cga tta ctc gac ctg cac aaa cga 499

Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu Asp Leu His Lys Arg
 120 125 130
 ggc gcg cta tcg ctc gac aaa gta gcg atc tta gtc ctc gat gaa gcc 547
 Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu Val Leu Asp Glu Ala
 135 140 145
 gac gaa atg ctc gat ctg ggc ttt ctg ccc gac atc gaa aaa atc ctc 595
 Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp Ile Glu Lys Ile Leu
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<210> 142

<211> 177

<212> PRT

<213> Corynebacterium glutamicum

<400> 142

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 20 25 30
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 35 40 45
 Pro Leu Leu Asp Arg Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp
 50 55 60
 Gly Thr Pro Arg Ala Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val
 65 70 75 80
 Gln Val Gly Asp Asp Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys
 85 90 95
 Ile Phe Thr Phe Tyr Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala
 100 105 110
 Leu Lys Val Gly Val Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu
 115 120 125
 Asp Leu His Lys Arg Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu
 130 135 140
 Val Leu Asp Glu Ala Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp
 145 150 155 160
 Ile Glu Lys Ile Leu Arg Ala Leu Thr His Gln His Gln Thr Met Leu
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Phe

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<211> 2319

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(2296)

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                                         Met Ser Asn Thr Glu
                                         1                               5

aac gtc aac ggc gac gta gaa cag ccg aat aac gtc att tcg tcg gaa 163
Asn Val Asn Gly Asp Val Glu Gln Pro Asn Asn Val Ile Ser Ser Glu
                               10                               15                               20

tct cag gaa acc ccg cag ggt gac tca gca tca gct gac ttc gct ctc 211
Ser Gln Glu Thr Pro Gln Gly Asp Ser Ala Ser Ala Asp Phe Ala Leu
                               25                               30                               35

gaa acc cca acc aac act gtt gaa gat gca cca gca tct gag ggt agc 259
Glu Thr Pro Thr Asn Thr Val Glu Asp Ala Pro Ala Ser Glu Gly Ser
                               40                               45                               50

gaa gag atc acc agg gtt gcg gat act tct gag gac gcc gac tct gca 307
Glu Glu Ile Thr Arg Val Ala Asp Thr Ser Glu Asp Ala Asp Ser Ala
                               55                               60                               65

gat gca gac aac gcg agc aat gta atc aat gag aat gag gac tcc tcg 355
Asp Ala Asp Asn Ala Ser Asn Val Ile Asn Glu Asn Glu Asp Ser Ser
                               70                               75                               80                               85

gaa ggt gct aac cag cct tca aac gag tca tcc tct acg gaa gcc aaa 403
Glu Gly Ala Asn Gln Pro Ser Asn Glu Ser Ser Ser Thr Glu Ala Lys
                               90                               95                               100

tcc ggc ttc gat gca ctc gga ctg cca gag cgt gtt ctt gac gct gtg 451
Ser Gly Phe Asp Ala Leu Gly Leu Pro Glu Arg Val Leu Asp Ala Val
                               105                               110                               115

cgc aag gtg ggt tac gaa act cct tcc cca att cag gca caa acc atc 499
Arg Lys Val Gly Tyr Glu Thr Pro Ser Pro Ile Gln Ala Gln Thr Ile
                               120                               125                               130

cca atc ctc atg gag ggc cag gat gtt gtt ggt cta gca cag acc ggt 547
Pro Ile Leu Met Glu Gly Gln Asp Val Val Gly Leu Ala Gln Thr Gly
                               135                               140                               145

acc ggt aag act gca gct ttc gcg ctg cca atc ctt gcc cgt att gac 595
Thr Gly Lys Thr Ala Ala Phe Ala Leu Pro Ile Leu Ala Arg Ile Asp
                               150                               155                               160                               165

aag tcc gtg cgc agc cca cag gca ctt gtg ctt gcc cct acc cgt gag 643
Lys Ser Val Arg Ser Pro Gln Ala Leu Val Leu Ala Pro Thr Arg Glu
                               170                               175                               180

ctg gca ctt cag gtt gct gac tcc ttc caa tcc ttc gct gac cac gtc 691
Leu Ala Leu Gln Val Ala Asp Ser Phe Gln Ser Phe Ala Asp His Val

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185	190	195	
ggt ggc ctg aac gtt ctg cca atc tat ggt gga cag gct tac ggc att Gly Gly Leu Asn Val Leu Pro Ile Tyr Gly Gly Gln Ala Tyr Gly Ile 200 205 210			739
cag ctc tct ggc ctg cgt cgt ggc gct cac atc gtc gtg ggt acc cca Gln Leu Ser Gly Leu Arg Arg Gly Ala His Ile Val Val Gly Thr Pro 215 220 225			787
ggc cga atc atc gat cac ctc gaa aag ggc tcc ctg gat atc tcc gga Gly Arg Ile Ile Asp His Leu Glu Lys Gly Ser Leu Asp Ile Ser Gly 230 235 240 245			835
ctg cgc ttc ctc gtg ctc gat gaa gca gac gag atg ctg aac atg ggc Leu Arg Phe Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Met Gly 250 255 260			883
ttc cag gaa gat gtc gag cgc atc ctc gag gac acc cca gac gag aag Phe Gln Glu Asp Val Glu Arg Ile Leu Glu Asp Thr Pro Asp Glu Lys 265 270 275			931
cag gtt gca cta ttc tcc gca acg atg cca aac ggc att cgt cgc ctg Gln Val Ala Leu Phe Ser Ala Thr Met Pro Asn Gly Ile Arg Arg Leu 280 285 290			979
tcc aag cag tac ctg aac aac cct gct gaa atc acc gtt aag tcc gag Ser Lys Gln Tyr Leu Asn Asn Pro Ala Glu Ile Thr Val Lys Ser Glu 295 300 305			1027
acc agg act aac acc aac atc acc cag cgc ttc ctc aac gtt gca cac Thr Arg Thr Asn Thr Asn Ile Thr Gln Arg Phe Leu Asn Val Ala His 310 315 320 325			1075
cgc aac aag atg gat gca ctg acc cgt att ctc gag gtc acc gag ttt Arg Asn Lys Met Asp Ala Leu Thr Arg Ile Leu Glu Val Thr Glu Phe 330 335 340			1123
gaa gca atg atc atg ttc gtg cgc acc aag cac gaa act gaa gaa gtt Glu Ala Met Ile Met Phe Val Arg Thr Lys His Glu Thr Glu Glu Val 345 350 355			1171
gct gaa aag ctc cgt gca cgc gga ttc tcc gca gca gcc atc aac ggc Ala Glu Lys Leu Arg Ala Arg Gly Phe Ser Ala Ala Ile Asn Gly 360 365 370			1219
gac att gct cag gca cag cgt gag cgc acc gtc gac cag ctg aag gac Asp Ile Ala Gln Ala Gln Arg Glu Arg Thr Val Asp Gln Leu Lys Asp 375 380 385			1267
ggc cgc ctg gac atc ctc gtt gca acc gac gtt gca gcc cgt ggt ctt Gly Arg Leu Asp Ile Leu Val Ala Thr Asp Val Ala Ala Arg Gly Leu 390 395 400 405			1315
gac gtt gag cgc atc tcc cac gtg ctt aac ttc gac att cca aac gac Asp Val Glu Arg Ile Ser His Val Leu Asn Phe Asp Ile Pro Asn Asp 410 415 420			1363
acc gag tcc tac gtt cac cgc atc ggc cgc acc ggc cgt gca gga cgt Thr Glu Ser Tyr Val His Arg Ile Gly Arg Thr Gly Arg Ala Gly Arg 425 430 435			1411

acc ggc gag gca atc ctg ttc gtg acc cca cgt gag cgt cgt atg ctt	1459
Thr Gly Glu Ala Ile Leu Phe Val Thr Pro Arg Glu Arg Arg Met Leu	
440 445 450	
cgc tcc atc gag cgc gca acc aac gca cca ctg cac gaa atg gaa ctg	1507
Arg Ser Ile Glu Arg Ala Thr Asn Ala Pro Leu His Glu Met Glu Leu	
455 460 465	
cca acc gtc gat cag gtc aac gac ttc cgc aag gtc aag ttc gdt gac	1555
Pro Thr Val Asp Gln Val Asn Asp Phe Arg Lys Val Lys Phe Ala Asp	
470 475 480 485	
tcc atc acc aag tcc ctc gag gac aag cag atg gac ctg ttc cgc acc	1603
Ser Ile Thr Lys Ser Leu Glu Asp Lys Gln Met Asp Leu Phe Arg Thr	
490 495 500	
ctg gtc aag gaa tac tcc cag gcc aac gac gtt cct cta gag gac atc	1651
Leu Val Lys Glu Tyr Ser Gln Ala Asn Asp Val Pro Leu Glu Asp Ile	
505 510 515	
gca gcg gca ctg gca acc cag gca cag tcc ggc gac ttc ctg ctc aag	1699
Ala Ala Ala Leu Ala Thr Gln Ala Gln Ser Gly Asp Phe Leu Leu Lys	
520 525 530	
gag ctc cca cca gag cgc cgt gag cgc aac gac cgc cgt cgt gac cgt	1747
Glu Leu Pro Pro Glu Arg Arg Glu Arg Asn Asp Arg Arg Arg Asp Arg	
535 540 545	
gac ttc gac gac cgt ggt gga cgt gga cgc gac cgt gac cgt ggc gac	1795
Asp Phe Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Arg Gly Asp	
550 555 560 565	
cgc gga gat cgt ggc tca cgc ttc gac cgc gac gac gag aac ctg gca	1843
Arg Gly Asp Arg Gly Ser Arg Phe Asp Arg Asp Asp Glu Asn Leu Ala	
570 575 580	
acc tac cgc ctc gca gtg ggc aag cgc cag cac atc cgc cca ggc gca	1891
Thr Tyr Arg Leu Ala Val Gly Lys Arg Gln His Ile Arg Pro Gly Ala	
585 590 595	
atc gtt ggt gca ctt gcc aac gaa ggt ggc ctg aac tcc aag gac ttc	1939
Ile Val Gly Ala Leu Ala Asn Glu Gly Gly Leu Asn Ser Lys Asp Phe	
600 605 610	
ggc cgc atc acc atc gca gcc gac cac acc ctg gtt gaa ctg cca aag	1987
Gly Arg Ile Thr Ile Ala Ala Asp His Thr Leu Val Glu Leu Pro Lys	
615 620 625	
gat ctc cca cag agc gtt ctt gac aac ctg cgc gac acc cgc atc tcc	2035
Asp Leu Pro Gln Ser Val Leu Asp Asn Leu Arg Asp Thr Arg Ile Ser	
630 635 640 645	
ggc cag ctc atc aac ata gaa cgc gac tcc ggt gga cgc cca cca cgc	2083
Gly Gln Leu Ile Asn Ile Glu Arg Asp Ser Gly Gly Arg Pro Pro Arg	
650 655 660	
cgc ttc gag cgc gat gac cgt ggc gga cgc ggc gga ttc cgc ggc gac	2131
Arg Phe Glu Arg Asp Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Asp	
665 670 675	

cgt gat gac cgc ggt gga cgt gga cgt gac cgt gac gat cgt gga agc 2179
 Arg Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Asp Arg Gly Ser
 680 685 690

cgt gga ggt ttc cgc ggt gga cgt gac cgt gat gat cgt ggc gga cgc 2227
 Arg Gly Gly Phe Arg Gly Gly Arg Asp Arg Asp Arg Arg Gly Gly Arg
 695 700 705

ggt gga ttc cgc gga cgc gac gac cgc gga gac cgt ggt ggc cgt ggc 2275
 Gly Gly Phe Arg Gly Arg Asp Asp Arg Gly Asp Arg Gly Gly Arg Gly
 710 715 720 725

ggt tac cgt ggc gga cgc gac taagagttcg ttttagcttc agc 2319
 Gly Tyr Arg Gly Gly Arg Asp
 730

<210> 144

<211> 732

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Met Ser Asn Thr Glu Asn Val Asn Gly Asp Val Glu Gln Pro Asn Asn
 1 5 10 15

Val Ile Ser Ser Glu Ser Gln Glu Thr Pro Gln Gly Asp Ser Ala Ser
 20 25 30

Ala Asp Phe Ala Leu Glu Thr Pro Thr Asn Thr Val Glu Asp Ala Pro
 35 40 45

Ala Ser Glu Gly Ser Glu Glu Ile Thr Arg Val Ala Asp Thr Ser Glu
 50 55 60

Asp Ala Asp Ser Ala Asp Ala Asp Asn Ala Ser Asn Val Ile Asn Glu
 65 70 75 80

Asn Glu Asp Ser Ser Glu Gly Ala Asn Gln Pro Ser Asn Glu Ser Ser
 85 90 95

Ser Thr Glu Ala Lys Ser Gly Phe Asp Ala Leu Gly Leu Pro Glu Arg
 100 105 110

Val Leu Asp Ala Val Arg Lys Val Gly Tyr Glu Thr Pro Ser Pro Ile
 115 120 125

Gln Ala Gln Thr Ile Pro Ile Leu Met Glu Gly Gln Asp Val Val Gly
 130 135 140

Leu Ala Gln Thr Gly Thr Gly Lys Thr Ala Ala Phe Ala Leu Pro Ile
 145 150 155 160

Leu Ala Arg Ile Asp Lys Ser Val Arg Ser Pro Gln Ala Leu Val Leu
 165 170 175

Ala Pro Thr Arg Glu Leu Ala Leu Gln Val Ala Asp Ser Phe Gln Ser
 180 185 190

Phe Ala Asp His Val Gly Gly Leu Asn Val Leu Pro Ile Tyr Gly Gly
 195 200 205

Gln Ala Tyr Gly Ile Gln Leu Ser Gly Leu Arg Arg Gly Ala His Ile
210 215 220

Val Val Gly Thr Pro Gly Arg Ile Ile Asp His Leu Glu Lys Gly Ser
225 230 235 240

Leu Asp Ile Ser Gly Leu Arg Phe Leu Val Leu Asp Glu Ala Asp Glu
245 250 255

Met Leu Asn Met Gly Phe Gln Glu Asp Val Glu Arg Ile Leu Glu Asp
260 265 270

Thr Pro Asp Glu Lys Gln Val Ala Leu Phe Ser Ala Thr Met Pro Asn
275 280 285

Gly Ile Arg Arg Leu Ser Lys Gln Tyr Leu Asn Asn Pro Ala Glu Ile
290 295 300

Thr Val Lys Ser Glu Thr Arg Thr Asn Thr Asn Ile Thr Gln Arg Phe
305 310 315 320

Leu Asn Val Ala His Arg Asn Lys Met Asp Ala Leu Thr Arg Ile Leu
325 330 335

Glu Val Thr Glu Phe Glu Ala Met Ile Met Phe Val Arg Thr Lys His
340 345 350

Glu Thr Glu Glu Val Ala Glu Lys Leu Arg Ala Arg Gly Phe Ser Ala
355 360 365

Ala Ala Ile Asn Gly Asp Ile Ala Gln Ala Gln Arg Glu Arg Thr Val
370 375 380

Asp Gln Leu Lys Asp Gly Arg Leu Asp Ile Leu Val Ala Thr Asp Val
385 390 395 400

Ala Ala Arg Gly Leu Asp Val Glu Arg Ile Ser His Val Leu Asn Phe
405 410 415

Asp Ile Pro Asn Asp Thr Glu Ser Tyr Val His Arg Ile Gly Arg Thr
420 425 430

Gly Arg Ala Gly Arg Thr Gly Glu Ala Ile Leu Phe Val Thr Pro Arg
435 440 445

Glu Arg Arg Met Leu Arg Ser Ile Glu Arg Ala Thr Asn Ala Pro Leu
450 455 460

His Glu Met Glu Leu Pro Thr Val Asp Gln Val Asn Asp Phe Arg Lys
465 470 475 480

Val Lys Phe Ala Asp Ser Ile Thr Lys Ser Leu Glu Asp Lys Gln Met
485 490 495

Asp Leu Phe Arg Thr Leu Val Lys Glu Tyr Ser Gln Ala Asn Asp Val
500 505 510

Pro Leu Glu Asp Ile Ala Ala Ala Leu Ala Thr Gln Ala Gln Ser Gly
515 520 525

Asp Phe Leu Leu Lys Glu Leu Pro Pro Glu Arg Arg Glu Arg Asn Asp
530 535 540

Arg Arg Arg Asp Arg Asp Phe Asp Asp Arg Gly Gly Arg Gly Arg Asp
545 550 555 560

Arg Asp Arg Gly Asp Arg Gly Asp Arg Gly Ser Arg Phe Asp Arg Asp
565 570 575

Asp Glu Asn Leu Ala Thr Tyr Arg Leu Ala Val Gly Lys Arg Gln His
580 585 590

Ile Arg Pro Gly Ala Ile Val Gly Ala Leu Ala Asn Glu Gly Gly Leu
595 600 605

Asn Ser Lys Asp Phe Gly Arg Ile Thr Ile Ala Ala Asp His Thr Leu
610 615 620

Val Glu Leu Pro Lys Asp Leu Pro Gln Ser Val Leu Asp Asn Leu Arg
625 630 635 640

Asp Thr Arg Ile Ser Gly Gln Leu Ile Asn Ile Glu Arg Asp Ser Gly
645 650 655

Gly Arg Pro Pro Arg Arg Phe Glu Arg Asp Asp Arg Gly Gly Arg Gly
660 665 670

Gly Phe Arg Gly Asp Arg Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg
675 680 685

Asp Asp Arg Gly Ser Arg Gly Gly Phe Arg Gly Gly Arg Asp Arg Asp
690 695 700

Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Arg Asp Asp Arg Gly Asp
705 710 715 720

Arg Gly Gly Arg Gly Gly Tyr Arg Gly Gly Arg Asp
725 730

<210> 145

<211> 450

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(427)

<223> RXA02682

<400> 145

tcccgatgct gctaggttcg tgtaaagcaa ccacaagttg caccaccatt cttccatcca 60

gagaatacga attcgtttac ctctagaaag gcactttccc atg tct tac cac gat 115
Met Ser Tyr His Asp
1 5

cac agc gac atc gaa tac ctc aag aag atc ggc gcc aac tcc cct gac 163
His Ser Asp Ile Glu Tyr Leu Lys Lys Ile Gly Ala Asn Ser Pro Asp
10 15 20

gcc ttc aaa gct ttt gtc cat ttt gat gag gca gct ctc cgc ggc ccg 211
Ala Phe Lys Ala Phe Val His Phe Asp Glu Ala Ala Leu Arg Gly Pro
25 30 35

aac aag aaa atc cca cgc aac tac acc gaa atg atc gca ctt gcg gtc 259
Asn Lys Lys Ile Pro Arg Asn Tyr Thr Glu Met Ile Ala Leu Ala Val
40 45 50

gca ttc aca acc caa tgc gcc tac tgc atc gac atc cac act gcc gct 307
Ala Phe Thr Thr Gln Cys Ala Tyr Cys Ile Asp Ile His Thr Ala Ala
55 60 65

gcg aag aag gaa ggt gtc acc acc gag gag ctc gct gag gtt gcg ctc 355
Ala Lys Lys Glu Gly Val Thr Thr Glu Glu Leu Ala Glu Val Ala Leu
70 75 80 85

atc gcc gca gca ctt cgg gca ggc ggc gcc atg acg cac ggc gca ctt 403
Ile Ala Ala Ala Leu Arg Ala Gly Gly Ala Met Thr His Gly Ala Leu
90 95 100

gcc atg aag ctt tac gac gaa aac tagaagcgat tctgcacatt ttt 450
Ala Met Lys Leu Tyr Asp Glu Asn
105

<210> 146

<211> 109

<212> PRT

<213> Corynebacterium glutamicum

<400> 146

Met Ser Tyr His Asp His Ser Asp Ile Glu Tyr Leu Lys Lys Ile Gly
1 5 10 15

Ala Asn Ser Pro Asp Ala Phe Lys Ala Phe Val His Phe Asp Glu Ala
20 25 30

Ala Leu Arg Gly Pro Asn Lys Lys Ile Pro Arg Asn Tyr Thr Glu Met
35 40 45

Ile Ala Leu Ala Val Ala Phe Thr Thr Gln Cys Ala Tyr Cys Ile Asp
50 55 60

Ile His Thr Ala Ala Ala Lys Lys Glu Gly Val Thr Thr Glu Glu Leu
65 70 75 80

Ala Glu Val Ala Leu Ile Ala Ala Ala Leu Arg Ala Gly Gly Ala Met
85 90 95

Thr His Gly Ala Leu Ala Met Lys Leu Tyr Asp Glu Asn
100 105

<210> 147

<211> 798

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXN00542

<400> 147

cgatcgtgtt ctgaacctga atgatggtgt cctgcgccacc aaggttctgc gactcgacaa 60

gtaaagaact ttaaggctct agagaggttag ttgaaggatt atg gca atc gga gat 115
Met Ala Ile Gly Asp
1 5

act aac atc acc gtc gtt ggc aac att gtt gct gac ccg gaa ctc cgc 163
Thr Asn Ile Thr Val Val Gly Asn Ile Val Ala Asp Pro Glu Leu Arg
10 15 20

ttc acc cca tcg ggt gca gca gtg gct aac ttc cgc att gca tca act 211
Phe Thr Pro Ser Gly Ala Ala Val Ala Asn Phe Arg Ile Ala Ser Thr
25 30 35

ccc cgc tcg ttc aac cgc caa acc aac cag tgg gaa gac ggc gaa gcc 259
Pro Arg Ser Phe Asn Arg Gln Thr Asn Gln Trp Glu Asp Gly Glu Ala
40 45 50

ctc ttt ctc acc gtt aac gtt tgg cgt cag gca gct gaa aac gtt gca 307
Leu Phe Leu Thr Val Asn Val Trp Arg Gln Ala Ala Glu Asn Val Ala
55 60 65

gag tcc ctg tcc aag ggt atg cgc gtt atc gtc acc ggt cgc ctc aag 355
Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val Thr Gly Arg Leu Lys
70 75 80 85

cag cgc tcc tat gaa acc cgt gag ggc gaa aag cgc agc gtt ttt gag 403
Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys Arg Ser Val Phe Glu
90 95 100

gtc gaa gcg gat gaa gtc gga cca tca cta aca ttt gcc aag gca gat 451
Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr Phe Ala Lys Ala Asp
105 110 115

gtc cag cgc aca ccg cgc ggt gga aac tct ggc gga aac tac ggt ggc 499
Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly Gly Asn Tyr Gly Gly
120 125 130

ggc aac caa ggt ggt ggc ctc ggt gga aac caa ggc aac cag caa ggt 547
Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln Gly Asn Gln Gln Gly
135 140 145

gga ttc agc aac cag aac tct ggc ggc ttc ggt gga aac caa ggc aac 595
Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly Gly Asn Gln Gly Asn
150 155 160 165

cag cag caa agc aac cag ggc gga ttt ggt gga aac caa aac cag tcc 643
Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly Asn Gln Asn Gln Ser
170 175 180

cag ggt aac aac ttc aac caa ggt gga ttt ggc gga ggc agc cca cag 691
Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly Gly Gly Ser Pro Gln
185 190 195

gca gca ccg gac aat gac cct tgg aat tct gca cca cca gct ggc tcc 739
Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala Pro Pro Ala Gly Ser
200 205 210

ggc ggg ttc ggc ggc gca gac gat gag cca ccg ttc taaagctttt 785
Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro Phe
215 220 225

cttttctaaa aca 798

<210> 148

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 148

Met Ala Ile Gly Asp Thr Asn Ile Thr Val Val Gly Asn Ile Val Ala
1 5 10 15

Asp Pro Glu Leu Arg Phe Thr Pro Ser Gly Ala Ala Val Ala Asn Phe
20 25 30

Arg Ile Ala Ser Thr Pro Arg Ser Phe Asn Arg Gln Thr Asn Gln Trp
35 40 45

Glu Asp Gly Glu Ala Leu Phe Leu Thr Val Asn Val Trp Arg Gln Ala
50 55 60

Ala Glu Asn Val Ala Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val
65 70 75 80

Thr Gly Arg Leu Lys Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys
85 90 95

Arg Ser Val Phe Glu Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr
100 105 110

Phe Ala Lys Ala Asp Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly
115 120 125

Gly Asn Tyr Gly Gly Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln
130 135 140

Gly Asn Gln Gln Gly Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly
145 150 155 160

Gly Asn Gln Gly Asn Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly
165 170 175

Asn Gln Asn Gln Ser Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly
180 185 190

Gly Gly Ser Pro Gln Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala
195 200 205

Pro Pro Ala Gly Ser Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro
210 215 220

Phe
225

<210> 149

<211> 542

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(519)

<223> FRXA00542

<400> 149

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Ala Leu Phe Leu Thr Val Asn Val Trp Arg Gln Ala Ala Glu Asn Val	
1 5 10 15	
gca gag tcc ctg tcc aag ggt atg cgc gtt atc gtc acc ggt cgc ctc	96
Ala Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val Thr Gly Arg Leu	
20 25 30	
aag cag cgc tcc tat gaa acc cgt gag ggc gaa aag cgc agc gtt ttt	144
Lys Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys Arg Ser Val Phe	
35 40 45	
gag gtc gaa gcg gat gaa gtc gga cca tca cta aca ttt gcc aag gca	192
Glu Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr Phe Ala Lys Ala	
50 55 60	
gat gtc cag cgc aca ccg cgc ggt gga aac tct ggc gga aac tac ggt	240
Asp Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly Gly Asn Tyr Gly	
65 70 75 80	
ggc ggc aac caa ggt ggt ggc ctc ggt gga aac caa ggc aac cag caa	288
Gly Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln Gly Asn Gln Gln	
85 90 95	
ggt gga ttc agc aac cag aac tct ggc ggc ttc ggt gga aac caa ggc	336
Gly Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly Gly Asn Gln Gly	
100 105 110	
aac cag cag caa agc aac cag ggc gga ttt ggt gga aac caa aac cag	384
Asn Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly Asn Gln Asn Gln	
115 120 125	
tcc cag ggt aac aac ttc aac caa ggt gga ttt ggc gga ggc agc cca	432
Ser Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly Gly Gly Ser Pro	
130 135 140	
cag gca gca ccg gac aat gac cct tgg aat tct gca cca cca gct ggc	480
Gln Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala Pro Pro Ala Gly	
145 150 155 160	
tcc ggc ggg ttc ggc ggc gca gac gat gag cca ccg ttc taaagctttt	529
Ser Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro Phe	
165 170	
cttttctaaa aca	542

<210> 150

<211> 173

<212> PRT

<213> Corynebacterium glutamicum

<400> 150

Ala Leu Phe Leu Thr Val Asn Val Trp Arg Gln Ala Ala Glu Asn Val
 1 5 10 15

Ala Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val Thr Gly Arg Leu
 20 25 30

Lys Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys Arg Ser Val Phe
 35 40 45

Glu Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr Phe Ala Lys Ala
 50 55 60

Asp Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly Gly Asn Tyr Gly
 65 70 75 80

Gly Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln Gly Asn Gln Gln
 85 90 95

Gly Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly Gly Asn Gln Gly
 100 105 110

Asn Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly Asn Gln Asn Gln
 115 120 125

Ser Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly Gly Gly Ser Pro
 130 135 140

Gln Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala Pro Pro Ala Gly
 145 150 155 160

Ser Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro Phe
 165 170

<210> 151

<211> 906

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(883)

<223> RXN02833

<400> 151

tagcttctcc gccacccttc atccacggct gaataaaatt atttttcgat agtttcgcca 60

aaaggagata cctaacatag tgagccagaa ctcatcttct ttg ctc gaa acc tgg 115
 Leu Leu Glu Thr Trp
 1 5

cgc caa gtt gtt gcc gat ctc aca act ttg agc cag caa gcg gac agt 163
 Arg Gln Val Val Ala Asp Leu Thr Thr Leu Ser Gln Gln Ala Asp Ser
 10 15 20

gga ttc gac cca ttg acg cca act caa cgt gca tat ttg aac ctg acg 211
 Gly Phe Asp Pro Leu Thr Pro Thr Gln Arg Ala Tyr Leu Asn Leu Thr
 25 30 35

aag ccg att gcc atc gtc gat ggc tac gcc gtg ctg tcc aca ccc aac 259

Lys Pro Ile Ala Ile Val Asp Gly Tyr Ala Val Leu Ser Thr Pro Asn
 40 45 50

 gcg atg gca aaa aat gtc att gaa aac gat ttg ggc gat gct ttg acc 307
 Ala Met Ala Lys Asn Val Ile Glu Asn Asp Leu Gly Asp Ala Leu Thr
 55 60 65

 cgt gtg ttg tgc ctg cgc atg ggc cga tca ttc agc ttg gct gtc agt 355
 Arg Val Leu Ser Leu Arg Met Gly Arg Ser Phe Ser Leu Ala Val Ser
 70 75 80 85

 gtg gag cct gag cag gaa att cca gaa acc cca gct cag cag gag ttt 403
 Val Glu Pro Glu Gln Glu Ile Pro Glu Thr Pro Ala Gln Gln Glu Phe
 90 95 100

 aaa tat cag cct gac gca cct gtg atc tct tcc aac aag gcg cca aag 451
 Lys Tyr Gln Pro Asp Ala Pro Val Ile Ser Ser Asn Lys Ala Pro Lys
 105 110 115

 cag tat gaa gtt ggt ggt cgg gga gag gcg tcg aca agc gac ggc tgg 499
 Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser Thr Ser Asp Gly Trp
 120 125 130

 gaa cgt acc cac tct gca ccg gct ccc gag ccg cac ccg gca cct atc 547
 Glu Arg Thr His Ser Ala Pro Ala Pro Glu Pro His Pro Ala Pro Ile
 135 140 145

 gcc gat cgt gag cca gag ctg gcc acc ccg cag cgc att ccg cgc gaa 595
 Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln Arg Ile Pro Arg Glu
 150 155 160 165

 acc cca gct cac aac cct aat cgg gaa gtg tcc ctc aac ccg aaa tac 643
 Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser Leu Asn Pro Lys Tyr
 170 175 180

 act ttt gaa agc ttc gtg atc ggg ccg ttc aac cgt ttc gcc aat gca 691
 Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn Arg Phe Ala Asn Ala
 185 190 195

 gcc gca gtt gct gtg gcg gaa agc cca gcg aaa gct ttc aac ccg ctg 739
 Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys Ala Phe Asn Pro Leu
 200 205 210

 ttt att tcc ggc ggt tcc ggc ttg ggc aaa act cac ctg ctg cac gca 787
 Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr His Leu Leu His Ala
 215 220 225

 gta gga aat tat gct caa gaa ttg cag cct ggc ccg cgg att aag tac 835
 Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly Pro Arg Ile Lys Tyr
 230 235 240 245

 gtc tca agt gag gaa tat cac caa cga cta cat caa ctc cgt gcg aga 883
 Val Ser Ser Glu Glu Tyr His Gln Arg Leu His Gln Leu Arg Ala Arg
 250 255 260

 tgaccgccag gaaaccttca agc 906

<210> 152

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

Leu Leu Glu Thr Trp Arg Gln Val Val Ala Asp Leu Thr Thr Leu Ser
1 5 10 15

Gln Gln Ala Asp Ser Gly Phe Asp Pro Leu Thr Pro Thr Gln Arg Ala
20 25 30

Tyr Leu Asn Leu Thr Lys Pro Ile Ala Ile Val Asp Gly Tyr Ala Val
35 40 45

Leu Ser Thr Pro Asn Ala Met Ala Lys Asn Val Ile Glu Asn Asp Leu
50 55 60

Gly Asp Ala Leu Thr Arg Val Leu Ser Leu Arg Met Gly Arg Ser Phe
65 70 75 80

Ser Leu Ala Val Ser Val Glu Pro Glu Gln Glu Ile Pro Glu Thr Pro
85 90 95

Ala Gln Gln Glu Phe Lys Tyr Gln Pro Asp Ala Pro Val Ile Ser Ser
100 105 110

Asn Lys Ala Pro Lys Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser
115 120 125

Thr Ser Asp Gly Trp Glu Arg Thr His Ser Ala Pro Ala Pro Glu Pro
130 135 140

His Pro Ala Pro Ile Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln
145 150 155 160

Arg Ile Pro Arg Glu Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser
165 170 175

Leu Asn Pro Lys Tyr Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn
180 185 190

Arg Phe Ala Asn Ala Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys
195 200 205

Ala Phe Asn Pro Leu Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr
210 215 220

His Leu Leu His Ala Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly
225 230 235 240

Pro Arg Ile Lys Tyr Val Ser Ser Glu Glu Tyr His Gln Arg Leu His
245 250 255

Gln Leu Arg Ala Arg
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<222> (1)..(579)

<223> FRXA02833

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Lys	Gln	Tyr	Glu	Val	Gly	Gly	Arg	Gly	Glu	Ala	Ser	Thr	Ser	Asp	Gly	
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Trp	Glu	Gly	Thr	His	Ser	Ala	Pro	Ala	Pro	Glu	Pro	His	Pro	Ala	Pro	
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Ile	Ala	Asp	Arg	Glu	Pro	Glu	Leu	Ala	Thr	Pro	Gln	Arg	Ile	Pro	Arg	
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gaa	acc	cca	gct	cac	aac	cct	aat	cgg	gaa	gtg	tcc	ctc	aac	ccg	aaa	336
Glu	Thr	Pro	Ala	His	Asn	Pro	Asn	Arg	Glu	Val	Ser	Leu	Asn	Pro	Lys	
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Tyr	Thr	Phe	Glu	Ser	Phe	Val	Ile	Gly	Pro	Phe	Asn	Arg	Phe	Ala	Asn	
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Ala	Ala	Ala	Val	Ala	Val	Ala	Glu	Ser	Pro	Ala	Lys	Ala	Phe	Asn	Pro	
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ctg	ttt	att	tcc	ggc	ggt	tcc	ggc	ttg	ggc	aaa	act	cac	ctg	ctg	cac	480
Leu	Phe	Ile	Ser	Gly	Gly	Ser	Gly	Leu	Gly	Lys	Thr	His	Leu	Leu	His	
145				150					155						160	
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Ala	Val	Gly	Asn	Tyr	Ala	Gln	Glu	Leu	Gln	Pro	Gly	Pro	Arg	Ile	Lys	
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tac	gtc	tca	agt	gag	gaa	tat	cac	caa	cga	cta	cat	caa	ctc	cgt	gcg	576
Tyr	Val	Ser	Ser	Glu	Glu	Tyr	His	Gln	Arg	Leu	His	Gln	Leu	Arg	Ala	
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Arg																

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<213> Corynebacterium glutamicum

<400> 154

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 20 25 30
 Phe Lys Tyr Gln Pro Asp Ala Leu Val Phe Ser Ser Asn Lys Ala Pro
 35 40 45
 Lys Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser Thr Ser Asp Gly
 50 55 60
 Trp Glu Gly Thr His Ser Ala Pro Ala Pro Glu Pro His Pro Ala Pro
 65 70 75 80
 Ile Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln Arg Ile Pro Arg
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 Glu Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser Leu Asn Pro Lys
 100 105 110
 Tyr Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn Arg Phe Ala Asn
 115 120 125
 Ala Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys Ala Phe Asn Pro
 130 135 140
 Leu Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr His Leu Leu His
 145 150 155 160
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 Tyr Val Ser Ser Glu Glu Tyr His Gln Arg Leu His Gln Leu Arg Ala
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Arg

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<222> (101)..(1993)

<223> RXA01480

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 Met Ala Lys Gly Arg
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 att ccg gaa agt gac att cag gca atc cgc gag cgc acc ccg atc gag 163

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Gly	Trp	Asp	Thr	Leu	Thr	Lys	His	Leu	Leu	Lys	Lys	Gly	Phe	Glu	Phe		
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Lys	Glu	Leu	Glu	Ala	Ala	Gly	Leu	Ser	Lys	Met	Gly	Lys	Arg	Gly	Pro		
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Ile	Asp	Gln	Phe	Gln	Arg	Arg	Leu	Leu	Trp	Pro	Ile	Lys	Asn	Leu	Ser		
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Lys	Val	Leu	Phe	Gly	Leu	Asp	Ser	Ala	Lys	Lys	Ala	Ile	Ala	Ala	Gly		

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His	Gln	Ala	Val	Val	Val	Glu	Gly	Tyr	Thr	Asp	Val	Met	Ala	Met	His				
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Ser	Phe	Val	Ser	Val	Ala	Pro	Asn	Gly	Met	Asp	Pro	Cys	Asp	Leu	Arg				
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Asp	Thr	Val	Glu	Gly	Arg	Leu	Ala	Ala	Leu	Arg	Arg	Ala	Val	Pro	Ile				
390								395					400					405	
gtg	gcg	gat	att	cgc	gat	aag	acg	ctg	cag	tct	gaa	tac	gcc	cgc	ctg	1363			
Val	Ala	Asp	Ile	Arg	Asp	Lys	Thr	Leu	Gln	Ser	Glu	Tyr	Ala	Arg	Leu				
410								415					420						
ctg	tct	ggt	tgg	gtc	ggc	tgg	tct	gat	cct	tca	gag	gtg	ctg	cgt	cag	1411			
Leu	Ser	Gly	Trp	Val	Gly	Trp	Ser	Asp	Pro	Ser	Glu	Val	Leu	Arg	Gln				
425								430					435						
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Ala	Lys	Arg	Phe	Asp	Gln	Pro	Leu	Glu	Asp	Gln	Ser	Leu	Arg	Pro	Thr				
455								460					465						
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470								475					480					485	
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His Ile Ser Phe Pro Glu Ala Val Glu Val Cys Ala Glu Lys Ile Gly
85 90 95

Tyr Gln Ile Asn Tyr Gln Gly Gly Gly Pro Gly Arg Arg Glu Glu Pro
 100 105 110
 Gly Thr Arg Gln Arg Leu Ile Leu Ala Asn Lys Ala Ala His Gln Phe
 115 120 125
 Tyr Arg Glu Gln Leu Glu Thr Pro Glu Ala Gln Pro Gly Arg Glu Phe
 130 135 140
 Leu Leu Gln Arg Gly Phe Gly Gln Gln His Ile Tyr His Phe Glu Cys
 145 150 155 160
 Gly Tyr Ala Pro Ala Gly Trp Asp Thr Leu Thr Lys His Leu Leu Lys
 165 170 175
 Lys Gly Phe Glu Phe Lys Glu Leu Glu Ala Ala Gly Leu Ser Lys Met
 180 185 190
 Gly Lys Arg Gly Pro Ile Asp Gln Phe Gln Arg Arg Leu Leu Trp Pro
 195 200 205
 Ile Lys Asn Leu Ser Gly Asp Val Ile Gly Phe Gly Ala Arg Lys Leu
 210 215 220
 Phe Asp Asp Asp Lys Met Gly Lys Tyr Met Asn Thr Pro Glu Thr Leu
 225 230 235 240
 Leu Tyr Lys Lys Ser Lys Val Leu Phe Gly Leu Asp Ser Ala Lys Lys
 245 250 255
 Ala Ile Ala Ala Gly His Gln Ala Val Val Val Glu Gly Tyr Thr Asp
 260 265 270
 Val Met Ala Met His Ala Ala Gly Ile Asp Thr Ala Val Ala Ser Cys
 275 280 285
 Gly Thr Ala Phe Gly Glu Glu His Leu Gln Met Leu Arg Arg Leu Met
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 Leu Asp Asp Asn Tyr Phe Arg Gly Glu Leu Ile Tyr Thr Phe Asp Gly
 305 310 315 320
 Asp Glu Ala Gly Gln Lys Ala Ala Met Arg Ala Phe Glu Gly Asp Gln
 325 330 335
 Lys Phe Thr Gly Gln Ser Phe Val Ser Val Ala Pro Asn Gly Met Asp
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 Pro Cys Asp Leu Arg Leu Glu Arg Gly Asp Ala Ala Val Arg Asp Leu
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 Val Ala Arg Arg Ile Pro Met Phe Glu Phe Val Ile Gln Ser Ile Ile
 370 375 380
 Ser Glu Tyr Thr Leu Asp Thr Val Glu Gly Arg Leu Ala Ala Leu Arg
 385 390 395 400
 Arg Ala Val Pro Ile Val Ala Asp Ile Arg Asp Lys Thr Leu Gln Ser
 405 410 415

Glu Tyr Ala Arg Leu Leu Ser Gly Trp Val Gly Trp Ser Asp Pro Ser
 420 425 430

Glu Val Leu Arg Gln Val His Glu Glu Ala Arg Arg Pro Lys Arg Asp
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Lys Lys Pro Val Arg Ala Lys Arg Phe Asp Gln Pro Leu Glu Asp Gln
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Ser Leu Arg Pro Thr Met Ala Leu Pro Asn Pro Arg Asn Pro Val Leu
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Trp Gln Glu Arg Glu Ser Leu Lys Ile Ala Leu Gln Tyr Pro Glu Leu
 485 490 495

Ala Gly Ser Tyr Phe Asp Gly Leu Pro Thr Asp Ser Phe Thr Asn Pro
 500 505 510

Ala Tyr Arg Met Val Arg Asp Ala Ile Ser Ala Ala Gly Gly Cys Glu
 515 520 525

Arg Ala Leu Asp Gly Thr Asp Trp Leu Pro Ala Val Ser Glu Asn Met
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Thr Asp Ile Leu Gly Thr Ser Leu Val Ser Glu Leu Ala Met Glu Pro
 545 550 555 560

Ile Glu Val Glu Ala Gln Asp Leu Glu Ser Tyr Thr Asp Gly Val Leu
 565 570 575

Ser Arg Leu Gln Glu Thr Arg Val Gly Asn Gln Ile Ala Ile Leu Lys
 580 585 590

Gly Gln Leu Gln Arg Met Arg Pro Ser Glu Asp Glu Gln Ala Tyr Asn
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<222> (101)..(1597)

<223> RXN03163

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 Met Ala Lys Thr Arg
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gtc ccc gct cct gaa aag tcg gtg gcg cgg gtt tta cct ctt ttg ggg 163

Val	Pro	Ala	Pro	Glu	Lys	Ser	Val	Ala	Arg	Val	Leu	Pro	Leu	Leu	Gly		
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Arg	Leu	Val	Asp	Ala	Ile	Val	Met	Ser	Arg	Thr	Ala	Gln	Thr	Ser	His		
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Glu	Gly	Lys	Leu	Met	Trp	Leu	Asp	Arg	Val	Ile	Ser	Pro	Ile	Val	Val		
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Tyr	Pro	Pro	Gln	Thr	Ala	Lys	Leu	Ile	Glu	Gln	Leu	Ser	Asp	Arg	Tyr		
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Gly	Gly	Val	Arg	Ser	Asp	Leu	Ile	Arg	Ser	Ala	Leu	Pro	Ala	Arg	His		
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gct	ggg	gca	gaa	gag	gca	gat	acc	tcc	acg	tcg	tgg	gag	tca	ttg	ggt	499	
Ala	Gly	Ala	Glu	Glu	Ala	Asp	Thr	Ser	Thr	Ser	Trp	Glu	Ser	Leu	Gly		
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Gln	Ser	Phe	Val	Asp	Ala	Val	Leu	Ala	Gly	Thr	Thr	Ala	Arg	Ala	Ser		
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Arg	Tyr	Arg	Arg	Phe	Leu	Ser	Val	Leu	Ser	Gly	Gln	Gly	Arg	Leu	Ile		
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Ile	Gly	Thr	Arg	Ser	Ala	Ala	Phe	Ala	Pro	Val	Lys	Asp	Leu	Lys	Leu		

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50 55 60
Ala Gln Thr Ser His Glu Gly Lys Leu Met Trp Leu Asp Arg Val Ile
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Leu Ser Asp Arg Tyr Gly Gly Val Arg Ser Asp Leu Ile Arg Ser Ala
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Leu Pro Ala Arg His Ala Gly Ala Glu Glu Ala Asp Thr Ser Thr Ser
115 120 125
Trp Glu Ser Leu Gly Glu Val Lys Glu Pro Asp Leu Ser Ser Trp Ser
130 135 140
Ala Tyr Gln His Gly Gln Ser Phe Val Asp Ala Val Leu Ala Gly Thr
145 150 155 160
Thr Ala Arg Ala Ser Trp Gln Ile Ala Pro Gly Asp Asp Trp Ala Leu
165 170 175
Ala Leu Ala Ser Leu Ala Val Lys Val Val Lys Asp Gly Gly Gly Ala
180 185 190
Leu Leu Val Val Pro Asp Gln Arg Asp Leu Asp Arg Leu Glu Ala Ala
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Leu Arg Gly Leu Val Ala Ala Lys Gln Ile Thr Val Leu Asn Ser Gly
210 215 220
Leu Gly Pro Gln Ala Arg Tyr Arg Arg Phe Leu Ser Val Leu Ser Gly
225 230 235 240
Gln Gly Arg Leu Ile Ile Gly Thr Arg Ser Ala Ala Phe Ala Pro Val
245 250 255
Lys Asp Leu Lys Leu Ala Val Ile Leu Asn Asp Gly Asp Asp Asn Leu
260 265 270
Val Asp Pro Arg Ala Pro Tyr Ala His Ala Arg Glu Val Leu Thr Thr
275 280 285

Arg Ser Ser Leu Glu Ala Ser Ser Leu Ile Ile Ala Gly His Ala Arg
290 295 300

Thr Ala Glu Thr Gln Leu Leu Val Glu Ser Gly Trp Met His Asn Leu
305 310 315 320

Ile Ala Pro Arg Asp Thr Ile Arg Thr Arg Met Pro Arg Ile Gln Ala
325 330 335

Val Gly Asp Ser Asp Phe Gln Met Glu Arg Asp Pro Met Ala Arg Ser
340 345 350

Ala Arg Leu Pro Gly Ile Ala Phe His Ala Val Arg Ser Ala Leu Glu
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Arg Asp Gln Pro Ala Leu Ile Gln Val Pro Arg Lys Gly Tyr Val Pro
370 375 380

Thr Leu Ala Cys Gly Asn Cys Arg Thr Pro Ala Arg Cys Arg His Cys
385 390 395 400

Asn Gly Pro Val Gly Leu Pro Gln Gly Ser Ser Asp Leu Ala Gly Val
405 410 415

Pro Thr Cys Arg Trp Cys Gly Arg Pro Asp Ser Arg Phe Lys Cys Gln
420 425 430

Asn Cys Gly Ser Pro Lys Leu Arg Ala Val Val Leu Gly Thr Glu Arg
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Thr Ala Glu Glu Leu Gly Arg Ala Phe Pro Ser Val Arg Val Ile Thr
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Val Ala Arg Val Leu

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5

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Ser Glu Asp Gln His Asp Asp Val Gln Pro Gly Val Arg Val Arg Val	
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Arg Phe Gly Gly Arg Leu Val Asp Ala Ile Val Met Ser Arg Thr Ala	
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Gln Thr Ser His Glu Gly Lys Leu Met Trp Leu Asp Arg Val Ile Ser	
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Ser Asp Arg Tyr Gly Gly Val Arg Ser Asp Leu Ile Arg Ser Ala Leu	
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Tyr Gln His Gly Gln Ser Phe Val Asp Ala Val Leu Ala Gly Thr Thr	
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Leu Ala Ser Leu Ala Val Lys Val Val Lys Asp Gly Gly Gly Ala Leu	
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Gly Arg Leu Ile Ile Gly Thr Arg Ser Ala Ala Phe Ala Pro Val Lys	
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<213> Corynebacterium glutamicum

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Asp Arg Val Ile Ser Pro Ile Val Val Tyr Pro Pro Gln Thr Ala Lys
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Ile Arg Ser Ala Leu Pro Ala Arg His Ala Gly Ala Glu Glu Ala Asp
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Thr Ser Thr Ser Trp Glu Ser Leu Gly Glu Val Lys Glu Pro Asp Leu
115 120 125
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130 135 140
Leu Ala Gly Thr Thr Ala Arg Ala Ser Trp Gln Ile Ala Pro Gly Asp
145 150 155 160
Asp Trp Ala Leu Ala Leu Ala Ser Leu Ala Val Lys Val Val Lys Asp
165 170 175
Gly Gly Gly Ala Leu Leu Val Val Pro Asp Gln Arg Asp Leu Asp Arg
180 185 190
Leu Glu Ala Ala Leu Arg Gly Leu Val Ala Ala Lys Gln Ile Thr Val
195 200 205
Leu Asn Ser Gly Leu Gly Pro Gln Ala Arg Tyr Arg Arg Phe Leu Ser
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Val Leu Ser Gly Gln Gly Arg Leu Ile Ile Gly Thr Arg Ser Ala Ala
225 230 235 240
Phe Ala Pro Val Lys Asp Leu Lys Leu Ala Val Ile Leu Asn Asp Gly
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Asp Asp Asn Leu Val Asp Pro Arg Ala Pro Tyr Ala His Ala Arg Glu
260 265 270
Val Leu Thr Thr Arg Ser Ser Leu Glu Ala Ser Ser Leu Ile Ile Ala
275 280 285
Gly His Ala Arg Thr Ala Glu Thr Gln Leu Leu Val Glu Ser Gly Trp
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Met His Asn Leu Ile Ala Pro Arg Asp Thr Ile Arg Thr Arg Met Pro
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Arg Ile Gln Ala Val Gly Asp Ser Asp Phe Gln Met Glu Arg Asp Pro
325 330 335
Met Ala Arg Ser Ala Arg Leu Pro Gly Ile Ala Phe His Ala Val Arg
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Ser Ala Leu Glu Arg Asp Gln Pro Ala Leu Ile Gln Val Pro Arg Lys

355 360 365

Gly Tyr Val Pro Thr Leu Ala Cys Gly Asn Cys Arg Thr Pro Ala Arg
370 375 380

Cys Arg His Cys Asn Gly Pro Val Gly Leu Pro Gln Gly Ser Ser Asp
385 390 395 400

Leu Ala Gly Val Pro Thr Cys Arg Trp Cys Gly Arg Pro Asp Ser Arg
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Phe Lys Cys Gln Asn Cys Gly Ser Pro Lys Leu Arg Ala Val Val Leu
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Gly Thr Glu Arg Thr Ala Glu Glu Leu Gly Arg Ala Phe Pro Ser Val
435 440 445

Arg Val Ile Thr Ser Gly Gly Asn Lys Val Val Asp Ser Val Glu Asn
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Arg Ala Ser Ile Val Val Ser Thr Pro Gly Ala Glu Pro Phe Val Ala
465 470 475 480

Asn Ser Pro Glu Arg Pro Glu Lys Ser Glu Lys Pro Glu His Lys Gly
 485 490 495

Ala Tyr Gly Ala Leu Leu Leu Leu Asp Thr Trp Ala Leu Met Gly Arg
 500 505 510

Gln Asp Leu Arg Ala Met Glu Asp Ala Leu His Lys Trp Ala Ala Ala
515 520 525

Ala Thr Leu Val His Ser His Leu His Gln Gly Gln Val Ile Val Val
530 535 540

Ala Asp Pro Ser Phe Pro Ala Val Gln Ser Leu Ile Arg Trp Asp Met
545 550 555 560

Ala Gly Ala Ala Ala Gln Glu Leu Ala Ser Arg Arg Glu Val Met Phe
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Pro Pro Ser Val His Met Ala Ala Ile Asp Gly Ala Thr Ala Ala Leu
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Glu Ser Phe Leu Asp Leu Ala Glu Leu Pro Asp His Ala Glu Val Leu
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Gly Pro Val Asp Leu Pro Pro Gly Val Ser Leu Pro Gly Glu Tyr Asp
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Glu Gln Arg Phe Gly Pro Pro Gln Arg Leu Leu Ile Arg Thr Pro Leu
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Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile Leu Lys Glu Val Leu
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Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys Pro Leu Gly Phe Lys
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Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe Gln Leu Val Asn Asp
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acc acc acg gtg ttg tat ccg atg aag ggc gtg tct gtg ctg cac cgt 595
Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val Ser Val Leu His Arg
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Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly Leu Thr Pro Arg Gln

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Tyr	Glu	Thr	Leu	Asp	Asn	Leu	Leu	Asp	His	Ala	Asp	Glu	Ile	Lys	Gly					
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aag	gtt	ggc	gcc	agc	ctg	cgt	gag	cgc	att	gag	cag	gtc	cgg	atg	aac	835				
Lys	Val	Gly	Ala	Ser	Leu	Arg	Glu	Arg	Ile	Glu	Gln	Val	Arg	Met	Asn					
230					235				240						245					
cgc	aag	ctc	acg	gag	atg	gtg	aag	gat	ctg	gag	ctg	ccg	ctt	ggg	ccg	883				
Arg	Lys	Leu	Thr	Glu	Met	Val	Lys	Asp	Leu	Glu	Leu	Pro	Leu	Gly	Pro					
			250						255					260						
gac	gat	ttt	gag	atg	aag	cct	gtg	cag	gtt	gcg	gag	gtt	gcg	gcg	aag	931				
Asp	Asp	Phe	Glu	Met	Lys	Pro	Val	Gln	Val	Ala	Glu	Val	Ala	Ala	Lys					
		265					270					275								
ttt	gac	gat	ctg	gag	ttt	ggg	acc	aat	ttg	cgt	gag	cgg	gtg	ctg	gcg	979				
Phe	Asp	Asp	Leu	Glu	Phe	Gly	Thr	Asn	Leu	Arg	Glu	Arg	Val	Leu	Ala					
		280					285					290								
gtg	gtg	aag	gcc	gag	ggg	tcc	gct	gcc	ccc	gtg	gag	gaa	gtg	gaa	gcg	1027				
Val	Val	Lys	Ala	Glu	Gly	Ser	Ala	Ala	Pro	Val	Glu	Glu	Val	Glu	Ala					
		295				300					305									
gaa	cag	gtt	gtc	gtc	gat	acg	caa	tct	ttg	gcg	caa	tgg	ctg	cct	gct	1075				
Glu	Gln	Val	Val	Val	Asp	Thr	Gln	Ser	Leu	Ala	Gln	Trp	Leu	Pro	Ala					
310					315					320					325					
agg	gct	ggc	cag	gcg	ctt	gct	tta	gcg	ctg	gct	gga	gtg	gct	aaa	cct	1123				
Arg	Ala	Gly	Gln	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Gly	Val	Ala	Lys	Pro					
			330						335					340						
gct	gct	ggc	gac	acg	tat	gcg	cta	gcg	att	gcg	gat	acc	aag	cgc	cat	1171				
Ala	Ala	Gly	Asp	Thr	Tyr	Ala	Leu	Ala	Ile	Ala	Asp	Thr	Lys	Arg	His					
			345				350						355							
gcg	gtg	ttg	gtt	gat	gtg	gct	gat	att	tca	gcg	gag	gat	gaa	aag	gcg	1219				
Ala	Val	Leu	Val	Asp	Val	Ala	Asp	Ile	Ser	Ala	Glu	Asp	Glu	Lys	Ala					
		360					365					370								
ctg	gcc	acg	tgg	ttg	gcg	tcg	gaa	gat	cca	aag	atg	ctg	cac	ggc	gct	1267				
Leu	Ala	Thr	Trp	Leu	Ala	Ser	Glu	Asp	Pro	Lys	Met	Leu	His	Gly	Ala					
		375				380					385									
aag	gcc	gcc	tat	cat	atg	ctc	gct	ggg	cgc	ggg	ttt	gag	ctg	cac	ggc	1315				
Lys	Ala	Ala	Tyr	His	Met	Leu	Ala	Gly	Arg	Gly	Phe	Glu	Leu	His	Gly					
390					395					400					405					
gtg	gtg	cat	gac	acg	gcg	atc	gcg	gca	tac	ttg	ctg	cgt	ccg	ggc	caa	1363				
Val	Val	His	Asp	Thr	Ala	Ile	Ala	Ala	Tyr	Leu	Leu	Arg	Pro	Gly	Gln					
			410						415					420						

cg	acc	tat	gag	ctt	gcc	gac	gtc	tac	cag	cg	cat	ctt	caa	cga	cag	1411
Arg	Thr	Tyr	Glu	Leu	Ala	Asp	Val	Tyr	Gln	Arg	His	Leu	Gln	Arg	Gln	
			425					430					435			
ttg	tct	aca	aac	gac	aat	ggc	ggc	cag	ctc	acg	ctg	ctc	gac	gca	gct	1459
Leu	Ser	Thr	Asn	Asp	Asn	Gly	Gly	Gln	Leu	Thr	Leu	Leu	Asp	Ala	Ala	
		440					445					450				
gat	gac	caa	tcg	ctt	gtt	gat	gat	gtc	att	gca	atc	ctt	gag	ctg	tct	1507
Asp	Asp	Gln	Ser	Leu	Val	Asp	Asp	Val	Ile	Ala	Ile	Leu	Glu	Leu	Ser	
		455				460					465					
gaa	gaa	ttg	acc	aaa	cag	ctt	cag	gag	att	caa	gct	ttt	gag	ctt	tac	1555
Glu	Glu	Leu	Thr	Lys	Gln	Leu	Gln	Glu	Ile	Gln	Ala	Phe	Glu	Leu	Tyr	
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cat	gac	ctg	gaa	att	ccg	ctg	tcg	gga	att	ctg	gcg	cg	atg	gag	gcc	1603
His	Asp	Leu	Glu	Ile	Pro	Leu	Ser	Gly	Ile	Leu	Ala	Arg	Met	Glu	Ala	
			490						495					500		
atc	ggt	atc	gct	gtt	gat	gtt	gcc	act	ttg	gaa	gag	cag	ttg	aag	act	1651
Ile	Gly	Ile	Ala	Val	Asp	Val	Ala	Thr	Leu	Glu	Glu	Gln	Leu	Lys	Thr	
			505					510					515			
ttc	att	ggt	cag	gtt	gct	cag	gaa	gag	gaa	gca	gct	cg	gag	ctc	gct	1699
Phe	Ile	Gly	Gln	Val	Ala	Gln	Glu	Glu	Glu	Ala	Ala	Arg	Glu	Leu	Ala	
		520					525					530				
gag	gat	cca	acc	ctg	aat	ctc	tcg	agc	ccg	aag	cag	ctg	caa	gtg	gtg	1747
Glu	Asp	Pro	Thr	Leu	Asn	Leu	Ser	Ser	Pro	Lys	Gln	Leu	Gln	Val	Val	
		535				540					545					
ctt	ttt	gag	acg	ttc	gga	atg	ccg	aaa	acc	aag	aaa	acc	aag	acc	ggc	1795
Leu	Phe	Glu	Thr	Phe	Gly	Met	Pro	Lys	Thr	Lys	Lys	Thr	Lys	Thr	Gly	
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tac	tct	acg	gct	gcc	gcg	gaa	att	gaa	gcc	cta	gcg	atc	aag	aat	ccg	1843
Tyr	Ser	Thr	Ala	Ala	Ala	Glu	Ile	Glu	Ala	Leu	Ala	Ile	Lys	Asn	Pro	
			570						575					580		
cac	cca	ttc	cta	gat	cac	ctg	ttg	gca	cac	cgt	cag	tac	caa	aag	atg	1891
His	Pro	Phe	Leu	Asp	His	Leu	Leu	Ala	His	Arg	Gln	Tyr	Gln	Lys	Met	
			585					590					595			
aag	acc	act	ctg	gaa	ggt	ctc	atc	cgt	gag	gtg	gct	cct	gat	ggc	cgt	1939
Lys	Thr	Thr	Leu	Glu	Gly	Leu	Ile	Arg	Glu	Val	Ala	Pro	Asp	Gly	Arg	
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att	cac	acc	acc	ttc	aac	cag	acg	gtg	gcg	tct	acg	gga	cgt	ttg	tca	1987
Ile	His	Thr	Thr	Phe	Asn	Gln	Thr	Val	Ala	Ser	Thr	Gly	Arg	Leu	Ser	
		615				620					625					
tcc	act	gat	ccc	aac	ctg	caa	aac	att	cct	gtg	cg	act	gag	gct	ggc	2035
Ser	Thr	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Glu	Ala	Gly	
630					635					640					645	
cga	aag	att	cgt	tcg	gga	ttc	gtc	gta	ggc	gag	ggg	tat	gaa	acc	ttg	2083
Arg	Lys	Ile	Arg	Ser	Gly	Phe	Val	Val	Gly	Glu	Gly	Tyr	Glu	Thr	Leu	
			650						655					660		

ctg act gcc gac tat tcg cag att gaa atg cgc gtg atg gct cac ctt	2131
Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg Val Met Ala His Leu	
665 670 675	
tcc cag gac cca ggc ttg att gag gcg tac cgc gaa ggc gaa gac ctg	2179
Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg Glu Gly Glu Asp Leu	
680 685 690	
cac aat tac gtg ggt tcc aag gtg ttt aat gtg ccc atc gat ggc gtg	2227
His Asn Tyr Val Gly Ser Lys Val Phe Asn Val Pro Ile Asp Gly Val	
695 700 705	
acc cct gag ctg cgt cgc cag gtc aag gcc atg tct tac ggt ctg gtg	2275
Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met Ser Tyr Gly Leu Val	
710 715 720 725	
tac ggc ttg tcc gcg ttt ggt ttg tct cag cag ctg agc att cct gct	2323
Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln Leu Ser Ile Pro Ala	
730 735 740	
ggc gaa gcg aag cag atc atg gag tcc tac ttc gag cgc ttc ggc gga	2371
Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe Glu Arg Phe Gly Gly	
745 750 755	
gta cag cgc tac ctc cgg gag atc gtg gag gag gct cga aaa gct ggc	2419
Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu Ala Arg Lys Ala Gly	
760 765 770	
tac acg gaa acg ctc ttt ggg cgt cgt cgc tac ctg ccg gaa ctg acc	2467
Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr Leu Pro Glu Leu Thr	
775 780 785	
tcg gat aac cgt gtc gct cgt gaa aac gct gaa cgt gcc gca ctg aac	2515
Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu Arg Ala Ala Leu Asn	
790 795 800 805	
gcc ccg att cag gga act gcc gca gac atc atc aag gtg gcc atg atc	2563
Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Val Ala Met Ile	
810 815 820	
cgg gtg gac cgt tca ctc aag gaa gct gcc gtg aaa tct cgc gtg ctg	2611
Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val Lys Ser Arg Val Leu	
825 830 835	
ctt cag gtg cat gat gaa ttg gtc gtg gaa gta gcg gcc ggt gag ttg	2659
Leu Gln Val His Asp Glu Leu Val Val Glu Val Ala Ala Gly Glu Leu	
840 845 850	
gaa caa gtc cgt gag att ctg gaa cgc gaa atg gat aac gcc atc aag	2707
Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala Ile Lys	
855 860 865	
ctg tcc gtt cct ttg gaa gtt tca gct ggt gat ggc gtt aac tgg gat	2755
Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp Gly Val Asn Trp Asp	
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Ala Ala Ala His	

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<212> PRT
<213> Corynebacterium glutamicum

<400> 162

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Ser	Gly	Gly	Gln	Ala	Thr	Asn	Ala	Val	Tyr	Gly	Phe	Leu	Ser	Met	Leu	
		35					40					45				
Ser	Thr	Leu	Leu	Lys	Asp	Glu	Gln	Pro	Thr	His	Val	Ala	Val	Ala	Phe	
	50					55					60					
Asp	Val	Gly	Arg	Lys	Thr	Phe	Arg	Thr	Asp	Met	Phe	Pro	Ala	Tyr	Lys	
65					70					75					80	
Ala	Gln	Arg	Glu	Ala	Thr	Pro	Pro	Glu	Phe	Lys	Gly	Gln	Val	Glu	Ile	
				85					90					95		
Leu	Lys	Glu	Val	Leu	Ser	Thr	Leu	Gly	Ile	Thr	Thr	Ile	Glu	Lys	Ile	
		100						105					110			
Asp	Phe	Glu	Ala	Asp	Asp	Val	Ile	Ala	Thr	Leu	Ser	Val	Ala	Ala	Lys	
	115						120					125				
Pro	Leu	Gly	Phe	Lys	Thr	Leu	Ile	Val	Thr	Gly	Asp	Arg	Asp	Ser	Phe	
	130					135					140					
Gln	Leu	Val	Asn	Asp	Thr	Thr	Thr	Val	Leu	Tyr	Pro	Met	Lys	Gly	Val	
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Ser	Val	Leu	His	Arg	Phe	Thr	Pro	Glu	Ala	Val	Glu	Glu	Lys	Tyr	Gly	
			165					170						175		
Leu	Thr	Pro	Arg	Gln	Tyr	Pro	Glu	Phe	Ala	Ala	Leu	Arg	Gly	Asp	Pro	
		180						185					190			
Ser	Asp	Asn	Leu	Pro	Asn	Ile	Pro	Gly	Val	Gly	Glu	Lys	Thr	Ala	Thr	
	195					200						205				
Lys	Trp	Ile	Ala	Gln	Tyr	Glu	Thr	Leu	Asp	Asn	Leu	Leu	Asp	His	Ala	
	210					215					220					
Asp	Glu	Ile	Lys	Gly	Lys	Val	Gly	Ala	Ser	Leu	Arg	Glu	Arg	Ile	Glu	
225					230					235					240	
Gln	Val	Arg	Met	Asn	Arg	Lys	Leu	Thr	Glu	Met	Val	Lys	Asp	Leu	Glu	
			245						250					255		
Leu	Pro	Leu	Gly	Pro	Asp	Asp	Phe	Glu	Met	Lys	Pro	Val	Gln	Val	Ala	
		260						265					270			
Glu	Val	Ala	Ala	Lys	Phe	Asp	Asp	Leu	Glu	Phe	Gly	Thr	Asn	Leu	Arg	
	275						280					285				
Glu	Arg	Val	Leu	Ala	Val	Val	Lys	Ala	Glu	Gly	Ser	Ala	Ala	Pro	Val	

290	295	300
Glu Glu Val Glu Ala	Glu Gln Val Val Val	Asp Thr Gln Ser Leu Ala
305	310	315 320
Gln Trp Leu Pro Ala Arg Ala Gly Gln Ala Leu Ala Leu Ala Leu Ala	325 330	335
Gly Val Ala Lys Pro Ala Ala Gly Asp Thr Tyr Ala Leu Ala Ile Ala	340 345	350
Asp Thr Lys Arg His Ala Val Leu Val Asp Val Ala Asp Ile Ser Ala	355 360	365
Glu Asp Glu Lys Ala Leu Ala Thr Trp Leu Ala Ser Glu Asp Pro Lys	370 375	380
Met Leu His Gly Ala Lys Ala Ala Tyr His Met Leu Ala Gly Arg Gly	385 390	395 400
Phe Glu Leu His Gly Val Val His Asp Thr Ala Ile Ala Ala Tyr Leu	405 410	415
Leu Arg Pro Gly Gln Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg	420 425	430
His Leu Gln Arg Gln Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr	435 440	445
Leu Leu Asp Ala Ala Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala	450 455	460
Ile Leu Glu Leu Ser Glu Glu Leu Thr Lys Gln Leu Gln Glu Ile Gln	465 470	475 480
Ala Phe Glu Leu Tyr His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu	485 490	495
Ala Arg Met Glu Ala Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu	500 505	510
Glu Gln Leu Lys Thr Phe Ile Gly Gln Val Ala Gln Glu Glu Glu Ala	515 520	525
Ala Arg Glu Leu Ala Glu Asp Pro Thr Leu Asn Leu Ser Ser Pro Lys	530 535	540
Gln Leu Gln Val Val Leu Phe Glu Thr Phe Gly Met Pro Lys Thr Lys	545 550	555 560
Lys Thr Lys Thr Gly Tyr Ser Thr Ala Ala Ala Glu Ile Glu Ala Leu	565 570	575
Ala Ile Lys Asn Pro His Pro Phe Leu Asp His Leu Leu Ala His Arg	580 585	590
Gln Tyr Gln Lys Met Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val	595 600	605
Ala Pro Asp Gly Arg Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser	610 615	620

Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val
625 630 635 640

Arg Thr Glu Ala Gly Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu
645 650 655

Gly Tyr Glu Thr Leu Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg
660 665 670

Val Met Ala His Leu Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg
675 680 685

Glu Gly Glu Asp Leu His Asn Tyr Val Gly Ser Lys Val Phe Asn Val
690 695 700

Pro Ile Asp Gly Val Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met
705 710 715 720

Ser Tyr Gly Leu Val Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln
725 730 735

Leu Ser Ile Pro Ala Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe
740 745 750

Glu Arg Phe Gly Gly Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu
755 760 765

Ala Arg Lys Ala Gly Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr
770 775 780

Leu Pro Glu Leu Thr Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu
785 790 795 800

Arg Ala Ala Leu Asn Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile
805 810 815

Lys Val Ala Met Ile Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val
820 825 830

Lys Ser Arg Val Leu Leu Gln Val His Asp Glu Leu Val Val Glu Val
835 840 845

Ala Ala Gly Glu Leu Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met
850 855 860

Asp Asn Ala Ile Lys Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp
865 870 875 880

Gly Val Asn Trp Asp Ala Ala Ala His
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<222> (101)..(2557)

<223> FRXA00060

<400> 163

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Val Thr Glu Lys Thr
1 5

gac cag acc tta atg ctt atc gac ggc cac tcg atg gct ttc cgc gca 163
Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser Met Ala Phe Arg Ala
10 15 20

ttc ttt gct ttg ccg gct gag aat ttc tcc acg tcg ggc ggg cag gcc 211
Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr Ser Gly Gly Gln Ala
25 30 35

acc aat gct gtc tat ggc ttt ctc tcg atg ctg tcc acg ttg ttg aag 259
Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu Ser Thr Leu Leu Lys
40 45 50

gat gag cag cct act cat gtg gcg gtg gct ttc gat gtg ggg cgt aag 307
Asp Glu Gln Pro Thr His Val Ala Val Ala Phe Asp Val Gly Arg Lys
55 60 65

acg ttc cgt acc gat atg ttc ccg gcg tat aag gcg cag cgt gaa gca 355
Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys Ala Gln Arg Glu Ala
70 75 80 85

acg cca cct gag ttt aag ggc cag gtg gaa atc ctc aag gag gtg ttg 403
Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile Leu Lys Glu Val Leu
90 95 100

tcc act ttg gga att acg act att gag aaa atc gat ttt gag gct gat 451
Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile Asp Phe Glu Ala Asp
105 110 115

gat gtg atc gcc acg ttg tct gtg gcg gcg aaa cct tta ggc ttt aag 499
Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys Pro Leu Gly Phe Lys
120 125 130

acg ctg att gtt acg ggt gac cgt gat tcc ttc cag ttg gtc aat gac 547
Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe Gln Leu Val Asn Asp
135 140 145

acc acc acg gtg ttg tat ccg atg aag ggc gtg tct gtg ctg cac cgt 595
Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val Ser Val Leu His Arg
150 155 160 165

ttc acg ccg gaa gca gtg gag gag aag tat gga ctg aca ccg agg cag 643
Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly Leu Thr Pro Arg Gln
170 175 180

tat ccg gag ttt gca gcg ctg cgt ggt gat cct tcc gat aac ttg cct 691
Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro Ser Asp Asn Leu Pro
185 190 195

aat att cct ggc gtg ggc gag aag act gct acc aag tgg att gcc cag 739
Asn Ile Pro Gly Val Gly Glu Lys Thr Ala Thr Lys Trp Ile Ala Gln
200 205 210

tat gaa act ttg gat aat ttg ctt gat cac gct gat gag atc aag ggc Tyr Glu Thr Leu Asp Asn Leu Leu Asp His Ala Asp Glu Ile Lys Gly 215 220 225	787
aag gtt ggc gcc agc ctg cgt gag cgc att gag cag gtc cgg atg aac Lys Val Gly Ala Ser Leu Arg Glu Arg Ile Glu Gln Val Arg Met Asn 230 235 240 245	835
cgc aag ctc acg gag atg gtg aag gat ctg gag ctg ccg ctt ggt ccg Arg Lys Leu Thr Glu Met Val Lys Asp Leu Glu Leu Pro Leu Gly Pro 250 255 260	883
gac gat ttt gag atg aag cct gtg cag gtt gcg gag gtt gcg gcg aag Asp Asp Phe Glu Met Lys Pro Val Gln Val Ala Glu Val Ala Ala Lys 265 270 275	931
ttt gac gat ctg gag ttt ggt acc aat ttg cgt gag cgg gtg ctg gcg Phe Asp Asp Leu Glu Phe Gly Thr Asn Leu Arg Glu Arg Val Leu Ala 280 285 290	979
gtg gtg aag gcc gag ggt tcc gct gcc ccc gtg gag gaa gtg gaa gcg Val Val Lys Ala Glu Gly Ser Ala Ala Pro Val Glu Glu Val Glu Ala 295 300 305	1027
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gct gct ggc gac acg tat gcg cta gcg att gcg gat acc aag cgc cat Ala Ala Gly Asp Thr Tyr Ala Leu Ala Ile Ala Asp Thr Lys Arg His 345 350 355	1171
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ctg gcc acg tgg ttg gcg tcg gaa gat cca aag atg ctg cac ggc gct Leu Ala Thr Trp Leu Ala Ser Glu Asp Pro Lys Met Leu His Gly Ala 375 380 385	1267
aag gcc gcc tat cat atg ctc gct ggg cgc ggt ttt gag ctg cac ggc Lys Ala Ala Tyr His Met Leu Ala Gly Arg Gly Phe Glu Leu His Gly 390 395 400 405	1315
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cgc acc tat gag ctt gcc gac gtc tac cag cgg cat ctt caa cga cag Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg His Leu Gln Arg Gln 425 430 435	1411
ttg tct aca aac gac aat ggc ggc cag ctc acg ctg ctc gac gca gct Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr Leu Leu Asp Ala Ala 440 445 450	1459
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Glu	Glu	Leu	Thr	Lys	Gln	Leu	Gln	Glu	Ile	Gln	Ala	Phe	Glu	Leu	Tyr		
470					475					480					485		
cat	gac	ctg	gaa	att	ccg	ctg	tcg	gga	att	ctg	gcg	cgc	atg	gag	gcc	1603	
His	Asp	Leu	Glu	Ile	Pro	Leu	Ser	Gly	Ile	Leu	Ala	Arg	Met	Glu	Ala		
				490					495					500			
atc	ggt	atc	gct	gtt	gat	gtt	gcc	act	ttg	gaa	gag	cag	ttg	aag	act	1651	
Ile	Gly	Ile	Ala	Val	Asp	Val	Ala	Thr	Leu	Glu	Glu	Gln	Leu	Lys	Thr		
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Phe	Ile	Gly	Gln	Val	Ala	Gln	Glu	Glu	Glu	Ala	Ala	Arg	Glu	Leu	Ala		
		520				525						530					
gag	gat	cca	acc	ctg	aat	ctc	tcg	agc	ccg	aag	cag	ctg	caa	gtg	gtg	1747	
Glu	Asp	Pro	Thr	Leu	Asn	Leu	Ser	Ser	Pro	Lys	Gln	Leu	Gln	Val	Val		
	535					540					545						
ctt	ttt	gag	acg	ttc	gga	atg	ccg	aaa	acc	aag	aaa	acc	aag	acc	ggc	1795	
Leu	Phe	Glu	Thr	Phe	Gly	Met	Pro	Lys	Thr	Lys	Lys	Thr	Lys	Thr	Gly		
550					555					560					565		
tac	tct	acg	gct	gcc	gcg	gaa	att	gaa	gcc	cta	gcg	atc	aag	aat	ccg	1843	
Tyr	Ser	Thr	Ala	Ala	Ala	Glu	Ile	Glu	Ala	Leu	Ala	Ile	Lys	Asn	Pro		
				570					575					580			
cac	cca	ttc	cta	gat	cac	ctg	ttg	gca	cac	cgt	cag	tac	caa	aag	atg	1891	
His	Pro	Phe	Leu	Asp	His	Leu	Leu	Ala	His	Arg	Gln	Tyr	Gln	Lys	Met		
			585					590					595				
aag	acc	act	ctg	gaa	ggt	ctc	atc	cgt	gag	gtg	gct	cct	gat	ggc	cgt	1939	
Lys	Thr	Thr	Leu	Glu	Gly	Leu	Ile	Arg	Glu	Val	Ala	Pro	Asp	Gly	Arg		
		600					605					610					
att	cac	acc	acc	ttc	aac	cag	acg	gtg	gcg	tct	acg	gga	cgt	ttg	tca	1987	
Ile	His	Thr	Thr	Phe	Asn	Gln	Thr	Val	Ala	Ser	Thr	Gly	Arg	Leu	Ser		
		615				620					625						
tcc	act	gat	ccc	aac	ctg	caa	aac	att	cct	gtg	cgc	act	gag	gct	ggc	2035	
Ser	Thr	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Glu	Ala	Gly		
					635					640					645		
cga	aag	att	cgt	tcg	gga	ttc	gtc	gta	ggc	gag	ggg	tat	gaa	acc	ttg	2083	
Arg	Lys	Ile	Arg	Ser	Gly	Phe	Val	Val	Gly	Glu	Gly	Tyr	Glu	Thr	Leu		
				650					655					660			
ctg	act	gcc	gac	tat	tcg	cag	att	gaa	atg	cgc	gtg	atg	gct	cac	ctt	2131	
Leu	Thr	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Met	Arg	Val	Met	Ala	His	Leu		
			665					670					675				
tcc	cag	gac	cca	ggc	ttg	att	gag	gcg	tac	cgc	gaa	ggc	gaa	gac	ctg	2179	
Ser	Gln	Asp	Pro	Gly	Leu	Ile	Glu	Ala	Tyr	Arg	Glu	Gly	Glu	Asp	Leu		
		680					685					690					
cac	aat	tac	gtg	ggt	tcc	aag	gtg	ttt	aat	gtg	ccc	atc	gat	ggc	gtg	2227	
His	Asn	Tyr	Val	Gly	Ser	Lys	Val	Phe	Asn	Val	Pro	Ile	Asp	Gly	Val		

695	700	705	
acc cct gag ctg cgt cgc cag gtc aag gcc atg tct tac ggt ctg gtg			2275
Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met Ser Tyr Gly Leu Val			
710	715	720	725
tac ggc ttg tcc gcg ttt ggt ttg tct cag cag ctg agc att cct gct			2323
Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln Leu Ser Ile Pro Ala			
	730	735	740
ggc gaa gcg aag cag atc atg gag tcc tac ttc gag cgc ttc ggc gga			2371
Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe Glu Arg Phe Gly Gly			
	745	750	755
gta cag cgc tac ctc cgg gag atc gtg gag gag gct cga aaa gct ggc			2419
Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu Ala Arg Lys Ala Gly			
	760	765	770
tac acg gaa acg ctc ttt ggg cgt cgt cgc tac ctg ccg gaa ctg acc			2467
Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr Leu Pro Glu Leu Thr			
	775	780	785
tcg gat aac cgt gtc gct cgt gaa aac gct gaa cgt gcc gca ctg aac			2515
Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu Arg Ala Ala Leu Asn			
	790	795	800
gcc ccg att agg gaa ctg ccg cag aca tca tca agg tgg cca			2557
Ala Pro Ile Arg Glu Leu Pro Gln Thr Ser Ser Arg Trp Pro			
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Ser Gly Gly Gln Ala Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu			
	35	40	45
Ser Thr Leu Leu Lys Asp Glu Gln Pro Thr His Val Ala Val Ala Phe			
	50	55	60
Asp Val Gly Arg Lys Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys			
	65	70	75
Ala Gln Arg Glu Ala Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile			
	85	90	95
Leu Lys Glu Val Leu Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile			
	100	105	110
Asp Phe Glu Ala Asp Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys			

115					120					125					
Pro	Leu	Gly	Phe	Lys	Thr	Leu	Ile	Val	Thr	Gly	Asp	Arg	Asp	Ser	Phe
130						135					140				
Gln	Leu	Val	Asn	Asp	Thr	Thr	Thr	Val	Leu	Tyr	Pro	Met	Lys	Gly	Val
145					150					155					160
Ser	Val	Leu	His	Arg	Phe	Thr	Pro	Glu	Ala	Val	Glu	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Thr	Pro	Arg	Gln	Tyr	Pro	Glu	Phe	Ala	Ala	Leu	Arg	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Asn	Ile	Pro	Gly	Val	Gly	Glu	Lys	Thr	Ala	Thr
		195					200					205			
Lys	Trp	Ile	Ala	Gln	Tyr	Glu	Thr	Leu	Asp	Asn	Leu	Leu	Asp	His	Ala
	210					215					220				
Asp	Glu	Ile	Lys	Gly	Lys	Val	Gly	Ala	Ser	Leu	Arg	Glu	Arg	Ile	Glu
225					230					235					240
Gln	Val	Arg	Met	Asn	Arg	Lys	Leu	Thr	Glu	Met	Val	Lys	Asp	Leu	Glu
				245					250					255	
Leu	Pro	Leu	Gly	Pro	Asp	Asp	Phe	Glu	Met	Lys	Pro	Val	Gln	Val	Ala
			260					265					270		
Glu	Val	Ala	Ala	Lys	Phe	Asp	Asp	Leu	Glu	Phe	Gly	Thr	Asn	Leu	Arg
		275					280					285			
Glu	Arg	Val	Leu	Ala	Val	Val	Lys	Ala	Glu	Gly	Ser	Ala	Ala	Pro	Val
	290					295					300				
Glu	Glu	Val	Glu	Ala	Glu	Gln	Val	Val	Val	Asp	Thr	Gln	Ser	Leu	Ala
305					310					315					320
Gln	Trp	Leu	Pro	Ala	Arg	Ala	Gly	Gln	Ala	Leu	Ala	Leu	Ala	Leu	Ala
				325					330					335	
Gly	Val	Ala	Lys	Pro	Ala	Ala	Gly	Asp	Thr	Tyr	Ala	Leu	Ala	Ile	Ala
			340					345				350			
Asp	Thr	Lys	Arg	His	Ala	Val	Leu	Val	Asp	Val	Ala	Asp	Ile	Ser	Ala
		355					360					365			
Glu	Asp	Glu	Lys	Ala	Leu	Ala	Thr	Trp	Leu	Ala	Ser	Glu	Asp	Pro	Lys
	370					375					380				
Met	Leu	His	Gly	Ala	Lys	Ala	Ala	Tyr	His	Met	Leu	Ala	Gly	Arg	Gly
385					390					395					400
Phe	Glu	Leu	His	Gly	Val	Val	His	Asp	Thr	Ala	Ile	Ala	Ala	Tyr	Leu
				405					410					415	
Leu	Arg	Pro	Gly	Gln	Arg	Thr	Tyr	Glu	Leu	Ala	Asp	Val	Tyr	Gln	Arg
			420					425					430		
His	Leu	Gln	Arg	Gln	Leu	Ser	Thr	Asn	Asp	Asn	Gly	Gly	Gln	Leu	Thr
		435					440					445			

Leu Leu Asp Ala Ala Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala
450 455 460

Ile Leu Glu Leu Ser Glu Glu Leu Thr Lys Gln Leu Gln Glu Ile Gln
465 470 475 480

Ala Phe Glu Leu Tyr His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu
485 490 495

Ala Arg Met Glu Ala Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu
500 505 510

Glu Gln Leu Lys Thr Phe Ile Gly Gln Val Ala Gln Glu Glu Glu Ala
515 520 525

Ala Arg Glu Leu Ala Glu Asp Pro Thr Leu Asn Leu Ser Ser Pro Lys
530 535 540

Gln Leu Gln Val Val Leu Phe Glu Thr Phe Gly Met Pro Lys Thr Lys
545 550 555 560

Lys Thr Lys Thr Gly Tyr Ser Thr Ala Ala Ala Glu Ile Glu Ala Leu
565 570 575

Ala Ile Lys Asn Pro His Pro Phe Leu Asp His Leu Leu Ala His Arg
580 585 590

Gln Tyr Gln Lys Met Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val
595 600 605

Ala Pro Asp Gly Arg Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser
610 615 620

Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val
625 630 635 640

Arg Thr Glu Ala Gly Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu
645 650 655

Gly Tyr Glu Thr Leu Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg
660 665 670

Val Met Ala His Leu Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg
675 680 685

Glu Gly Glu Asp Leu His Asn Tyr Val Gly Ser Lys Val Phe Asn Val
690 695 700

Pro Ile Asp Gly Val Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met
705 710 715 720

Ser Tyr Gly Leu Val Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln
725 730 735

Leu Ser Ile Pro Ala Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe
740 745 750

Glu Arg Phe Gly Gly Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu
755 760 765

Ala Arg Lys Ala Gly Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr
770 775 780

Leu Pro Glu Leu Thr Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu
785 790 795 800

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Arg Trp Pro

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Met Ile Arg Val Asp
1 5

cgt tca ctc aag gaa gct gcc gtg aaa tct cgc gtg ctg ctt cag gtg 163
Arg Ser Leu Lys Glu Ala Ala Val Lys Ser Arg Val Leu Leu Gln Val
10 15 20

cat gat gaa ttg gtc gtg gaa gta gcg gcc ggt gag ttg gaa caa gtc 211
His Asp Glu Leu Val Val Glu Val Ala Ala Gly Glu Leu Glu Gln Val
25 30 35

cgt gag att ctg gaa cgc gaa atg gat aac gcc atc aag ctg tcc gtt 259
Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala Ile Lys Leu Ser Val
40 45 50

cct ttg gaa gtt tca gct ggt gat ggc gtt aac tgg gat gct gca gcg 307
Pro Leu Glu Val Ser Ala Gly Asp Gly Val Asn Trp Asp Ala Ala Ala
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His
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<210> 166

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Val Leu Leu Gln Val His Asp Glu Leu Val Val Glu Val Ala Ala Gly

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	35						40					45			
Ile	Lys	Leu	Ser	Val	Pro	Leu	Glu	Val	Ser	Ala	Gly	Asp	Gly	Val	Asn
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 Met Ala Arg Leu Ser
 1 5
 cac atg gcc aag caa tcc tca ttt gta cat ctt cac aac cac acc gag 163
 His Met Ala Lys Gln Ser Ser Phe Val His Leu His Asn His Thr Glu
 10 15 20
 ttt tcc atg ctt gat gga atg gcc aag atc gat atg ttg gcc gat gag 211
 Phe Ser Met Leu Asp Gly Met Ala Lys Ile Asp Met Leu Ala Asp Glu
 25 30 35
 gtt aaa gcc cag gga atg cct gcg gtc gga atc acc gac cac ggc aat 259
 Val Lys Ala Gln Gly Met Pro Ala Val Gly Ile Thr Asp His Gly Asn
 40 45 50
 atg tat ggc tcc aac ccc ttt tat cgc aag atg aca gag atg ggc att 307
 Met Tyr Gly Ser Asn Pro Phe Tyr Arg Lys Met Thr Glu Met Gly Ile
 55 60 65
 aag ccc atc att ggc att gaa acg tat atg gca cct gag tct cgt ttt 355
 Lys Pro Ile Ile Gly Ile Glu Thr Tyr Met Ala Pro Glu Ser Arg Phe
 70 75 80 85
 aag aaa gag cgt gtg cgt tgg ggc gaa cca cac caa aaa tca gat gat 403
 Lys Lys Glu Arg Val Arg Trp Gly Glu Pro His Gln Lys Ser Asp Asp
 90 95 100
 gtt tct ggt tcc ggt gcg tat ttg cac cag acg atg ctt gca gaa aac 451
 Val Ser Gly Ser Gly Ala Tyr Leu His Gln Thr Met Leu Ala Glu Asn
 105 110 115
 acc aca ggt tta aga aac ctc ttt tat cta tct tcg atg gca tcg tac 499
 Thr Thr Gly Leu Arg Asn Leu Phe Tyr Leu Ser Ser Met Ala Ser Tyr
 120 125 130

gaa ggc cag cta ggc aag tgg ccc cgc atg gac gcc gat atc atc gct	547
Glu Gly Gln Leu Gly Lys Trp Pro Arg Met Asp Ala Asp Ile Ile Ala	
135 140 145	
gag cac gcc gaa ggc atc atc gcc acc acg ggt tgc cct tcc ggc gat	595
Glu His Ala Glu Gly Ile Ile Ala Thr Thr Gly Cys Pro Ser Gly Asp	
150 155 160 165	
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Val Gln Thr Arg Leu Arg Leu Gly Gln Phe Asp Glu Ala Leu Glu Ala	
170 175 180	
gcc gcc atg tgg cag gac atc tat ggt cgc gac aac tac ttc ctc gag	691
Ala Ala Met Trp Gln Asp Ile Tyr Gly Arg Asp Asn Tyr Phe Leu Glu	
185 190 195	
ttg atg gac cac ggg ctc gac att gaa acc cgt gtg cgc agt gag ctg	739
Leu Met Asp His Gly Leu Asp Ile Glu Thr Arg Val Arg Ser Glu Leu	
200 205 210	
ctc gaa atc gga cgc aag ctc aat ttg cca ccc ctg gtc acc aac gac	787
Leu Glu Ile Gly Arg Lys Leu Asn Leu Pro Pro Leu Val Thr Asn Asp	
215 220 225	
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Cys His Tyr Val Leu Glu Ser Gln Ala Gln Ala His Glu Ala Met Leu	
230 235 240 245	
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Cys Val Gln Thr Gly Lys Thr Leu His Asp Glu Asp Arg Phe Lys Phe	
250 255 260	
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Gly Gly Thr Gly Tyr Tyr Val Lys Ser Ala Glu Gln Met Arg Ala Leu	
265 270 275	
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Trp Asp Asp Met Val Pro Asp Gly Cys Asp Asn Thr Leu Trp Ile Ala	
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Glu Arg Val Gln Ser Tyr Asp Glu Ile Trp Glu Glu His Ser His Asp	
295 300 305	
cgc atg cct atc gct gat gtt cca gaa ggc tac acc cca acc act tgg	1075
Arg Met Pro Ile Ala Asp Val Pro Glu Gly Tyr Thr Pro Thr Thr Trp	
310 315 320 325	
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Leu His His Glu Val Met Ala Gly Leu Glu Asp Arg Phe Ser Gly Gln	
330 335 340	
caa gtt cct gag gat tat att gag cgc gcg gag tat gag atc tcc gtt	1171
Gln Val Pro Glu Asp Tyr Ile Glu Arg Ala Glu Tyr Glu Ile Ser Val	
345 350 355	
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Ile Asp Met Lys Gly Tyr Pro Ser Tyr Phe Leu Ile Val Ala Glu Ile	
360 365 370	
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Ile Lys His Ala Arg Ser Ile Gly Ile Arg Val Gly Pro Gly Arg Gly	
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Ser Ala Ala Gly Ala Leu Val Ala Tyr Ala Leu Thr Ile Thr Asn Ile	
390 395 400 405	
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Asp Pro Met Glu His Gly Leu Leu Phe Glu Arg Phe Leu Asn Pro Glu	
410 415 420	
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Arg Pro Ser Ala Pro Asp Ile Asp Ile Asp Phe Asp Asp Arg Arg Arg	
425 430 435	
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Gly Glu Met Ile Arg Tyr Ala Ala Asp Arg Trp Gly Glu Asp Lys Ile	
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Ala Gln Val Ile Thr Phe Gly Thr Val Lys Thr Lys Gln Ala Leu Lys	
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Asp Ser Ala Arg Val Gln Met Gly Gln Pro Gly Tyr Gln Ile Ala Asp	
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Arg Val Ile Lys Glu Leu Pro Pro Ala Ile Met Ala Lys Asp Ile Pro	
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Ala Val Arg Gln Leu Ile Glu Thr Asp Pro Asp Val Lys Arg Ile Tyr	
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Asp Thr Ala Arg Gly Leu Glu Gly Val Val Arg Gln Ser Gly Val His	
535 540 545	
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Ala Cys Ala Val Ile Met Ser Ser Val Pro Leu Leu Asp Cys Ile Pro	
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Met Trp Lys Arg Pro Ala Asp Gly Ala Leu Ile Thr Gly Trp Asp Tyr	
570 575 580	
cca gca tgt gag gcc att ggc ctg ttg aag atg gac ttc ctg gga ctt	1891
Pro Ala Cys Glu Ala Ile Gly Leu Lys Met Asp Phe Leu Gly Leu	
585 590 595	
cga aac ctt acc gtt att ggc gat gcg att gaa aac att aag gcc aac	1939
Arg Asn Leu Thr Val Ile Gly Asp Ala Ile Glu Asn Ile Lys Ala Asn	
600 605 610	
cgc gat ggg gaa gtg ctt gat cta gaa aac cta gcg atc gag gat gaa	1987
Arg Asp Gly Glu Val Leu Asp Leu Glu Asn Leu Ala Ile Glu Asp Glu	

615	620	625	
gaa acc tac aag ctg cta ggc cgt gga gaa acc ctt ggt gtg ttc cag Glu Thr Tyr Lys Leu Leu Gly Arg Gly Glu Thr Leu Gly Val Phe Gln 630 635 640 645			2035
ctt gat ggt ggt ggc atg cag gag ctg ctg aag cgt atg cag cca acc Leu Asp Gly Gly Gly Met Gln Glu Leu Leu Lys Arg Met Gln Pro Thr 650 655 660			2083
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atc ctt ggt gaa acc tat ggt ctg att gtg tac cag gag cag atc atg Ile Leu Gly Glu Thr Tyr Gly Leu Ile Val Tyr Gln Glu Gln Ile Met 710 715 720 725			2275
agg atc tcc cag aag gtc gca aac tac acc gct ggt caa gca gat ggt Arg Ile Ser Gln Lys Val Ala Asn Tyr Thr Ala Gly Gln Ala Asp Gly 730 735 740			2323
ttc cgt aaa gcc atg ggt aag aag aag ccc gag gtc ctg gaa aag gag Phe Arg Lys Ala Met Gly Lys Lys Lys Pro Glu Val Leu Glu Lys Glu 745 750 755			2371
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gcg att aag act ttg tgg gat acc att ctg ccg ttc gcc ggc tac gcg Ala Ile Lys Thr Leu Trp Asp Thr Ile Leu Pro Phe Ala Gly Tyr Ala 775 780 785			2467
ttc aac aag tct cac gcc gca ggt tat gga ctt gta tcc ttc tgg act Phe Asn Lys Ser His Ala Ala Gly Tyr Gly Leu Val Ser Phe Trp Thr 790 795 800 805			2515
gcc tat ttg aag gcg cac tac gcg ccg gaa tac atg gca gca ctg ctg Ala Tyr Leu Lys Ala His Tyr Ala Pro Glu Tyr Met Ala Ala Leu Leu 810 815 820			2563
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tgc cga cac ctt gga att cga gtg ctt tcg ccg gat att aac gag tcc Cys Arg His Leu Gly Ile Arg Val Leu Ser Pro Asp Ile Asn Glu Ser 840 845 850			2659
tcg ttg aac ttc ctt cct gtt ggc acc gat att cgc tat ggc ctg gga Ser Leu Asn Phe Leu Pro Val Gly Thr Asp Ile Arg Tyr Gly Leu Gly 855 860 865			2707

gcc att aga aac gtg ggt gct gaa gtt gtg gat tcc att ttg gat acc 2755
 Ala Ile Arg Asn Val Gly Ala Glu Val Val Asp Ser Ile Leu Asp Thr
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cgc aag gaa aag ggc cta ttt aag gac ttc tca gac tac ttg gac aag 2803
 Arg Lys Glu Lys Gly Leu Phe Lys Asp Phe Ser Asp Tyr Leu Asp Lys
 890 895 900

atc gat acc ctg ccg tgt aac aag cgc atc acc gag tct ttg atc aag 2851
 Ile Asp Thr Leu Pro Cys Asn Lys Arg Ile Thr Glu Ser Leu Ile Lys
 905 910 915

ggt ggc gct ttt gac tcc ctt gga cac gca cga aaa ggc ctc atg ctg 2899
 Gly Gly Ala Phe Asp Ser Leu Gly His Ala Arg Lys Gly Leu Met Leu
 920 925 930

gtc ttc gaa gat gcc gtt gat tcc gtc atc gct acc aaa aaa gct gct 2947
 Val Phe Glu Asp Ala Val Asp Ser Val Ile Ala Thr Lys Lys Ala Ala
 935 940 945

gac aag gga caa ttt gat ctc ttt gca gct ttc gac tcg gat aac aac 2995
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gac gat gtg gca agt ttc ttc cag atc acc gtt cct gat gac gaa tgg 3043
 Asp Asp Val Ala Ser Phe Phe Gln Ile Thr Val Pro Asp Asp Glu Trp
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gac cgt aag cat gag ctc gca ctc gag cga gaa atg ctg ggt ctg tat 3091
 Asp Arg Lys His Glu Leu Ala Leu Glu Arg Glu Met Leu Gly Leu Tyr
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gtt tct gga cac cca ctc gat ggc tat gaa gat gcc att gct gcc cag 3139
 Val Ser Gly His Pro Leu Asp Gly Tyr Glu Asp Ala Ile Ala Ala Gln
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 Val Asp Thr Ala Leu Thr Thr Ile Val Ala Gly Glu Leu Lys His Gly
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gca gaa gtg acc gtg ggt ggc att atc tct ggt gtg gat cga cgg ttc 3235
 Ala Glu Val Thr Val Gly Gly Ile Ile Ser Gly Val Asp Arg Arg Phe
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tcc aag aag gac ggt tcc cct tgg gcg att gtc acc att gaa gat cac 3283
 Ser Lys Lys Asp Gly Ser Pro Trp Ala Ile Val Thr Ile Glu Asp His
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 Asn Gly Ala Ser Val Glu Leu Leu Val Phe Asn Lys Val Tyr Ser Ile
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 Ser Met Arg Thr Asp Gln Cys Thr Met Ser Asn Ile Ala Lys Leu Lys
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 Ile Asp Gly Asp Asn Ser Thr Val Met Ile Leu Gly Asp His Leu Arg
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 Val Asn Arg Ser Ala Ser Leu Met Gly Asp Leu Lys Ala Thr Met Gly
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Thr Asp His Gly Asn Met Tyr Gly Ser Asn Pro Phe Tyr Arg Lys Met
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Thr Glu Met Gly Ile Lys Pro Ile Ile Gly Ile Glu Thr Tyr Met Ala
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Pro Glu Ser Arg Phe Lys Lys Glu Arg Val Arg Trp Gly Glu Pro His
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Gln Lys Ser Asp Asp Val Ser Gly Ser Gly Ala Tyr Leu His Gln Thr
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Ser Met Ala Ser Tyr Glu Gly Gln Leu Gly Lys Trp Pro Arg Met Asp
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Cys Pro Ser Gly Asp Val Gln Thr Arg Leu Arg Leu Gly Gln Phe Asp
165 170 175

Glu Ala Leu Glu Ala Ala Ala Met Trp Gln Asp Ile Tyr Gly Arg Asp
180 185 190

Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Asp Ile Glu Thr Arg
195 200 205

Val Arg Ser Glu Leu Leu Glu Ile Gly Arg Lys Leu Asn Leu Pro Pro
210 215 220

Leu Val Thr Asn Asp Cys His Tyr Val Leu Glu Ser Gln Ala Gln Ala
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His Glu Ala Met Leu Cys Val Gln Thr Gly Lys Thr Leu His Asp Glu
245 250 255

Asp Arg Phe Lys Phe Gly Gly Thr Gly Tyr Tyr Val Lys Ser Ala Glu
260 265 270

Gln Met Arg Ala Leu Trp Asp Asp Met Val Pro Asp Gly Cys Asp Asn
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Thr Leu Trp Ile Ala Glu Arg Val Gln Ser Tyr Asp Glu Ile Trp Glu
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Glu His Ser His Asp Arg Met Pro Ile Ala Asp Val Pro Glu Gly Tyr
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Thr Pro Thr Thr Trp Leu His His Glu Val Met Ala Gly Leu Glu Asp
325 330 335

Arg Phe Ser Gly Gln Gln Val Pro Glu Asp Tyr Ile Glu Arg Ala Glu
340 345 350

Tyr Glu Ile Ser Val Ile Asp Met Lys Gly Tyr Pro Ser Tyr Phe Leu
355 360 365

Ile Val Ala Glu Ile Ile Lys His Ala Arg Ser Ile Gly Ile Arg Val
370 375 380

Gly Pro Gly Arg Gly Ser Ala Ala Gly Ala Leu Val Ala Tyr Ala Leu
385 390 395 400

Thr Ile Thr Asn Ile Asp Pro Met Glu His Gly Leu Leu Phe Glu Arg
405 410 415

Phe Leu Asn Pro Glu Arg Pro Ser Ala Pro Asp Ile Asp Ile Asp Phe
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Asp Asp Arg Arg Arg Gly Glu Met Ile Arg Tyr Ala Ala Asp Arg Trp
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Gly Glu Asp Lys Ile Ala Gln Val Ile Thr Phe Gly Thr Val Lys Thr
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465 470 475 480

Tyr Gln Ile Ala Asp Arg Val Ile Lys Glu Leu Pro Pro Ala Ile Met

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Ile Tyr Leu Ser Asp Cys Arg His Leu Gly Ile Arg Val Leu Ser Pro
835 840 845

Asp Ile Asn Glu Ser Ser Leu Asn Phe Leu Pro Val Gly Thr Asp Ile
850 855 860

Arg Tyr Gly Leu Gly Ala Ile Arg Asn Val Gly Ala Glu Val Val Asp
865 870 875 880

Ser Ile Leu Asp Thr Arg Lys Glu Lys Gly Leu Phe Lys Asp Phe Ser
885 890 895

Asp Tyr Leu Asp Lys Ile Asp Thr Leu Pro Cys Asn Lys Arg Ile Thr
900 905 910

Glu Ser Leu Ile Lys Gly Gly Ala Phe Asp Ser Leu Gly His Ala Arg
915 920 925

Lys Gly Leu Met Leu Val Phe Glu Asp Ala Val Asp Ser Val Ile Ala
930 935 940

Thr Lys Lys Ala Ala Asp Lys Gly Gln Phe Asp Leu Phe Ala Ala Phe
945 950 955 960

Asp Ser Asp Asn Asn Asp Asp Val Ala Ser Phe Phe Gln Ile Thr Val
965 970 975

Pro Asp Asp Glu Trp Asp Arg Lys His Glu Leu Ala Leu Glu Arg Glu
980 985 990

Met Leu Gly Leu Tyr Val Ser Gly His Pro Leu Asp Gly Tyr Glu Asp
995 1000 1005

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Glu Leu Lys His Gly Ala Glu Val Thr Val Gly Gly Ile Ile Ser Gly
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Lys Val Tyr Ser Ile Val Gly Ser Met Ile Val Glu Asp Asn Ile Ile
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Leu Ala Lys Ala His Ile Ser Ile Arg Asp Asp Arg Met Ser Leu Phe
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Leu Pro Leu Arg Leu Ser Met Arg Thr Asp Gln Cys Thr Met Ser Asn
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Val Tyr Leu Asn Leu Ile Asp Gly Asp Asn Ser Thr Val Met Ile Leu
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<223> RXA01238

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 Val Ile Ala Ala Tyr
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 Gly Ala Ser Ile Ser Leu Asp Asp Ser Thr Leu Thr Ile Ser Tyr Ser
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cct ctt ctt gct gct ctt tct aag tcc agc gca caa tcg gaa tcg gtt 211
 Pro Leu Leu Ala Ala Leu Ser Lys Ser Ser Ala Gln Ser Glu Ser Val
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gat ctg aca cag gtc tct gga gta tct gtg cag gat ccc act gct ttt 259
 Asp Leu Thr Gln Val Ser Gly Val Ser Val Gln Asp Pro Thr Ala Phe
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 Thr His Gly Phe Leu Asn Leu Glu Gly Val Asp Lys Ser Ile Ala Phe
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 Ala Val Leu Lys Gly Glu Lys Pro Gln His Leu Gly Gly Gly Ala Pro
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 Val Val Pro Ser Ala Pro Ser Thr Val Ala Gly Leu Asn Phe Val Gly
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Ala Asp Leu Val Pro Lys Met Val Glu Phe Val Gly Asp Leu Pro Leu	
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Thr Leu Ala Arg Asn Glu Lys Leu Gln Val Glu Asn His Lys Leu Pro	
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Thr Val Ala Ser His Leu Gly Phe Glu Leu Lys Asn His His Asp Ala	
250 255 260	
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Ala Glu Asp Ala Arg Ala Cys Ala Ala Ile Thr Ile Ala Leu Ala Lys	
265 270 275	
cgc cac agc ttt gag ggc agc ttt gtg gat ttc gtt cac agc cgt ggt	979
Arg His Ser Phe Glu Gly Ser Phe Val Asp Phe Val His Ser Arg Gly	
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Phe Thr Met Gly Thr Val Asp Asn Ala Arg Val Tyr Pro Val Leu Lys	
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Asp Arg Ser Gly Ala Asn Val Ala Leu Gln Arg Arg Asn Phe Gly Leu	
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Asp Ala Gly Lys Thr Glu Val Pro Val Gln Pro Ala Val Asp Pro Ala	
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Trp Glu Thr Pro Lys Ala Glu Pro Lys Lys Gln Ser Gly Arg Arg Ala	
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Lys Ser Ile Ala Phe Ala Pro Asn Ser Ser Ala Asp Leu Ala Ala Leu
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Ala Ala Asp Ile Asp Ala Val Leu Lys Gly Glu Lys Pro Gln His Leu
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Gly Gly Gly Ala Pro Val Val Pro Ser Ala Pro Ser Thr Val Ala Gly
100 105 110

Leu Asn Phe Val Gly Phe Asp Val Glu Thr Ala Asn Asp Asp Trp Gly
115 120 125

Ser Ile Cys Gln Ile Gly Leu Val Lys Tyr Val Asp Gly Val Glu Glu
130 135 140

Ser Ser Glu Ser Trp Leu Cys Thr Pro Pro Glu Ser Leu Asn Phe Phe

145 150 155 160
Asn Glu Ile Asn Ile Gly Ile His Gly Ile Thr Pro Glu Met Val Ala
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Asp Gln Pro Arg Phe Ala Asp Leu Val Pro Lys Met Val Glu Phe Val
 180 185 190
Gly Asp Leu Pro Leu Val Ala His Asn Ala Gln Phe Asp Phe Thr Ala
 195 200 205
Leu Ser Arg Ala Cys Ala Ala Ser Gly Ile Asp Val Pro Glu Met Ile
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Tyr Gly Cys Ser Leu Thr Leu Ala Arg Asn Glu Lys Leu Gln Val Glu
225 230 235 240
Asn His Lys Leu Pro Thr Val Ala Ser His Leu Gly Phe Glu Leu Lys
 245 250 255
Asn His His Asp Ala Ala Glu Asp Ala Arg Ala Cys Ala Ala Ile Thr
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Ile Ala Leu Ala Lys Arg His Ser Phe Glu Gly Ser Phe Val Asp Phe
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Val His Ser Arg Gly Phe Thr Met Gly Thr Val Asp Asn Ala Arg Val
290 295 300
Tyr Pro Val Leu Lys Asp Arg Ser Gly Ala Asn Val Ala Leu Gln Arg
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Ala Val Asp Pro Ala Trp Glu Thr Pro Lys Ala Glu Pro Lys Lys Gln
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Ser Gly Arg Arg Ala Pro Trp Asp Lys Val Ala Thr Pro Glu Val Ile
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Pro Asp Pro Asn Pro Asp Ala Asp Pro Ser Ser Ile Leu Tyr Gly Gln
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Trp Gln Arg Ile Ala Asp Gln Gly Ala Leu Ile Gly Lys Asn Val Thr
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Lys Lys Thr Thr Ile Leu Val Ala Gly Pro Trp Ala Thr Ile Thr Ser
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Lys Gln Lys Arg Ala Glu Glu Leu Lys Glu Lys Gly Gln Asp Ile Gln
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170										175					180									
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Gln	Tyr	Val	Tyr	Glu	Lys	Tyr	Gly	Arg	Asp	Asn	Ala	Ala	Gln	Val	Ala									
280										285					290									
aat	gtc	att	acc	tac	cga	aca	aaa	ggc	gcg	atg	cgt	gat	gct	gcc	cgt	1027								
Asn	Val	Ile	Thr	Tyr	Arg	Thr	Lys	Gly	Ala	Met	Arg	Asp	Ala	Ala	Arg									
295										300					305									
gca	ctg	ggt	tac	ccg	caa	ggt	gct	gcc	gat	gcc	tgg	gct	aaa	gga	acc	1075								
Ala	Leu	Gly	Tyr	Pro	Gln	Gly	Ala	Ala	Asp	Ala	Trp	Ala	Lys	Gly	Thr									
310										315					320					325				
tcg	gaa	cca	ccc	gat	gat	gtg	ctg	gaa	tta	gct	gcg	caa	ttt	aaa	ggg	1123								
Ser	Glu	Pro	Pro	Asp	Asp	Val	Leu	Glu	Leu	Ala	Ala	Gln	Phe	Lys	Gly									
330										335					340									
caa	cca	cgg	cat	ttg	ggt	att	cac	tcc	ggt	ggc	atg	gtc	att	tgc	gat	1171								
Gln	Pro	Arg	His	Leu	Gly	Ile	His	Ser	Gly	Gly	Met	Val	Ile	Cys	Asp									
345										350					355									
cgc	ccc	atc	gcc	gat	gtg	gtg	cca	gtg	gaa	tgg	gct	cgg	atg	gat	aac	1219								
Arg	Pro	Ile	Ala	Asp	Val	Val	Pro	Val	Glu	Trp	Ala	Arg	Met	Asp	Asn									
360										365					370									
cgc	tcg	gtt	gtg	caa	tgg	gat	aaa	gat	gac	tgt	gcc	acg	gca	ggc	ttg	1267								
Arg	Ser	Val	Val	Gln	Trp	Asp	Lys	Asp	Asp	Cys	Ala	Thr	Ala	Gly	Leu									
375										380					385									
gtc	aaa	ttc	gac	ctt	ttg	gga	ttg	ggc	atg	ttg	gaa	gcc	atc	cat	cac	1315								
Val	Lys	Phe	Asp	Leu	Leu	Gly	Leu	Gly	Met	Leu	Glu	Ala	Ile	His	His									
390										395					400					405				
atg	ctg	gat	ctg	gtg	gca	gaa	cac	cga	ggt	aaa	aag	atc	aat	ttg	tgg	1363								
Met	Leu	Asp	Leu	Val	Ala	Glu	His	Arg	Gly	Lys	Lys	Ile	Asn	Leu	Trp									
410										415					420									

gaa cta gat ctg gcg gaa ccg gag gtc tat gac atg ttg tgc aag gca	1411
Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp Met Leu Cys Lys Ala	
425 430 435	
gat gcc gtg ggt gtg ttc cag gtg gaa tca cgt gcg cag tta tcc acg	1459
Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg Ala Gln Leu Ser Thr	
440 445 450	
ctg cct cga ctc aag ccc cgc acc ttc ttt gac ctg gtc gtg gag gta	1507
Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp Leu Val Val Glu Val	
455 460 465	
gct ctg att cgt cca ggt ccc atc caa ggc gga tcg gtg cac ccg tat	1555
Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly Ser Val His Pro Tyr	
470 475 480 485	
ttg cgg cgc cgt gct ggt gaa gag gcc atc act tat gac cac ccc gtg	1603
Leu Arg Arg Arg Ala Gly Glu Glu Ala Ile Thr Tyr Asp His Pro Val	
490 495 500	
ttg gaa aag tct ttg ggt aaa acc tta gga atc cca ctg ttt cag gaa	1651
Leu Glu Lys Ser Leu Gly Lys Thr Leu Gly Ile Pro Leu Phe Gln Glu	
505 510 515	
cag ctc atg cag gta gct gtt gat gct gca ggt ttt agt ggt ggg gaa	1699
Gln Leu Met Gln Val Ala Val Asp Ala Ala Gly Phe Ser Gly Gly Glu	
520 525 530	
gcg gat tcc ttg cgc aga gcg atg ggg tcg aaa cgc tca cct gaa cgc	1747
Ala Asp Ser Leu Arg Arg Ala Met Gly Ser Lys Arg Ser Pro Glu Arg	
535 540 545	
atg gct gcg ttg cgc tcg cgg ttt ttc caa ggg ctg aaa gat acc aat	1795
Met Ala Ala Leu Arg Ser Arg Phe Phe Gln Gly Leu Lys Asp Thr Asn	
550 555 560 565	
ggg att gtg ggg gag acc gcc gag aaa ctg tgg aac aaa att gtg gcc	1843
Gly Ile Val Gly Glu Thr Ala Glu Lys Leu Trp Asn Lys Ile Val Ala	
570 575 580	
ttt gct gcc tac ggt ttt ccg gaa tcg cat tcg cag tcg ttt gcg tcc	1891
Phe Ala Ala Tyr Gly Phe Pro Glu Ser His Ser Gln Ser Phe Ala Ser	
585 590 595	
ttg gtg tat ttc tcc gcg tgg ttt aaa tac cac tac ccg gct gaa ttc	1939
Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His Tyr Pro Ala Glu Phe	
600 605 610	
tgc gtg gga tta ttg cgg gca caa ccc atg ggt ttc tat tca cca cag	1987
Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly Phe Tyr Ser Pro Gln	
615 620 625	
tct ttg atc agt gat gcc aga cgc cac ggc gtg agt atc ctg ccg atc	2035
Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val Ser Ile Leu Pro Ile	
630 635 640 645	
acg gtc aat gat tcc ggt gtg gag gcc gat gct ccg aat ggt gcg att	2083
Thr Val Asn Asp Ser Gly Val Glu Ala Asp Ala Pro Asn Gly Ala Ile	
650 655 660	

cga ttg ggg ctc aac ctg gtg aaa ggc ctt ggc cac gat gcc gcg caa	2131
Arg Leu Gly Leu Asn Leu Val Lys Gly Leu Gly His Asp Ala Ala Gln	
665 670 675	
aga ata gag gac aac gcc ccg ttt gat tcc att ccg gat tta tcg cgc	2179
Arg Ile Glu Asp Asn Ala Pro Phe Asp Ser Ile Pro Asp Leu Ser Arg	
680 685 690	
cgg gct gat ctt aat gtt gct caa gtt gag gca ttg gcg cga gcg gga	2227
Arg Ala Asp Leu Asn Val Ala Gln Val Glu Ala Leu Ala Arg Ala Gly	
695 700 705	
gcg gtg gac tgc ttg ggg gtc gga cgt cga caa gca tta tgg caa gcg	2275
Ala Val Asp Cys Leu Gly Val Gly Arg Arg Gln Ala Leu Trp Gln Ala	
710 715 720 725	
ggc gtc gca gcg acc gaa aaa cct gga atg ctg cct ggc ctt tcg gtg	2323
Gly Val Ala Ala Thr Glu Lys Pro Gly Met Leu Pro Gly Leu Ser Val	
730 735 740	
att gaa gct ccg gcg ttg ccg ggg atg agc gcc ttt gag ctg atg gcg	2371
Ile Glu Ala Pro Ala Leu Pro Gly Met Ser Ala Phe Glu Leu Met Ala	
745 750 755	
acc aat att tcc gcc acg gga gtc acc gcg gat tat cag ccg atg gcg	2419
Thr Asn Ile Ser Ala Thr Gly Val Thr Ala Asp Tyr Gln Pro Met Ala	
760 765 770	
ttg att ccg gag ccg atg gag gag ctg ggg atc gtg ccg gcg gat ccg	2467
Leu Ile Arg Glu Arg Met Glu Glu Leu Gly Ile Val Pro Ala Asp Arg	
775 780 785	
cta ttg gag gtg gaa gat ggc acg ccg ctg ccg atc gct ggc att gtc	2515
Leu Leu Glu Val Glu Asp Gly Thr Arg Leu Arg Ile Ala Gly Ile Val	
790 795 800 805	
acg cac ccg cag cgc ccg caa act gcg tcg ggg ctg aca ttt tta ggg	2563
Thr His Arg Gln Arg Pro Gln Thr Ala Ser Gly Leu Thr Phe Leu Gly	
810 815 820	
atg gag gat gag acc ggg ctg atg aat gtg atg gtg tcc gtt ggg ttg	2611
Met Glu Asp Glu Thr Gly Leu Met Asn Val Met Val Ser Val Gly Leu	
825 830 835	
tgg cag ccg cag cgc gtg ctg gcc aga aat gcc aag gcg ttg att att	2659
Trp Gln Arg Gln Arg Val Leu Ala Arg Asn Ala Lys Ala Leu Ile Ile	
840 845 850	
cga ggg att gtg cag aat gcg caa ggg gtg gcg aca gtt gtc gct gac	2707
Arg Gly Ile Val Gln Asn Ala Gln Gly Val Ala Thr Val Val Ala Asp	
855 860 865	
cgg ttg gaa ccg ttg gac atg ggg gag ttt ctc agc cgt ggc tca cga	2755
Arg Leu Glu Pro Leu Asp Met Gly Glu Phe Leu Ser Arg Gly Ser Arg	
870 875 880 885	
gat ttt cga taatttgga aagtggacat tat	2787
Asp Phe Arg	

<210> 172

<211> 888

<212> PRT

<213> Corynebacterium glutamicum

<400> 172

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Gln Trp Leu Asp Lys Ile Asp Tyr Val Ile Asp Cys Phe Lys Pro Glu
20 25 30

Asn Ile Val Leu Glu Phe Gly Ser Thr Met Thr Pro Glu Asp Ala Asp
35 40 45

Arg Asn Glu Tyr Leu Arg Arg Thr Gln Ala Lys Phe Gln Leu Arg Gly
50 55 60

Ile Leu Ser Thr Asn Pro Glu Ser Ala Ala Arg Gly Ser Val Arg Leu
65 70 75 80

Ala Gly Ala Lys Gln Ala Leu Ala Arg Lys Met Pro Leu Ala Asp Ala
85 90 95

Glu Ser Glu Leu His Pro Met Gly Thr Thr Trp Met Arg Ser Gly Asp
100 105 110

Thr Leu Leu Lys Ala His Pro Asp Tyr Ala Asp Leu Ile Ala Thr Thr
115 120 125

Val Glu Leu Ala Ala Glu Cys Ala Phe Thr Leu Asp Leu Val Ala Pro
130 135 140

Asn Leu Pro Lys Trp Asp Thr Pro Gly Glu His Thr Glu Met Ser Trp
145 150 155 160

Leu Ala His Leu Val Ser Thr Arg Ile Asp Thr Arg Tyr Val Gly Arg
165 170 175

Ser Ala Asp Ile Lys Ala Arg Ala Ala Thr Gln Ile Asp Tyr Glu Leu
180 185 190

Gly Val Ile Glu Lys Leu Gly Phe Pro Gly Tyr Phe Leu Val Val Asn
195 200 205

Asp Leu Val Glu Phe Cys Arg Asp Ser Asn Ile Leu Cys Gln Gly Arg
210 215 220

Gly Ser Ala Ala Asn Ser Ala Val Cys Phe Val Leu Gly Ile Thr Asn
225 230 235 240

Ala Glu Pro Ile Ser Ala Gly Leu Leu Phe Glu Arg Phe Leu Ser Pro
245 250 255

Asp Arg Asp Gly Pro Pro Asp Ile Asp Ile Asp Ile Glu Ser Gly Arg
260 265 270

Arg Glu Glu Val Ile Gln Tyr Val Tyr Glu Lys Tyr Gly Arg Asp Asn
275 280 285

Ala Ala Gln Val Ala Asn Val Ile Thr Tyr Arg Thr Lys Gly Ala Met

290	295	300
Arg Asp Ala Ala Arg Ala Leu Gly Tyr Pro Gln Gly Ala Ala Asp Ala 305 310 315 320		
Trp Ala Lys Gly Thr Ser Glu Pro Pro Asp Asp Val Leu Glu Leu Ala 325 330 335		
Ala Gln Phe Lys Gly Gln Pro Arg His Leu Gly Ile His Ser Gly Gly 340 345 350		
Met Val Ile Cys Asp Arg Pro Ile Ala Asp Val Val Pro Val Glu Trp 355 360 365		
Ala Arg Met Asp Asn Arg Ser Val Val Gln Trp Asp Lys Asp Asp Cys 370 375 380		
Ala Thr Ala Gly Leu Val Lys Phe Asp Leu Leu Gly Leu Gly Met Leu 385 390 395 400		
Glu Ala Ile His His Met Leu Asp Leu Val Ala Glu His Arg Gly Lys 405 410 415		
Lys Ile Asn Leu Trp Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp 420 425 430		
Met Leu Cys Lys Ala Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg 435 440 445		
Ala Gln Leu Ser Thr Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp 450 455 460		
Leu Val Val Glu Val Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly 465 470 475 480		
Ser Val His Pro Tyr Leu Arg Arg Arg Ala Gly Glu Glu Ala Ile Thr 485 490 495		
Tyr Asp His Pro Val Leu Glu Lys Ser Leu Gly Lys Thr Leu Gly Ile 500 505 510		
Pro Leu Phe Gln Glu Gln Leu Met Gln Val Ala Val Asp Ala Ala Gly 515 520 525		
Phe Ser Gly Gly Glu Ala Asp Ser Leu Arg Arg Ala Met Gly Ser Lys 530 535 540		
Arg Ser Pro Glu Arg Met Ala Ala Leu Arg Ser Arg Phe Phe Gln Gly 545 550 555 560		
Leu Lys Asp Thr Asn Gly Ile Val Gly Glu Thr Ala Glu Lys Leu Trp 565 570 575		
Asn Lys Ile Val Ala Phe Ala Ala Tyr Gly Phe Pro Glu Ser His Ser 580 585 590		
Gln Ser Phe Ala Ser Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His 595 600 605		
Tyr Pro Ala Glu Phe Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly 610 615 620		

Phe Tyr Ser Pro Gln Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val
625 630 635 640

Ser Ile Leu Pro Ile Thr Val Asn Asp Ser Gly Val Glu Ala Asp Ala
645 650 655

Pro Asn Gly Ala Ile Arg Leu Gly Leu Asn Leu Val Lys Gly Leu Gly
660 665 670

His Asp Ala Ala Gln Arg Ile Glu Asp Asn Ala Pro Phe Asp Ser Ile
675 680 685

Pro Asp Leu Ser Arg Arg Ala Asp Leu Asn Val Ala Gln Val Glu Ala
690 695 700

Leu Ala Arg Ala Gly Ala Val Asp Cys Leu Gly Val Gly Arg Arg Gln
705 710 715 720

Ala Leu Trp Gln Ala Gly Val Ala Ala Thr Glu Lys Pro Gly Met Leu
725 730 735

Pro Gly Leu Ser Val Ile Glu Ala Pro Ala Leu Pro Gly Met Ser Ala
740 745 750

Phe Glu Leu Met Ala Thr Asn Ile Ser Ala Thr Gly Val Thr Ala Asp
755 760 765

Tyr Gln Pro Met Ala Leu Ile Arg Glu Arg Met Glu Glu Leu Gly Ile
770 775 780

Val Pro Ala Asp Arg Leu Leu Glu Val Glu Asp Gly Thr Arg Leu Arg
785 790 795 800

Ile Ala Gly Ile Val Thr His Arg Gln Arg Pro Gln Thr Ala Ser Gly
805 810 815

Leu Thr Phe Leu Gly Met Glu Asp Glu Thr Gly Leu Met Asn Val Met
820 825 830

Val Ser Val Gly Leu Trp Gln Arg Gln Arg Val Leu Ala Arg Asn Ala
835 840 845

Lys Ala Leu Ile Ile Arg Gly Ile Val Gln Asn Ala Gln Gly Val Ala
850 855 860

Thr Val Val Ala Asp Arg Leu Glu Pro Leu Asp Met Gly Glu Phe Leu
865 870 875 880

Ser Arg Gly Ser Arg Asp Phe Arg
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<210> 173

<211> 599

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(576)

<223> FRXA00407

<400> 173

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Leu	Asn	Val	Ala	Gln	Val	Glu	Ala	Leu	Ala	Arg	Ala	Gly	Ala	Val	Asp	
1				5				10						15		
tgc	ttg	ggg	gtc	gga	cgt	cga	caa	gca	tta	tgg	caa	gcg	ggc	gtc	gca	96
Cys	Leu	Gly	Val	Gly	Arg	Arg	Gln	Ala	Leu	Trp	Gln	Ala	Gly	Val	Ala	
			20					25						30		
gcg	acc	gaa	aaa	cct	gga	atg	ctg	cct	ggc	ctt	tcg	gtg	att	gaa	gct	144
Ala	Thr	Glu	Lys	Pro	Gly	Met	Leu	Pro	Gly	Leu	Ser	Val	Ile	Glu	Ala	
		35					40					45				
ccg	gcg	ttg	ccg	ggg	atg	agc	gcc	ttt	gag	ctg	atg	gcg	acc	aat	att	192
Pro	Ala	Leu	Pro	Gly	Met	Ser	Ala	Phe	Glu	Leu	Met	Ala	Thr	Asn	Ile	
	50					55					60					
tcc	gcc	acg	gga	gtc	acc	gcg	gat	tat	cag	ccg	atg	gcg	ttg	att	cgg	240
Ser	Ala	Thr	Gly	Val	Thr	Ala	Asp	Tyr	Gln	Pro	Met	Ala	Leu	Ile	Arg	
65					70				75						80	
gag	cgg	atg	gag	gag	ctg	ggg	atc	gtg	ccg	gcg	gat	cgg	cta	ttg	gag	288
Glu	Arg	Met	Glu	Glu	Leu	Gly	Ile	Val	Pro	Ala	Asp	Arg	Leu	Leu	Glu	
				85					90					95		
gtg	gaa	gat	ggc	acg	cgg	ctg	cgg	atc	gct	ggc	att	gtc	acg	cac	cgg	336
Val	Glu	Asp	Gly	Thr	Arg	Leu	Arg	Ile	Ala	Gly	Ile	Val	Thr	His	Arg	
			100					105					110			
cag	cgc	ccg	caa	act	gcg	tcg	ggg	ctg	aca	ttt	tta	ggg	atg	gag	gat	384
Gln	Arg	Pro	Gln	Thr	Ala	Ser	Gly	Leu	Thr	Phe	Leu	Gly	Met	Glu	Asp	
		115					120					125				
gag	acc	ggg	ctg	atg	aat	gtg	atg	gtg	tcc	gtt	ggg	ttg	tgg	cag	cgg	432
Glu	Thr	Gly	Leu	Met	Asn	Val	Met	Val	Ser	Val	Gly	Leu	Trp	Gln	Arg	
	130					135					140					
cag	cgc	gtg	ctg	gcc	aga	aat	gcc	aag	gcg	ttg	att	att	cga	ggg	att	480
Gln	Arg	Val	Leu	Ala	Arg	Asn	Ala	Lys	Ala	Leu	Ile	Ile	Arg	Gly	Ile	
145					150					155					160	
gtg	cag	aat	gcg	caa	ggg	gtg	gcg	aca	gtt	gtc	gct	gac	cgg	ttg	gaa	528
Val	Gln	Asn	Ala	Gln	Gly	Val	Ala	Thr	Val	Val	Ala	Asp	Arg	Leu	Glu	
				165					170					175		
ccg	ttg	gac	atg	ggg	gag	ttt	ctc	agc	cgt	ggc	tca	cga	gat	ttt	cga	576
Pro	Leu	Asp	Met	Gly	Glu	Phe	Leu	Ser	Arg	Gly	Ser	Arg	Asp	Phe	Arg	
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taatttggca	aagtggacat	tat														599

<210> 174

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 174

Leu Asn Val Ala Gln Val Glu Ala Leu Ala Arg Ala Gly Ala Val Asp

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Cys Leu Gly Val Gly Arg Arg Gln Ala Leu Trp Gln Ala Gly Val Ala	20	25	30
Ala Thr Glu Lys Pro Gly Met Leu Pro Gly Leu Ser Val Ile Glu Ala	35	40	45
Pro Ala Leu Pro Gly Met Ser Ala Phe Glu Leu Met Ala Thr Asn Ile	50	55	60
Ser Ala Thr Gly Val Thr Ala Asp Tyr Gln Pro Met Ala Leu Ile Arg	65	70	75
Glu Arg Met Glu Glu Leu Gly Ile Val Pro Ala Asp Arg Leu Leu Glu	85	90	95
Val Glu Asp Gly Thr Arg Leu Arg Ile Ala Gly Ile Val Thr His Arg	100	105	110
Gln Arg Pro Gln Thr Ala Ser Gly Leu Thr Phe Leu Gly Met Glu Asp	115	120	125
Glu Thr Gly Leu Met Asn Val Met Val Ser Val Gly Leu Trp Gln Arg	130	135	140
Gln Arg Val Leu Ala Arg Asn Ala Lys Ala Leu Ile Ile Arg Gly Ile	145	150	155
Val Gln Asn Ala Gln Gly Val Ala Thr Val Val Ala Asp Arg Leu Glu	165	170	175
Pro Leu Asp Met Gly Glu Phe Leu Ser Arg Gly Ser Arg Asp Phe Arg	180	185	190

<210> 175

<211> 2062

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2062)

<223> FRXA00415

<400> 175

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	Met Val Ala Glu His	
	1 5	

gct gca ggg gat tgg gtg gtc ctt gca ggt ttt cag tgg ttg gac aaa	163
Ala Ala Gly Asp Trp Val Val Leu Ala Gly Phe Gln Trp Leu Asp Lys	
10 15 20	

atc gac tat gtg atc gat tgc ttt aaa ccg gaa aat att gtg ctg gaa	211
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Ile	Asp	Tyr	Val	Ile	Asp	Cys	Phe	Lys	Pro	Glu	Asn	Ile	Val	Leu	Glu		
			25					30					35				
ttc	ggt	tca	acc	atg	aca	ccg	gaa	gac	gcc	gac	cgc	aat	gaa	tac	ctc	259	
Phe	Gly	Ser	Thr	Met	Thr	Pro	Glu	Asp	Ala	Asp	Arg	Asn	Glu	Tyr	Leu		
		40					45					50					
aga	aga	acg	caa	gcc	aaa	ttc	cag	ctt	cga	ggc	atc	cta	agc	acc	aac	307	
Arg	Arg	Thr	Gln	Ala	Lys	Phe	Gln	Leu	Arg	Gly	Ile	Leu	Ser	Thr	Asn		
		55				60					65						
cca	gaa	tcc	gct	gcc	cgg	ggg	agc	gtg	cgg	ctt	gcc	ggc	gcc	aag	cag	355	
Pro	Glu	Ser	Ala	Ala	Arg	Gly	Ser	Val	Arg	Leu	Ala	Gly	Ala	Lys	Gln		
	70				75				80						85		
gca	cta	gcc	cgc	aag	atg	ccg	ctt	gcc	gac	gcc	gaa	agc	gag	cta	cat	403	
Ala	Leu	Ala	Arg	Lys	Met	Pro	Leu	Ala	Asp	Ala	Glu	Ser	Glu	Leu	His		
				90					95					100			
ccc	atg	ggc	act	acc	tgg	atg	cgc	agc	ggg	gat	aca	ttg	tta	aaa	gca	451	
Pro	Met	Gly	Thr	Thr	Trp	Met	Arg	Ser	Gly	Asp	Thr	Leu	Leu	Lys	Ala		
			105					110					115				
cac	cct	gat	tac	gcg	gat	ctc	att	gca	acc	acg	gtg	gaa	tta	gct	gct	499	
His	Pro	Asp	Tyr	Ala	Asp	Leu	Ile	Ala	Thr	Thr	Val	Glu	Leu	Ala	Ala		
		120					125					130					
gaa	tgt	gct	ttc	acc	cta	gat	ttg	gtg	gcc	ccg	aat	ctg	ccc	aag	tgg	547	
Glu	Cys	Ala	Phe	Thr	Leu	Asp	Leu	Val	Ala	Pro	Asn	Leu	Pro	Lys	Trp		
	135					140					145						
gat	acc	cct	ggt	gaa	cac	acg	gaa	atg	tcc	tgg	ctt	gcg	cac	ctg	gtt	595	
Asp	Thr	Pro	Gly	Glu	His	Thr	Glu	Met	Ser	Trp	Leu	Ala	His	Leu	Val		
	150				155					160					165		
tcc	act	cgg	att	gat	acc	cgc	tat	gtg	ggg	cgc	tcc	gca	gac	atc	aaa	643	
Ser	Thr	Arg	Ile	Asp	Thr	Arg	Tyr	Val	Gly	Arg	Ser	Ala	Asp	Ile	Lys		
			170						175					180			
gca	cga	gct	gcc	aca	caa	att	gac	tat	gaa	tta	ggc	gtt	att	gaa	aag	691	
Ala	Arg	Ala	Ala	Thr	Gln	Ile	Asp	Tyr	Glu	Leu	Gly	Val	Ile	Glu	Lys		
			185					190					195				
ctg	ggt	ttt	cca	ggc	tat	ttc	ctc	gtc	gtt	aat	gat	ctg	gtg	gag	ttt	739	
Leu	Gly	Phe	Pro	Gly	Tyr	Phe	Leu	Val	Val	Asn	Asp	Leu	Val	Glu	Phe		
		200					205					210					
tgt	cgc	gat	tcc	aat	att	ttg	tgc	caa	ggc	aga	ggt	tcc	gcg	gcg	aac	787	
Cys	Arg	Asp	Ser	Asn	Ile	Leu	Cys	Gln	Gly	Arg	Gly	Ser	Ala	Ala	Asn		
	215					220					225						
tcg	gcg	gtg	tgc	ttt	gtc	cta	ggc	atc	acc	aac	gcg	gag	ccg	atc	tct	835	
Ser	Ala	Val	Cys	Phe	Val	Leu	Gly	Ile	Thr	Asn	Ala	Glu	Pro	Ile	Ser		
	230				235					240					245		
gct	gga	ttg	ttg	ttt	gaa	cgg	ttt	tta	tct	cct	gac	cgg	gat	ggt	cca	883	
Ala	Gly	Leu	Leu	Phe	Glu	Arg	Phe	Leu	Ser	Pro	Asp	Arg	Asp	Gly	Pro		
				250					255					260			
cca	gat	att	gac	att	gat	att	gaa	tcc	ggc	agg	cgc	gaa	gaa	gta	atc	931	
Pro	Asp	Ile	Asp	Ile	Asp	Ile	Glu	Ser	Gly	Arg	Arg	Glu	Glu	Val	Ile		

265	270	275	
caa tac gtg tat gaa aaa tac gga agg gat aac gca gct caa gta gcc Gln Tyr Val Tyr Glu Lys Tyr Gly Arg Asp Asn Ala Ala Gln Val Ala 280 285 290			979
aat gtc att acc tac cga aca aaa ggc gcg atg cgt gat gct gcc cgt Asn Val Ile Thr Tyr Arg Thr Lys Gly Ala Met Arg Asp Ala Ala Arg 295 300 305			1027
gca ctg ggt tac ccg caa ggt gct gcc gat gcc tgg gct aaa gga acc Ala Leu Gly Tyr Pro Gln Gly Ala Ala Asp Ala Trp Ala Lys Gly Thr 310 315 320 325			1075
tcg gaa cca ccc gat gat gtg ctg gaa tta gct gcg caa ttt aaa ggg Ser Glu Pro Pro Asp Asp Val Leu Glu Leu Ala Ala Gln Phe Lys Gly 330 335 340			1123
caa cca cgg cat ttg ggt att cac tcc ggt ggc atg gtc att tgc gat Gln Pro Arg His Leu Gly Ile His Ser Gly Gly Met Val Ile Cys Asp 345 350 355			1171
cgc ccc atc gcc gat gtg gtg cca gtg gaa tgg gct cgg atg gat aac Arg Pro Ile Ala Asp Val Val Pro Val Glu Trp Ala Arg Met Asp Asn 360 365 370			1219
cgc tcg gtt gtg caa tgg gat aaa gat gac tgt gcc acg gca ggc ttg Arg Ser Val Val Gln Trp Asp Lys Asp Asp Cys Ala Thr Ala Gly Leu 375 380 385			1267
gtc aaa ttc gac ctt ttg gga ttg ggc atg ttg gaa gcc atc cat cac Val Lys Phe Asp Leu Leu Gly Leu Gly Met Leu Glu Ala Ile His His 390 395 400 405			1315
atg ctg gat ctg gtg gca gaa cac cga ggt aaa aag atc aat ttg tgg Met Leu Asp Leu Val Ala Glu His Arg Gly Lys Lys Ile Asn Leu Trp 410 415 420			1363
gaa cta gat ctg gcg gaa ccg gag gtc tat gac atg ttg tgc aag gca Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp Met Leu Cys Lys Ala 425 430 435			1411
gat gcc gtg ggt gtg ttc cag gtg gaa tca cgt gcg cag tta tcc acg Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg Ala Gln Leu Ser Thr 440 445 450			1459
ctg cct cga ctc aag ccc cgc acc ttc ttt gac ctg gtc gtg gag gta Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp Leu Val Val Glu Val 455 460 465			1507
gct ctg att cgt cca ggt ccc atc caa ggc gga tcg gtg cac ccg tat Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly Ser Val His Pro Tyr 470 475 480 485			1555
ttg cgg cgc cgt gct ggt gaa gag gcc atc act tat gac cac ccc gtg Leu Arg Arg Arg Ala Gly Glu Glu Ala Ile Thr Tyr Asp His Pro Val 490 495 500			1603
ttg gaa aag tct ttg ggt aaa acc tta gga atc cca ctg ttt cag gaa Leu Glu Lys Ser Leu Gly Lys Thr Leu Gly Ile Pro Leu Phe Gln Glu 505 510 515			1651

cag ctc atg cag gta gct gtt gat gct gca ggt ttt agt ggt ggg gaa 1699
 Gln Leu Met Gln Val Ala Val Asp Ala Ala Gly Phe Ser Gly Gly Glu
 520 525 530
 gcg gat tcc ttg cgc aga gcg atg ggg tcg aaa cgc tca cct gaa cgc 1747
 Ala Asp Ser Leu Arg Arg Ala Met Gly Ser Lys Arg Ser Pro Glu Arg
 535 540 545
 atg gct gcg ttg cgc tcg cgg ttt ttc caa ggg ctg aaa gat acc aat 1795
 Met Ala Ala Leu Arg Ser Arg Phe Phe Gln Gly Leu Lys Asp Thr Asn
 550 555 560 565
 ggg att gtg ggg gag acc gcc gag aaa ctg tgg aac aaa att gtg gcc 1843
 Gly Ile Val Gly Glu Thr Ala Glu Lys Leu Trp Asn Lys Ile Val Ala
 570 575 580
 ttt gct gcc tac ggt ttt ccg gaa tcg cat tcg cag tcg ttt gcg tcc 1891
 Phe Ala Ala Tyr Gly Phe Pro Glu Ser His Ser Gln Ser Phe Ala Ser
 585 590 595
 ttg gtg tat ttc tcc gcg tgg ttt aaa tac cac tac ccg gct gaa ttc 1939
 Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His Tyr Pro Ala Glu Phe
 600 605 610
 tgc gtg gga tta ttg cgg gca caa ccc atg ggt ttc tat tca cca cag 1987
 Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly Phe Tyr Ser Pro Gln
 615 620 625
 tct ttg atc agt gat gcc aga cgc cac ggc gtg agt atc ctg ccg atc 2035
 Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val Ser Ile Leu Pro Ile
 630 635 640 645
 acg gtc aat gat tcc ggt gtg gag gcc 2062
 Thr Val Asn Asp Ser Gly Val Glu Ala
 650

<210> 176

<211> 654

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 176

Met Val Ala Glu His Ala Ala Gly Asp Trp Val Val Leu Ala Gly Phe
 1 5 10 15
 Gln Trp Leu Asp Lys Ile Asp Tyr Val Ile Asp Cys Phe Lys Pro Glu
 20 25 30
 Asn Ile Val Leu Glu Phe Gly Ser Thr Met Thr Pro Glu Asp Ala Asp
 35 40 45
 Arg Asn Glu Tyr Leu Arg Arg Thr Gln Ala Lys Phe Gln Leu Arg Gly
 50 55 60
 Ile Leu Ser Thr Asn Pro Glu Ser Ala Ala Arg Gly Ser Val Arg Leu
 65 70 75 80
 Ala Gly Ala Lys Gln Ala Leu Ala Arg Lys Met Pro Leu Ala Asp Ala
 85 90 95

Glu Ser Glu Leu His Pro Met Gly Thr Thr Trp Met Arg Ser Gly Asp
100 105 110

Thr Leu Leu Lys Ala His Pro Asp Tyr Ala Asp Leu Ile Ala Thr Thr
115 120 125

Val Glu Leu Ala Ala Glu Cys Ala Phe Thr Leu Asp Leu Val Ala Pro
130 135 140

Asn Leu Pro Lys Trp Asp Thr Pro Gly Glu His Thr Glu Met Ser Trp
145 150 155 160

Leu Ala His Leu Val Ser Thr Arg Ile Asp Thr Arg Tyr Val Gly Arg
165 170 175

Ser Ala Asp Ile Lys Ala Arg Ala Ala Thr Gln Ile Asp Tyr Glu Leu
180 185 190

Gly Val Ile Glu Lys Leu Gly Phe Pro Gly Tyr Phe Leu Val Val Asn
195 200 205

Asp Leu Val Glu Phe Cys Arg Asp Ser Asn Ile Leu Cys Gln Gly Arg
210 215 220

Gly Ser Ala Ala Asn Ser Ala Val Cys Phe Val Leu Gly Ile Thr Asn
225 230 235 240

Ala Glu Pro Ile Ser Ala Gly Leu Leu Phe Glu Arg Phe Leu Ser Pro
245 250 255

Asp Arg Asp Gly Pro Pro Asp Ile Asp Ile Asp Ile Glu Ser Gly Arg
260 265 270

Arg Glu Glu Val Ile Gln Tyr Val Tyr Glu Lys Tyr Gly Arg Asp Asn
275 280 285

Ala Ala Gln Val Ala Asn Val Ile Thr Tyr Arg Thr Lys Gly Ala Met
290 295 300

Arg Asp Ala Ala Arg Ala Leu Gly Tyr Pro Gln Gly Ala Ala Asp Ala
305 310 315 320

Trp Ala Lys Gly Thr Ser Glu Pro Pro Asp Asp Val Leu Glu Leu Ala
325 330 335

Ala Gln Phe Lys Gly Gln Pro Arg His Leu Gly Ile His Ser Gly Gly
340 345 350

Met Val Ile Cys Asp Arg Pro Ile Ala Asp Val Val Pro Val Glu Trp
355 360 365

Ala Arg Met Asp Asn Arg Ser Val Val Gln Trp Asp Lys Asp Asp Cys
370 375 380

Ala Thr Ala Gly Leu Val Lys Phe Asp Leu Leu Gly Leu Gly Met Leu
385 390 395 400

Glu Ala Ile His His Met Leu Asp Leu Val Ala Glu His Arg Gly Lys
405 410 415

Lys Ile Asn Leu Trp Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp
420 425 430

Met Leu Cys Lys Ala Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg
435 440 445

Ala Gln Leu Ser Thr Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp
450 455 460

Leu Val Val Glu Val Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly
465 470 475 480

Ser Val His Pro Tyr Leu Arg Arg Arg Ala Gly Glu Glu Ala Ile Thr
485 490 495

Tyr Asp His Pro Val Leu Glu Lys Ser Leu Gly Lys Thr Leu Gly Ile
500 505 510

Pro Leu Phe Gln Glu Gln Leu Met Gln Val Ala Val Asp Ala Ala Gly
515 520 525

Phe Ser Gly Gly Glu Ala Asp Ser Leu Arg Arg Ala Met Gly Ser Lys
530 535 540

Arg Ser Pro Glu Arg Met Ala Ala Leu Arg Ser Arg Phe Phe Gln Gly
545 550 555 560

Leu Lys Asp Thr Asn Gly Ile Val Gly Glu Thr Ala Glu Lys Leu Trp
565 570 575

Asn Lys Ile Val Ala Phe Ala Ala Tyr Gly Phe Pro Glu Ser His Ser
580 585 590

Gln Ser Phe Ala Ser Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His
595 600 605

Tyr Pro Ala Glu Phe Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly
610 615 620

Phe Tyr Ser Pro Gln Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val
625 630 635 640

Ser Ile Leu Pro Ile Thr Val Asn Asp Ser Gly Val Glu Ala
645 650

<210> 177

<211> 477

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(454)

<223> RXN00414

<400> 177

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ggtgctgcat gagccggatg cgcaggcgcc ttcattctgcc atg cag ggg gaa gcg 115
Met Gln Gly Glu Ala

	1	5	
tcg gtt cct ttt gcc gag ctg cat gcc acc agc agt tat aac ttt ctc			163
Ser Val Pro Phe Ala Glu Leu His Ala Thr Ser Ser Tyr Asn Phe Leu			
	10	20	
act ggc gca tcg gat ccg tct gat gtg gtt gtg cag gcc aaa aag tta			211
Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val Gln Ala Lys Lys Leu			
	25	35	
gga ctt gct gct cta tca gtc atg gat agg gat ggt ttt tat ggt gca			259
Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp Gly Phe Tyr Gly Ala			
	40	50	
gtg aga ttt gcg gaa gct gcc gcg gaa gct gga atg cat acc gtt tat			307
Val Arg Phe Ala Glu Ala Ala Glu Ala Gly Met His Thr Val Tyr			
	55	65	
ggt gcg gag ctg agt ctg caa gaa ggc gtg ttg aca gtc ttg tgt aaa			355
Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu Thr Val Leu Cys Lys			
	70	80	85
aat ccg gaa ggc tac aaa aag ctc agt cac ctg atc agt gac gcg aaa			403
Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu Ile Ser Asp Ala Lys			
	90	95	100
atg gca cgg gag aaa agg gga agt tcg cta tcc gcc gct gcc aat ggt			451
Met Ala Arg Glu Lys Arg Gly Ser Ser Leu Ser Ala Ala Ala Asn Gly			
	105	110	115
tgc tgaacatgct gcaggggatt ggg			477
Cys			

<210> 178

<211> 118

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Met Gln Gly Glu Ala Ser Val Pro Phe Ala Glu Leu His Ala Thr Ser			
1	5	10	15
Ser Tyr Asn Phe Leu Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val			
	20	25	30
Gln Ala Lys Lys Leu Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp			
	35	40	45
Gly Phe Tyr Gly Ala Val Arg Phe Ala Glu Ala Ala Ala Glu Ala Gly			
	50	55	60
Met His Thr Val Tyr Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu			
	65	70	75
Thr Val Leu Cys Lys Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu			
	85	90	95
Ile Ser Asp Ala Lys Met Ala Arg Glu Lys Arg Gly Ser Ser Leu Ser			
	100	105	110

Ala Ala Ala Asn Gly Cys
115

<210> 179

<211> 543

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(520)

<223> FRXA00414

<400> 179

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ggtgctgcat gagccggatg cgcaggcgcc ttcattctgcc atg cag ggg gaa gcg 115
Met Gln Gly Glu Ala
1 5

tcg gtt cct ttt gcc gag ctg cat gcc acc agc agt tat aac ttt ctc 163
Ser Val Pro Phe Ala Glu Leu His Ala Thr Ser Ser Tyr Asn Phe Leu
10 15 20

act ggc gca tcg gat ccg tct gat gtg gtt gtg cag gcc aaa aag tta 211
Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val Gln Ala Lys Lys Leu
25 30 35

gga ctt gct gct cta tca gtc atg gat agg gat ggt ttt tat ggt gca 259
Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp Gly Phe Tyr Gly Ala
40 45 50

gtg aga ttt gcg gaa gct gcc gcg gaa gct gga atg cat acc gtt tat 307
Val Arg Phe Ala Glu Ala Ala Ala Glu Ala Gly Met His Thr Val Tyr
55 60 65

ggt gcg gag ctg agt ctg caa gaa ggc gtg ttg aca gtc ttg tgt aaa 355
Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu Thr Val Leu Cys Lys
70 75 80 85

aat ccg gaa ggc tac aaa aag ctc agt cac ctg atc agt gac gcg aaa 403
Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu Ile Ser Asp Ala Lys
90 95 100

atg gca cgg gga gaa aag ggg aag ttc gct atc cgc cgc tgc caa tgg 451
Met Ala Arg Gly Glu Lys Gly Lys Phe Ala Ile Arg Arg Cys Gln Trp
105 110 115

ttg ctg aac atg ctg cag ggg att ggg tgg tcc ttg cag gtt ttc agt 499
Leu Leu Asn Met Leu Gln Gly Ile Gly Trp Ser Leu Gln Val Phe Ser
120 125 130

ggt tgg aca aaa tcg act atg tgatcgattg ctttaaaccg gaa 543
Gly Trp Thr Lys Ser Thr Met
135 140

<210> 180

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

Met Gln Gly Glu Ala Ser Val Pro Phe Ala Glu Leu His Ala Thr Ser
 1 5 10 15

Ser Tyr Asn Phe Leu Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val
 20 25 30

Gln Ala Lys Lys Leu Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp
 35 40 45

Gly Phe Tyr Gly Ala Val Arg Phe Ala Glu Ala Ala Ala Glu Ala Gly
 50 55 60

Met His Thr Val Tyr Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu
 65 70 75 80

Thr Val Leu Cys Lys Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu
 85 90 95

Ile Ser Asp Ala Lys Met Ala Arg Gly Glu Lys Gly Lys Phe Ala Ile
 100 105 110

Arg Arg Cys Gln Trp Leu Leu Asn Met Leu Gln Gly Ile Gly Trp Ser
 115 120 125

Leu Gln Val Phe Ser Gly Trp Thr Lys Ser Thr Met
 130 135 140

<210> 181

<211> 1365

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1342)

<223> RXN00807

<400> 181

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gtagtgagga agtagtntag agatcgtgac taattcgagt gtg ttt gac agt ctc 115
 Val Phe Asp Ser Leu
 1 5

gcc ggc tcc aaa aca gtg tcc aag acg ctt ttc gac gcg gcc tcc agc 163
 Ala Gly Ser Lys Thr Val Ser Lys Thr Leu Phe Asp Ala Ala Ser Ser
 10 15 20

gcg cgt gcc ctt gtc cgc gcc cga acc aca gaa cgt gcc cgc gcc cgg 211
 Ala Arg Ala Leu Val Arg Ala Arg Thr Thr Glu Arg Ala Arg Ala Arg
 25 30 35

gca gaa cac caa aac cct gca atg atc cac gac tcc ggc ttt gcc cag 259
 Ala Glu His Gln Asn Pro Ala Met Ile His Asp Ser Gly Phe Ala Gln
 40 45 50

tca tgg ctg ttt aca ggc cct ccc gga tcg gga cgt tct gtg gca gcc	307
Ser Trp Leu Phe Thr Gly Pro Pro Gly Ser Gly Arg Ser Val Ala Ala	
55 60 65	
aag gtt ttc gcc gct acg ctc gta tgt tcg aat ccg gat gtt gtg ggc	355
Lys Val Phe Ala Ala Thr Leu Val Cys Ser Asn Pro Asp Val Val Gly	
70 75 80 85	
tgt gga caa tgc gag gat tgc cgc gcc gcc atg gga ggc agc cac ccc	403
Cys Gly Gln Cys Glu Asp Cys Arg Ala Ala Met Gly Gly Ser His Pro	
90 95 100	
gat att gaa cac atc gtc ccg cag caa ttg tct atc ggt gtt gat gca	451
Asp Ile Glu His Ile Val Pro Gln Gln Leu Ser Ile Gly Val Asp Ala	
105 110 115	
gct aga gag gtc atc aaa gcc gca gcg gtc agt cct gtt gca gga aac	499
Ala Arg Glu Val Ile Lys Ala Ala Val Ser Pro Val Ala Gly Asn	
120 125 130	
tgg cga gtc gtc atc ttc gaa aac gcc gac cga ctc acc atg caa gcc	547
Trp Arg Val Val Ile Phe Glu Asn Ala Asp Arg Leu Thr Met Gln Ala	
135 140 145	
gcc aac gcc ttg ctg aaa acc gtg gag gaa cca acc gaa agc acc gtg	595
Ala Asn Ala Leu Leu Lys Thr Val Glu Glu Pro Thr Glu Ser Thr Val	
150 155 160 165	
atg att ctg tgc gca ccc acc aca gac ccc cgc gac att gcg atc acc	643
Met Ile Leu Cys Ala Pro Thr Thr Asp Pro Arg Asp Ile Ala Ile Thr	
170 175 180	
ctc cgc tcc cgc tgc agg cac ctc tac att ccc acc ccc tcc atc gcg	691
Leu Arg Ser Arg Cys Arg His Leu Tyr Ile Pro Thr Pro Ser Ile Ala	
185 190 195	
gaa gtc gca cga atc ctc gta gct gaa ggc aac gtc agc caa gcg gat	739
Glu Val Ala Arg Ile Leu Val Ala Glu Gly Asn Val Ser Gln Ala Asp	
200 205 210	
gca gaa tta gcg gcg gct gcc tca ggc gct cac atc ggc agg gct cga	787
Ala Glu Leu Ala Ala Ala Ala Ser Gly Ala His Ile Gly Arg Ala Arg	
215 220 225	
tac tta gcg cac aac aac gcc gcc caa cgc aga cgc gcc agc atc ctc	835
Tyr Leu Ala His Asn Asn Ala Ala Gln Arg Arg Arg Ala Ser Ile Leu	
230 235 240 245	
aac ctg gcc gaa tta atc ttc cac ggt gat gtc gcc ttc cgc tcc gta	883
Asn Leu Ala Glu Leu Ile Phe His Gly Asp Val Ala Phe Arg Ser Val	
250 255 260	
aac acc ttg gtc aaa atg gtg gaa acc gaa gcc aaa gac agc aac aaa	931
Asn Thr Leu Val Lys Met Val Glu Thr Glu Ala Lys Asp Ser Asn Lys	
265 270 275	
gaa aaa gaa gaa ggc gat ctc gaa gcc gta aga atc tca ctc ggc atg	979
Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg Ile Ser Leu Gly Met	
280 285 290	
ggg gcc aaa ggc aaa ggt gtc cac aaa gca gta cgt gga gga gcg gga	1027

Gly Ala Lys Gly Lys Gly Val His Lys Ala Val Arg Gly Gly Ala Gly
 295 300 305
 gat ttc aaa gca ctc gaa gac caa caa aaa ctc cga cgc acc cga ttc 1075
 Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu Arg Arg Thr Arg Phe
 310 315 320 325
 ctc cgc gac agc ctc gac ctc gca ctc gtc gac cta gcc ggc atc tac 1123
 Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp Leu Ala Gly Ile Tyr
 330 335 340
 cgc gat gcc atc atc att tcc tcc caa gcc caa gtc gga ctc aca cac 1171
 Arg Asp Ala Ile Ile Ile Ser Ser Gln Ala Gln Val Gly Leu Thr His
 345 350 355
 ccc gat atg gaa ggc ctc tcc caa gaa ctc gca aca aaa gta agc caa 1219
 Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala Thr Lys Val Ser Gln
 360 365 370
 gaa gga ctc ctg gca tgc ctc gac gcg atc tcc aaa tgc cgc gaa tcc 1267
 Glu Gly Leu Leu Ala Cys Leu Asp Ala Ile Ser Lys Cys Arg Glu Ser
 375 380 385
 ttc ggc ttc aat gta cga ccc atc gtg gcc atg gac gcc ctg gta gga 1315
 Phe Gly Phe Asn Val Arg Pro Ile Val Ala Met Asp Ala Leu Val Gly
 390 395 400 405
 cgc ctg cgc aaa gcc tac aaa gtg tcc taaacacccc aaattattga 1362
 Arg Leu Arg Lys Ala Tyr Lys Val Ser
 410
 agt 1365
 <210> 182
 <211> 414
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 182
 Val Phe Asp Ser Leu Ala Gly Ser Lys Thr Val Ser Lys Thr Leu Phe
 1 5 10 15
 Asp Ala Ala Ser Ser Ala Arg Ala Leu Val Arg Ala Arg Thr Thr Glu
 20 25 30
 Arg Ala Arg Ala Arg Ala Glu His Gln Asn Pro Ala Met Ile His Asp
 35 40 45
 Ser Gly Phe Ala Gln Ser Trp Leu Phe Thr Gly Pro Pro Gly Ser Gly
 50 55 60
 Arg Ser Val Ala Ala Lys Val Phe Ala Ala Thr Leu Val Cys Ser Asn
 65 70 75 80
 Pro Asp Val Val Gly Cys Gly Gln Cys Glu Asp Cys Arg Ala Ala Met
 85 90 95
 Gly Gly Ser His Pro Asp Ile Glu His Ile Val Pro Gln Gln Leu Ser
 100 105 110

Ile Gly Val Asp Ala Ala Arg Glu Val Ile Lys Ala Ala Ala Val Ser
115 120 125

Pro Val Ala Gly Asn Trp Arg Val Val Ile Phe Glu Asn Ala Asp Arg
130 135 140

Leu Thr Met Gln Ala Ala Asn Ala Leu Leu Lys Thr Val Glu Glu Pro
145 150 155 160

Thr Glu Ser Thr Val Met Ile Leu Cys Ala Pro Thr Thr Asp Pro Arg
165 170 175

Asp Ile Ala Ile Thr Leu Arg Ser Arg Cys Arg His Leu Tyr Ile Pro
180 185 190

Thr Pro Ser Ile Ala Glu Val Ala Arg Ile Leu Val Ala Glu Gly Asn
195 200 205

Val Ser Gln Ala Asp Ala Glu Leu Ala Ala Ala Ser Gly Ala His
210 215 220

Ile Gly Arg Ala Arg Tyr Leu Ala His Asn Asn Ala Ala Gln Arg Arg
225 230 235 240

Arg Ala Ser Ile Leu Asn Leu Ala Glu Leu Ile Phe His Gly Asp Val
245 250 255

Ala Phe Arg Ser Val Asn Thr Leu Val Lys Met Val Glu Thr Glu Ala
260 265 270

Lys Asp Ser Asn Lys Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg
275 280 285

Ile Ser Leu Gly Met Gly Ala Lys Gly Lys Gly Val His Lys Ala Val
290 295 300

Arg Gly Gly Ala Gly Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu
305 310 315 320

Arg Arg Thr Arg Phe Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp
325 330 335

Leu Ala Gly Ile Tyr Arg Asp Ala Ile Ile Ile Ser Ser Gln Ala Gln
340 345 350

Val Gly Leu Thr His Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala
355 360 365

Thr Lys Val Ser Gln Glu Gly Leu Leu Ala Cys Leu Asp Ala Ile Ser
370 375 380

Lys Cys Arg Glu Ser Phe Gly Phe Asn Val Arg Pro Ile Val Ala Met
385 390 395 400

Asp Ala Leu Val Gly Arg Leu Arg Lys Ala Tyr Lys Val Ser
405 410

<210> 183
<211> 1242
<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1219)

<223> FRXA00807

<400> 183

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gtagtgagga agtagtgtag agatcgtgac taattcgagt  gtg ttt gac agt ctc 115
                                         Val Phe Asp Ser Leu
                                         1                               5

gcc ggc tcc aaa aca gtg tcc aag acg ctt ttc gac gcg gcc tcc agc 163
Ala Gly Ser Lys Thr Val Ser Lys Thr Leu Phe Asp Ala Ala Ser Ser
                               10                               15                               20

gcg cgt gcc ctt gtc cgc gcc cga acc aca gaa cgt gcc cgc gcc cgg 211
Ala Arg Ala Leu Val Arg Ala Arg Thr Thr Glu Arg Ala Arg Ala Arg
                               25                               30                               35

gca gaa cac caa aac cct gca atg atc cac gac tcc ggc ttt gcc cag 259
Ala Glu His Gln Asn Pro Ala Met Ile His Asp Ser Gly Phe Ala Gln
                               40                               45                               50

tca tgg ctg ttt aca ggc cct ccc gga tgc gga cgt tct gtg gca gcc 307
Ser Trp Leu Phe Thr Gly Pro Pro Gly Ser Gly Arg Ser Val Ala Ala
                               55                               60                               65

aag gtt ttc gcc gct acg ctc gta tgt tgc aat ccg gat gtt gtg ggc 355
Lys Val Phe Ala Ala Thr Leu Val Cys Ser Asn Pro Asp Val Val Gly
                               70                               75                               80                               85

tgt gga caa tgc gag gat tgc cgc gcc gcc atg gga ggc agc cac ccc 403
Cys Gly Gln Cys Glu Asp Cys Arg Ala Ala Met Gly Gly Ser His Pro
                               90                               95                               100

gat att gaa cac atc gtc ccg cag caa ttg tct atc ggt gtt gat gca 451
Asp Ile Glu His Ile Val Pro Gln Gln Leu Ser Ile Gly Val Asp Ala
                               105                               110                               115

gct aga gag gtc atc aaa gcc gca gcg gtc agt cct gtt gca gga aac 499
Ala Arg Glu Val Ile Lys Ala Ala Val Ser Pro Val Ala Gly Asn
                               120                               125                               130

tgg cga gtc gtc atc ttc gaa aac gcc gac cga ctc acc atg caa gcc 547
Trp Arg Val Val Ile Phe Glu Asn Ala Asp Arg Leu Thr Met Gln Ala
                               135                               140                               145

gcc aac gcc ttg ctg aaa acc gtg gag gaa cca acc gaa agc acc gtg 595
Ala Asn Ala Leu Leu Lys Thr Val Glu Glu Pro Thr Glu Ser Thr Val
                               150                               155                               160                               165

atg att ctg tgc gca ccc acc aca gac ccc cgc gac att gcg atc acc 643
Met Ile Leu Cys Ala Pro Thr Thr Asp Pro Arg Asp Ile Ala Ile Thr
                               170                               175                               180

ctc cgc tcc cgc tgc agg cac ctc tac att ccc acc ccc tcc atc gcg 691
Leu Arg Ser Arg Cys Arg His Leu Tyr Ile Pro Thr Pro Ser Ile Ala
                               185                               190                               195

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gaa gtc gca cga atc ctc gta gct gaa ggc aac gtc agc caa gcg gat 739
 Glu Val Ala Arg Ile Leu Val Ala Glu Gly Asn Val Ser Gln Ala Asp
 200 205 210

gca gaa tta gcg gcg gct gcc tca ggc gct cac atc ggc agg gct cga 787
 Ala Glu Leu Ala Ala Ala Ser Gly Ala His Ile Gly Arg Ala Arg
 215 220 225

tac tta gcg cac aac aac gcc gcc caa cgc aga cgc gcc agc atc ctc 835
 Tyr Leu Ala His Asn Asn Ala Ala Gln Arg Arg Arg Ala Ser Ile Leu
 230 235 240 245

aac ctg gcc gaa tta atc ttc cac ggt gat gtc gcc ttc cgc tcc gta 883
 Asn Leu Ala Glu Leu Ile Phe His Gly Asp Val Ala Phe Arg Ser Val
 250 255 260

aac acc ttg gtc aaa atg gtg gaa acc gaa gcc aaa gac agc aac aaa 931
 Asn Thr Leu Val Lys Met Val Glu Thr Glu Ala Lys Asp Ser Asn Lys
 265 270 275

gaa aaa gaa gaa ggc gat ctc gaa gcc gta aga atc tca ctc ggc atg 979
 Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg Ile Ser Leu Gly Met
 280 285 290

gcg gcc aaa ggc aaa ggt gtc cac aaa gca gta cgt gga gga gcg gga 1027
 Ala Ala Lys Gly Lys Gly Val His Lys Ala Val Arg Gly Gly Ala Gly
 295 300 305

gat ttc aaa gca ctc gaa gac caa caa aaa ctc cga cgc acc cga ttc 1075
 Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu Arg Arg Thr Arg Phe
 310 315 320 325

ctc cgc gac agc ctc gac ctc gca ctc gtc gac cta gcc ggc atc tac 1123
 Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp Leu Ala Gly Ile Tyr
 330 335 340

cgc gat gcc atc atc att tcc tcc caa gcc caa gtc gga ctc aca cac 1171
 Arg Asp Ala Ile Ile Ile Ser Ser Gln Ala Gln Val Gly Leu Thr His
 345 350 355

ccc gat atg gaa ggc ctc tcc caa gaa ctc gca aca aaa gta agc caa 1219
 Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala Thr Lys Val Ser Gln
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taagcactcc tggcatgcct cca 1242

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<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 184

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Arg Ala Arg Ala Arg Ala Glu His Gln Asn Pro Ala Met Ile His Asp

35					40					45					
Ser	Gly	Phe	Ala	Gln	Ser	Trp	Leu	Phe	Thr	Gly	Pro	Pro	Gly	Ser	Gly
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Arg	Ser	Val	Ala	Ala	Lys	Val	Phe	Ala	Ala	Thr	Leu	Val	Cys	Ser	Asn
65					70					75					80
Pro	Asp	Val	Val	Gly	Cys	Gly	Gln	Cys	Glu	Asp	Cys	Arg	Ala	Ala	Met
				85					90					95	
Gly	Gly	Ser	His	Pro	Asp	Ile	Glu	His	Ile	Val	Pro	Gln	Gln	Leu	Ser
			100					105					110		
Ile	Gly	Val	Asp	Ala	Ala	Arg	Glu	Val	Ile	Lys	Ala	Ala	Ala	Val	Ser
		115					120					125			
Pro	Val	Ala	Gly	Asn	Trp	Arg	Val	Val	Ile	Phe	Glu	Asn	Ala	Asp	Arg
		130				135					140				
Leu	Thr	Met	Gln	Ala	Ala	Asn	Ala	Leu	Leu	Lys	Thr	Val	Glu	Glu	Pro
145					150					155					160
Thr	Glu	Ser	Thr	Val	Met	Ile	Leu	Cys	Ala	Pro	Thr	Thr	Asp	Pro	Arg
				165					170					175	
Asp	Ile	Ala	Ile	Thr	Leu	Arg	Ser	Arg	Cys	Arg	His	Leu	Tyr	Ile	Pro
			180					185					190		
Thr	Pro	Ser	Ile	Ala	Glu	Val	Ala	Arg	Ile	Leu	Val	Ala	Glu	Gly	Asn
		195					200					205			
Val	Ser	Gln	Ala	Asp	Ala	Glu	Leu	Ala	Ala	Ala	Ala	Ser	Gly	Ala	His
		210				215					220				
Ile	Gly	Arg	Ala	Arg	Tyr	Leu	Ala	His	Asn	Asn	Ala	Ala	Gln	Arg	Arg
225					230					235					240
Arg	Ala	Ser	Ile	Leu	Asn	Leu	Ala	Glu	Leu	Ile	Phe	His	Gly	Asp	Val
				245					250					255	
Ala	Phe	Arg	Ser	Val	Asn	Thr	Leu	Val	Lys	Met	Val	Glu	Thr	Glu	Ala
			260					265					270		
Lys	Asp	Ser	Asn	Lys	Glu	Lys	Glu	Glu	Gly	Asp	Leu	Glu	Ala	Val	Arg
		275					280					285			
Ile	Ser	Leu	Gly	Met	Ala	Ala	Lys	Gly	Lys	Gly	Val	His	Lys	Ala	Val
		290					295					300			
Arg	Gly	Gly	Ala	Gly	Asp	Phe	Lys	Ala	Leu	Glu	Asp	Gln	Gln	Lys	Leu
305					310					315					320
Arg	Arg	Thr	Arg	Phe	Leu	Arg	Asp	Ser	Leu	Asp	Leu	Ala	Leu	Val	Asp
				325					330					335	
Leu	Ala	Gly	Ile	Tyr	Arg	Asp	Ala	Ile	Ile	Ile	Ser	Ser	Gln	Ala	Gln
			340					345					350		
Val	Gly	Leu	Thr	His	Pro	Asp	Met	Glu	Gly	Leu	Ser	Gln	Glu	Leu	Ala
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Thr Lys Val Ser Gln
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<211> 834

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(811)

<223> RXA00214

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Met Asn Ser Pro Ser
1 5

aat cca tct ccc acc gtc cca agc ttg gac acc acc aag atg ctc tcc 163
Asn Pro Ser Pro Thr Val Pro Ser Leu Asp Thr Thr Lys Met Leu Ser
10 15 20

ttc gac ctg gaa aca acg ggc gtc aat ccc ttt gac acc cgc atc gtc 211
Phe Asp Leu Glu Thr Thr Gly Val Asn Pro Phe Asp Thr Arg Ile Val
25 30 35

acc tcc gca atg gtt acg atc acc agc aaa ggc gct gag cct att gag 259
Thr Ser Ala Met Val Thr Ile Thr Ser Lys Gly Ala Glu Pro Ile Glu
40 45 50

cta ttg gct gac ccc ggc atc gaa atc ccc gag gcc gcc act gca gtc 307
Leu Leu Ala Asp Pro Gly Ile Glu Ile Pro Glu Ala Ala Thr Ala Val
55 60 65

cac ggc atc acc acc gaa cat gcc cgc gcc aac ggc cgt ccg cac gat 355
His Gly Ile Thr Thr Glu His Ala Arg Ala Asn Gly Arg Pro His Asp
70 75 80 85

gag gtg tta gcc gaa acc atc tcc agg ctg cgc gcc ggc tgg cag gca 403
Glu Val Leu Ala Glu Thr Ile Ser Arg Leu Arg Ala Gly Trp Gln Ala
90 95 100

gga ctg tcg gtc att gtc ttc aac gca tcc tat gac ctg acc gta tta 451
Gly Leu Ser Val Ile Val Phe Asn Ala Ser Tyr Asp Leu Thr Val Leu
105 110 115

aga aac cat gat cca agc ttc acc atc gac ggc cta gtt tat gac ccc 499
Arg Asn His Asp Pro Ser Phe Thr Ile Asp Gly Leu Val Tyr Asp Pro
120 125 130

ttc gtt atc gac aaa gtc aaa gac cgt tac cgc aaa ggc aag cgc aca 547
Phe Val Ile Asp Lys Val Lys Asp Arg Tyr Arg Lys Gly Lys Arg Thr
135 140 145

ctc act gat atg tgt gct cac tac gac gtt caa tta ggc aac gcc cac 595
Leu Thr Asp Met Cys Ala His Tyr Asp Val Gln Leu Gly Asn Ala His
150 155 160 165

gaa gcc acc tca gat gcg ctc gca gcc gca cgc atc gcc tgg aag cag 643
Glu Ala Thr Ser Asp Ala Leu Ala Ala Ala Arg Ile Ala Trp Lys Gln
170 175 180

gtc cgc ctg tgg cca gaa ctc acc aag atg aca ggc gaa gaa ctc atg 691
Val Arg Leu Trp Pro Glu Leu Thr Lys Met Thr Gly Glu Glu Leu Met
185 190 195

gag ttc caa gca gtc aac tat tac gag caa caa aag agc ttc cgt agc 739
Glu Phe Gln Ala Val Asn Tyr Tyr Glu Gln Gln Lys Ser Phe Arg Ser
200 205 210

tat ctc atc ggg caa ggc cgc gat gcc agc gat gtg aac act tca tgg 787
Tyr Leu Ile Gly Gln Gly Arg Asp Ala Ser Asp Val Asn Thr Ser Trp
215 220 225

cca gtg caa act gac ccc gca tcc taaaccgcgc cagatttcta cct 834
Pro Val Gln Thr Asp Pro Ala Ser
230 235

<210> 186
<211> 237
<212> PRT
<213> Corynebacterium glutamicum

<400> 186
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35 40 45
Ala Glu Pro Ile Glu Leu Leu Ala Asp Pro Gly Ile Glu Ile Pro Glu
50 55 60
Ala Ala Thr Ala Val His Gly Ile Thr Thr Glu His Ala Arg Ala Asn
65 70 75 80
Gly Arg Pro His Asp Glu Val Leu Ala Glu Thr Ile Ser Arg Leu Arg
85 90 95
Ala Gly Trp Gln Ala Gly Leu Ser Val Ile Val Phe Asn Ala Ser Tyr
100 105 110
Asp Leu Thr Val Leu Arg Asn His Asp Pro Ser Phe Thr Ile Asp Gly
115 120 125
Leu Val Tyr Asp Pro Phe Val Ile Asp Lys Val Lys Asp Arg Tyr Arg
130 135 140
Lys Gly Lys Arg Thr Leu Thr Asp Met Cys Ala His Tyr Asp Val Gln
145 150 155 160
Leu Gly Asn Ala His Glu Ala Thr Ser Asp Ala Leu Ala Ala Ala Arg
165 170 175

Ile Ala Trp Lys Gln Val Arg Leu Trp Pro Glu Leu Thr Lys Met Thr
 180 185 190

Gly Glu Glu Leu Met Glu Phe Gln Ala Val Asn Tyr Tyr Glu Gln Gln
 195 200 205

Lys Ser Phe Arg Ser Tyr Leu Ile Gly Gln Gly Arg Asp Ala Ser Asp
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Val Asn Thr Ser Trp Pro Val Gln Thr Asp Pro Ala Ser
 225 230 235

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 <222> (101)..(1180)
 <223> RXA01255

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 Met Ser Thr Thr Ser
 1 5

gaa tca caa gat cac gcc gca aga atc gaa gct gag cgc caa gaa gct 163
 Glu Ser Gln Asp His Ala Ala Arg Ile Glu Ala Glu Arg Gln Glu Ala
 10 15 20

att gag gcg gct cct ttt gtt tcc gtc agc att caa tca agt gga atc 211
 Ile Glu Ala Ala Pro Phe Val Ser Val Ser Ile Gln Ser Ser Gly Ile
 25 30 35

cac cca tcg act tca cgc atg gtc acc att gat ttg gta acg ctg tcc 259
 His Pro Ser Thr Ser Arg Met Val Thr Ile Asp Leu Val Thr Leu Ser
 40 45 50

cct aat ttg gag ccg gtg gaa act ttt cat gcc gtg ttg gat tcc aaa 307
 Pro Asn Leu Glu Pro Val Glu Thr Phe His Ala Val Leu Asp Ser Lys
 55 60 65

act gat cct ggc ccc ttc cac ctt cat ggc gtg aca gag gaa gaa ttt 355
 Thr Asp Pro Gly Pro Phe His Leu His Gly Val Thr Glu Glu Glu Phe
 70 75 80 85

gcc agc gct aag cgt ttc ggc cag att ttg aaa agc ttg gac cgc ctc 403
 Ala Ser Ala Lys Arg Phe Gly Gln Ile Leu Lys Ser Leu Asp Arg Leu
 90 95 100

atc gat ggt cgt acc ctg ttg atc cac aat gct gcg cga agt tgg ggc 451
 Ile Asp Gly Arg Thr Leu Leu Ile His Asn Ala Ala Arg Ser Trp Gly
 105 110 115

ttt att gtt tcc gaa gcc aag cgc gct atg aat gat gct gcg cgc gcc 499
 Phe Ile Val Ser Glu Ala Lys Arg Ala Met Asn Asp Ala Ala Arg Ala
 120 125 130

aat cgc aac agc aat cgt gga aat cgc cgt ggt ggt cgc gga cgc cgc	547
Asn Arg Asn Ser Asn Arg Gly Asn Arg Arg Gly Gly Arg Gly Arg Arg	
135 140 145	
agg cag cgc gtg ggg cac atc cca aag ccg ctg gtg atc gtc gat acg	595
Arg Gln Arg Val Gly His Ile Pro Lys Pro Leu Val Ile Val Asp Thr	
150 155 160 165	
ctt gca tcg gcg cgt cga caa gca atc gct tta gac gac gtg cgc atc	643
Leu Ala Ser Ala Arg Arg Gln Ala Ile Ala Leu Asp Asp Val Arg Ile	
170 175 180	
cgg ggt gtc gca cac acc ctc ggc ctt gac gcg cct gca gcg gag gcg	691
Arg Gly Val Ala His Thr Leu Gly Leu Asp Ala Pro Ala Ala Glu Ala	
185 190 195	
tcg gtg gaa cgc gcg cag gtg tcg cac cgc cag ttg tgc cgc gaa gaa	739
Ser Val Glu Arg Ala Gln Val Ser His Arg Gln Leu Cys Arg Glu Glu	
200 205 210	
act ttg ctt gtg gca cgg ctt tat ggt gcg ttg aag cag tca gga ccg	787
Thr Leu Leu Val Ala Arg Leu Tyr Gly Ala Leu Lys Gln Ser Gly Pro	
215 220 225	
ctg gcg gaa atc gat ccc cag tcc ttg cgc gcc gat aag ttt ggt ttg	835
Leu Ala Glu Ile Asp Pro Gln Ser Leu Arg Ala Asp Lys Phe Gly Leu	
230 235 240 245	
caa cgc tcg atc atc cgg gtg cag gcg cag gaa gct tcg cca acg ctg	883
Gln Arg Ser Ile Ile Arg Val Gln Ala Gln Glu Ala Ser Pro Thr Leu	
250 255 260	
gtc aac cct ggt acg tat gag ccg gga aag acg ctg atc gct ggg atg	931
Val Asn Pro Gly Thr Tyr Glu Pro Gly Lys Thr Leu Ile Ala Gly Met	
265 270 275	
gaa gtt gtg gtc gcg ccg gaa att gag atg gat ccg gac atc att atc	979
Glu Val Val Val Ala Pro Glu Ile Glu Met Asp Pro Asp Ile Ile Ile	
280 285 290	
caa gcg tgc gtc gat gca gat ttg tcc tat tct gag aag ctc acc cgg	1027
Gln Ala Cys Val Asp Ala Asp Leu Ser Tyr Ser Glu Lys Leu Thr Arg	
295 300 305	
caa acc tca gtg gtg gtg tgc aat caa acc cgc gac att gac ggc aaa	1075
Gln Thr Ser Val Val Val Cys Asn Gln Thr Arg Asp Ile Asp Gly Lys	
310 315 320 325	
gcg atg cat gcc cag cgt aaa gga att ccg ctg ctg tcc gat gtt gcc	1123
Ala Met His Ala Gln Arg Lys Gly Ile Pro Leu Leu Ser Asp Val Ala	
330 335 340	
ttc tta gca gct gtt aaa agg gta aaa gaa ggg aag aaa gtg gac gtc	1171
Phe Leu Ala Ala Val Lys Arg Val Lys Glu Gly Lys Lys Val Asp Val	
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Glu Lys Arg	
360	

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<212> PRT
<213> Corynebacterium glutamicum

<400> 188

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Glu	Arg	Gln	Glu	Ala	Ile	Glu	Ala	Ala	Pro	Phe	Val	Ser	Val	Ser	Ile
			20					25						30	
Gln	Ser	Ser	Gly	Ile	His	Pro	Ser	Thr	Ser	Arg	Met	Val	Thr	Ile	Asp
		35					40					45			
Leu	Val	Thr	Leu	Ser	Pro	Asn	Leu	Glu	Pro	Val	Glu	Thr	Phe	His	Ala
	50					55					60				
Val	Leu	Asp	Ser	Lys	Thr	Asp	Pro	Gly	Pro	Phe	His	Leu	His	Gly	Val
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Thr	Glu	Glu	Glu	Phe	Ala	Ser	Ala	Lys	Arg	Phe	Gly	Gln	Ile	Leu	Lys
				85					90					95	
Ser	Leu	Asp	Arg	Leu	Ile	Asp	Gly	Arg	Thr	Leu	Leu	Ile	His	Asn	Ala
			100					105					110		
Ala	Arg	Ser	Trp	Gly	Phe	Ile	Val	Ser	Glu	Ala	Lys	Arg	Ala	Met	Asn
		115					120					125			
Asp	Ala	Ala	Arg	Ala	Asn	Arg	Asn	Ser	Asn	Arg	Gly	Asn	Arg	Arg	Gly
	130					135					140				
Gly	Arg	Gly	Arg	Arg	Arg	Gln	Arg	Val	Gly	His	Ile	Pro	Lys	Pro	Leu
145					150					155					160
Val	Ile	Val	Asp	Thr	Leu	Ala	Ser	Ala	Arg	Arg	Gln	Ala	Ile	Ala	Leu
				165					170					175	
Asp	Asp	Val	Arg	Ile	Arg	Gly	Val	Ala	His	Thr	Leu	Gly	Leu	Asp	Ala
			180					185					190		
Pro	Ala	Ala	Glu	Ala	Ser	Val	Glu	Arg	Ala	Gln	Val	Ser	His	Arg	Gln
		195					200					205			
Leu	Cys	Arg	Glu	Glu	Thr	Leu	Leu	Val	Ala	Arg	Leu	Tyr	Gly	Ala	Leu
	210					215					220				
Lys	Gln	Ser	Gly	Pro	Leu	Ala	Glu	Ile	Asp	Pro	Gln	Ser	Leu	Arg	Ala
225					230					235					240
Asp	Lys	Phe	Gly	Leu	Gln	Arg	Ser	Ile	Ile	Arg	Val	Gln	Ala	Gln	Glu
				245					250					255	
Ala	Ser	Pro	Thr	Leu	Val	Asn	Pro	Gly	Thr	Tyr	Glu	Pro	Gly	Lys	Thr
			260					265					270		
Leu	Ile	Ala	Gly	Met	Glu	Val	Val	Val	Ala	Pro	Glu	Ile	Glu	Met	Asp
		275					280					285			

Pro Asp Ile Ile Ile Gln Ala Cys Val Asp Ala Asp Leu Ser Tyr Ser
 290 295 300

Glu Lys Leu Thr Arg Gln Thr Ser Val Val Val Cys Asn Gln Thr Arg
 305 310 315 320

Asp Ile Asp Gly Lys Ala Met His Ala Gln Arg Lys Gly Ile Pro Leu
 325 330 335

Leu Ser Asp Val Ala Phe Leu Ala Ala Val Lys Arg Val Lys Glu Gly
 340 345 350

Lys Lys Val Asp Val Glu Lys Arg
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(913)
 <223> RXN00066

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 Val Thr Asp Pro Leu
 1 5

tcc gca gct ttg gat agc ggg cgc atc aac cat gcg tac ctt ttt tcg 163
 Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His Ala Tyr Leu Phe Ser
 10 15 20

ggg ccg cgt ggt tgt ggc aag acg tcg tcg gca cgc atc ctt gcc cgg 211
 Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala Arg Ile Leu Ala Arg
 25 30 35

tcc ctc aac tgc gtg gaa ggc cca act tcc acg ccg tgt ggg gtg tgt 259
 Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr Pro Cys Gly Val Cys
 40 45 50

aat tct tgc gta gcg ctg gcc ccg ggt ggc cct gga acc ctt gat gta 307
 Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro Gly Thr Leu Asp Val
 55 60 65

aca gag ctc gac gcc gcg agt aac aat ggt gtc gat gac atg cgt gaa 355
 Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val Asp Asp Met Arg Glu
 70 75 80 85

ctg cgc gaa cgc gcg aac tac gcc ccg gcg gaa tct cgc tac cgc gtg 403
 Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu Ser Arg Tyr Arg Val
 90 95 100

ttc atc att gac gaa gcc cac atg atc agt acc caa ggc ttc aac gcc 451
 Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr Gln Gly Phe Asn Ala
 105 110 115

Gly Thr Leu Asp Val Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val
65 70 75 80

Asp	Asp	Met	Arg	Glu 85	Leu	Arg	Glu	Arg	Ala	Asn	Tyr	Ala	Pro	Ala	Glu
Ser	Arg	Tyr	Arg	Val 100	Phe	Ile	Ile	Asp	Glu	Ala	His	Met	Ile	Ser	Thr
Gln	Gly	Phe	Asn	Ala	Leu	Leu	Lys	Ile	Val	Glu	Glu	Pro	Pro	Ala	His
Leu	Ile	Phe	Ile	Phe	Ala	Thr	Thr	Glu	Pro	Asp	Lys	Met	Ile	Gly	Thr
Ile	Arg	Ser	Arg	Thr	His	Asn	Tyr	Pro	Phe	Arg	Leu	Leu	Thr	Pro	Gly
Asp	Met	Arg	Lys	Val 165	Leu	Lys	Asn	Ala	Val	Asp	Gly	Glu	Gly	Val	His
Val	Asp	Asp	Ser	Val 180	Tyr	Pro	Leu	Val	Ile	Arg	Ala	Gly	Gly	Gly	Ser
Pro	Arg	Asp	Ser	Leu	Ser	Ile	Leu	Asp	Gln	Leu	Ile	Ala	Gly	Ser	Gly
Pro	Glu	Gly	Leu	Thr	Tyr	Glu	Arg	Ala	Leu	Pro	Leu	Leu	Gly	Val	Thr
Ser	Phe	Thr	Leu	Ile	Asp	Asp	Ser	Ile	His	Ala	Leu	Ala	Ser	Lys	Asp
Asn	Ala	Ser	Met	Phe	Thr	Thr	Ile	Asp	Asn	Val	Ile	Glu	Glu	Gly	Leu
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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

$\langle 222 \rangle$ (101) .. (913)

<223> FRXA00066

<400> 191

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Val Thr Asp Pro Leu
1 5

tcc gca gct ttg gat agc ggg cgc atc aac cat gcg tac ctt ttt tcg 163
Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His Ala Tyr Leu Phe Ser
10 15 20

ggt ccg cgt ggt tgt ggc aag acg tcg tcg gca cgc atc ctt gcc cgg 211
Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala Arg Ile Leu Ala Arg

25										30					35					
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Ser	Leu	Asn	Cys	Val	Glu	Gly	Pro	Thr	Ser	Thr	Pro	Cys	Gly	Val	Cys					
40					45					50										
aat	tct	tgc	gta	gcg	ctg	gcc	ccg	ggg	ggc	cct	gga	acc	ctt	gat	gta	307				
Asn	Ser	Cys	Val	Ala	Leu	Ala	Pro	Gly	Gly	Pro	Gly	Thr	Leu	Asp	Val					
55					60					65										
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Thr	Glu	Leu	Asp	Ala	Ala	Ser	Asn	Asn	Gly	Val	Asp	Asp	Met	Arg	Glu					
70					75					80					85					
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Leu	Arg	Glu	Arg	Ala	Asn	Tyr	Ala	Pro	Ala	Glu	Ser	Arg	Tyr	Arg	Val					
90					95					100										
ttc	atc	att	gac	gaa	gcc	cac	atg	atc	agt	acc	caa	ggc	ttc	aac	gcc	451				
Phe	Ile	Ile	Asp	Glu	Ala	His	Met	Ile	Ser	Thr	Gln	Gly	Phe	Asn	Ala					
105					110					115										
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120					125					130										
gcc	acc	acc	gag	ccg	gac	aaa	atg	atc	ggg	acg	atc	cgt	tcc	cgc	acg	547				
Ala	Thr	Thr	Glu	Pro	Asp	Lys	Met	Ile	Gly	Thr	Ile	Arg	Ser	Arg	Thr					
135					140					145										
cac	aat	tac	cca	ttc	cgc	ctg	ctc	acc	cca	ggg	gat	atg	cgc	aaa	gtg	595				
His	Asn	Tyr	Pro	Phe	Arg	Leu	Leu	Thr	Pro	Gly	Asp	Met	Arg	Lys	Val					
150					155					160					165					
ctg	aaa	aat	gcg	gtc	gat	ggc	gaa	ggc	gtc	cac	gtc	gac	gat	tcc	gtt	643				
Leu	Lys	Asn	Ala	Val	Asp	Gly	Glu	Gly	Val	His	Val	Asp	Asp	Ser	Val					
170					175					180										
tac	cca	ctg	gtc	atc	cgc	gcc	ggc	ggc	ggc	agc	ccc	cgc	gac	agc	ctc	691				
Tyr	Pro	Leu	Val	Ile	Arg	Ala	Gly	Gly	Gly	Ser	Pro	Arg	Asp	Ser	Leu					
185					190					195										
tcc	atc	ctc	gac	cag	ctc	atc	gcc	ggc	tcg	ggc	ccg	gag	ggc	ttg	aca	739				
Ser	Ile	Leu	Asp	Gln	Leu	Ile	Ala	Gly	Ser	Gly	Pro	Glu	Gly	Leu	Thr					
200					205					210										
tat	gag	cgc	gcc	ttg	ccg	ctg	ctc	ggg	gtc	aca	agc	ttc	acg	ctt	atc	787				
Tyr	Glu	Arg	Ala	Leu	Pro	Leu	Leu	Gly	Val	Thr	Ser	Phe	Thr	Leu	Ile					
215					220					225										
gac	gat	tcg	atc	cat	gcc	ctt	gca	tct	aaa	gac	aac	gca	agc	atg	ttc	835				
Asp	Asp	Ser	Ile	His	Ala	Leu	Ala	Ser	Lys	Asp	Asn	Ala	Ser	Met	Phe					
230					235					240					245					
acc	acg	atc	gat	aac	gtc	atc	gaa	gaa	ggc	ctc	gaa	ccg	cga	cgc	ttc	883				
Thr	Thr	Ile	Asp	Asn	Val	Ile	Glu	Glu	Gly	Leu	Glu	Pro	Arg	Arg	Phe					
250					255					260										
acg	atc	gac	ctt	cct	tcg	gac	ccg	ctc	cgg							913				
Thr	Ile	Asp	Leu	Pro	Ser	Asp	Pro	Leu	Arg											
265					270															

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<212> PRT
<213> Corynebacterium glutamicum

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Arg Ile Leu Ala Arg Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr
35 40 45
Pro Cys Gly Val Cys Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro
50 55 60
Gly Thr Leu Asp Val Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val
65 70 75 80
Asp Asp Met Arg Glu Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu
85 90 95
Ser Arg Tyr Arg Val Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr
100 105 110
Gln Gly Phe Asn Ala Leu Leu Lys Ile Val Glu Glu Pro Pro Ala His
115 120 125
Leu Ile Phe Ile Phe Ala Thr Thr Glu Pro Asp Lys Met Ile Gly Thr
130 135 140
Ile Arg Ser Arg Thr His Asn Tyr Pro Phe Arg Leu Leu Thr Pro Gly
145 150 155 160
Asp Met Arg Lys Val Leu Lys Asn Ala Val Asp Gly Glu Gly Val His
165 170 175
Val Asp Asp Ser Val Tyr Pro Leu Val Ile Arg Ala Gly Gly Gly Ser
180 185 190
Pro Arg Asp Ser Leu Ser Ile Leu Asp Gln Leu Ile Ala Gly Ser Gly
195 200 205
Pro Glu Gly Leu Thr Tyr Glu Arg Ala Leu Pro Leu Leu Gly Val Thr
210 215 220
Ser Phe Thr Leu Ile Asp Asp Ser Ile His Ala Leu Ala Ser Lys Asp
225 230 235 240
Asn Ala Ser Met Phe Thr Thr Ile Asp Asn Val Ile Glu Glu Gly Leu
245 250 255
Glu Pro Arg Arg Phe Thr Ile Asp Leu Pro Ser Asp Pro Leu Arg
260 265 270

<210> 193

<211> 751
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (89)..(751)
 <223> RXN01637

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 Met Val Asn Ser Gly Leu Asp Asp
 1 5

atg cgt ggt gcc acc tca ccg cgc ctc ctt ctg gaa atc ctc tgc gcc 160
 Met Arg Gly Ala Thr Ser Pro Arg Leu Leu Leu Glu Ile Leu Cys Ala
 10 15 20

cga ctg ctc ctg gca agc aat acc gtg gca ggt cca gcg gtc agt agt 208
 Arg Leu Leu Leu Ala Ser Asn Thr Val Ala Gly Pro Ala Val Ser Ser
 25 30 35 40

tcg act gac gct gcg cct gca gct act ccg ggt ggt ctc act ggt att 256
 Ser Thr Asp Ala Ala Pro Ala Ala Thr Pro Gly Gly Leu Thr Gly Ile
 45 50 55

gct gct gcc cgc gcg aaa gca cgg gag tat gga cag aag aag gca gct 304
 Ala Ala Ala Arg Ala Lys Ala Arg Glu Tyr Gly Gln Lys Lys Ala Ala
 60 65 70

cca gct cct gca cca act cct gcg ccc gag cca gtg cgc gaa cag tct 352
 Pro Ala Pro Ala Pro Thr Pro Ala Pro Glu Pro Val Arg Glu Gln Ser
 75 80 85

ctt gca cca acg cct gaa cca acg cca gcg gct gaa cct aca tct cag 400
 Leu Ala Pro Thr Pro Glu Pro Thr Pro Ala Ala Glu Pro Thr Ser Gln
 90 95 100

ccc gcg ccg gaa ccg gaa ccc gcc agg gaa cca gtg gtg gaa gtg cgg 448
 Pro Ala Pro Glu Pro Glu Pro Ala Arg Glu Pro Val Val Glu Val Arg
 105 110 115 120

gag gcg agc gtc gaa aag cag cct gca agc agt gat ccc ctc gaa acc 496
 Glu Ala Ser Val Glu Lys Gln Pro Ala Ser Ser Asp Pro Leu Glu Thr
 125 130 135

att cga agc cgc tgg tca gag ctg cgc aac atc gtg gaa aaa caa agt 544
 Ile Arg Ser Arg Trp Ser Glu Leu Arg Asn Ile Val Glu Lys Gln Ser
 140 145 150

gtg cgc acc tca atc atg ctg acc gaa gcg cga gtt ttg gga ctg cga 592
 Val Arg Thr Ser Ile Met Leu Thr Glu Ala Arg Val Leu Gly Leu Arg
 155 160 165

ggc gat acc ctc gtg ctc ggt cac agc acc ggg gcg ttg gct gcg cgt 640
 Gly Asp Thr Leu Val Leu Gly His Ser Thr Gly Ala Leu Ala Ala Arg
 170 175 180

ttg aac gct gct gat cac aac gga att ttg gtc aag gtg ttg gct gag 688
 Leu Asn Ala Ala Asp His Asn Gly Ile Leu Val Lys Val Leu Ala Glu

185 190 195 200
 gaa act ggt ctg cag ctc aag gtc gaa tgc att gtg ggc acg aac cca 736
 Glu Thr Gly Leu Gln Leu Lys Val Glu Cys Ile Val Gly Thr Asn Pro
 205 210 215

gcc gaa gct gga .ttt 751
 Ala Glu Ala Gly Phe
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<210> 194
 <211> 221
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 194
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Leu Leu Leu Glu Ile Leu Cys Ala Arg Leu Leu Leu Ala Ser Asn Thr
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Val Ala Gly Pro Ala Val Ser Ser Ser Thr Asp Ala Ala Pro Ala Ala
 35 40 45

Thr Pro Gly Gly Leu Thr Gly Ile Ala Ala Ala Arg Ala Lys Ala Arg
 50 55 60

Glu Tyr Gly Gln Lys Lys Ala Ala Pro Ala Pro Ala Pro Thr Pro Ala
 65 70 75 80

Pro Glu Pro Val Arg Glu Gln Ser Leu Ala Pro Thr Pro Glu Pro Thr
 85 90 95

Pro Ala Ala Glu Pro Thr Ser Gln Pro Ala Pro Glu Pro Glu Pro Ala
 100 105 110

Arg Glu Pro Val Val Glu Val Arg Glu Ala Ser Val Glu Lys Gln Pro
 115 120 125

Ala Ser Ser Asp Pro Leu Glu Thr Ile Arg Ser Arg Trp Ser Glu Leu
 130 135 140

Arg Asn Ile Val Glu Lys Gln Ser Val Arg Thr Ser Ile Met Leu Thr
 145 150 155 160

Glu Ala Arg Val Leu Gly Leu Arg Gly Asp Thr Leu Val Leu Gly His
 165 170 175

Ser Thr Gly Ala Leu Ala Ala Arg Leu Asn Ala Ala Asp His Asn Gly
 180 185 190

Ile Leu Val Lys Val Leu Ala Glu Glu Thr Gly Leu Gln Leu Lys Val
 195 200 205

Glu Cys Ile Val Gly Thr Asn Pro Ala Glu Ala Gly Phe
 210 215 220

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(409)

<223> FRXA01637

<400> 195

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                               Val Arg Glu Ala Ser
                               1 5

gtc gaa aag cag cct gca agc agt gat ccc ctc gaa acc att cga agc 163
Val Glu Lys Gln Pro Ala Ser Ser Asp Pro Leu Glu Thr Ile Arg Ser
                10                15                20

cgc tgg tca gag ctg cgc aac atc gtg gaa aaa caa agt gtg cgc acc 211
Arg Trp Ser Glu Leu Arg Asn Ile Val Glu Lys Gln Ser Val Arg Thr
                25                30                35

tca atc atg ctg acc gaa gcg cga gtt ttg gga ctg cga ggc gat acc 259
Ser Ile Met Leu Thr Glu Ala Arg Val Leu Gly Leu Arg Gly Asp Thr
                40                45                50

ctc gtg ctc ggt cac agc acc ggg gcg ttg gct gcg cgt ttg aac gct 307
Leu Val Leu Gly His Ser Thr Gly Ala Leu Ala Ala Arg Leu Asn Ala
                55                60                65

gct gat cac aac gga att ttg gtc aag gtg ttg gct gag gaa act ggt 355
Ala Asp His Asn Gly Ile Leu Val Lys Val Leu Ala Glu Glu Thr Gly
                70                75                80                85

ctg cag ctc aag gtc gaa tgc att gtg ggc acg aac cca gcc gaa gct 403
Leu Gln Leu Lys Val Glu Cys Ile Val Gly Thr Asn Pro Ala Glu Ala
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gga ttt 409
Gly Phe

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<210> 196

<211> 103

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

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Glu Thr Ile Arg Ser Arg Trp Ser Glu Leu Arg Asn Ile Val Glu Lys
 20 25 30

Gln Ser Val Arg Thr Ser Ile Met Leu Thr Glu Ala Arg Val Leu Gly
 35 40 45

Leu Arg Gly Asp Thr Leu Val Leu Gly His Ser Thr Gly Ala Leu Ala
 50 55 60

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Ala Arg Leu Asn Ala Ala Asp His Asn Gly Ile Leu Val Lys Val Leu
65 70 75 80

Ala Glu Glu Thr Gly Leu Gln Leu Lys Val Glu Cys Ile Val Gly Thr
85 90 95

Asn Pro Ala Glu Ala Gly Phe
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<210> 197

<211> 1683

<212> DNA

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<220>

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<223> RXA00212

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cgcgtgatcg aagatatccc gcaccagctt cagggcactg atg aat atc ctg tgc 115
Met Asn Ile Leu Cys
1 5

ctg ctg tgc tgg aaa ttc gcg gtg agg tgt tca tca ctg tgg agg att 163
Leu Leu Cys Trp Lys Phe Ala Val Arg Cys Ser Ser Leu Trp Arg Ile
10 15 20

tcc cag gag gtc aac gcg cag cgc att gct gat ggt ggc aag ccg ttt 211
Ser Gln Glu Val Asn Ala Gln Arg Ile Ala Asp Gly Gly Lys Pro Phe
25 30 35

gcc aac ccg cgt aat gct gcg gct ggt tct ctg cgt cag aaa aat att 259
Ala Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg Gln Lys Asn Ile
40 45 50

gag gac gtg aag aag cgc cgc ctg cgg atg atc agc cat ggc atc ggt 307
Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile Ser His Gly Ile Gly
55 60 65

ttc act gaa ggc ttt agc cct gcg tct cag cat gat gcg tat ctg gca 355
Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His Asp Ala Tyr Leu Ala
70 75 80 85

ttg gct gcc tgg ggt ttg ccc acc tcg ccg tac aca gag gct gtg act 403
Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr Thr Glu Ala Val Thr
90 95 100

gat cca gaa gat gtg gtg aaa aag gtc agc tac tgg gct gat cac cgc 451
Asp Pro Glu Asp Val Val Lys Lys Val Ser Tyr Trp Ala Asp His Arg
105 110 115

cac gac gca ctc cat gag atg gat ggc ctg gtg att aag gtc gat gac 499
His Asp Ala Leu His Glu Met Asp Gly Leu Val Ile Lys Val Asp Asp
120 125 130

atc gca tct cag cgt gct ttg ggt tcc acc agc cgc gcg cct cgc tgg 547

Ile	Ala	Ser	Gln	Arg	Ala	Leu	Gly	Ser	Thr	Ser	Arg	Ala	Pro	Arg	Trp		
135						140					145						
gcc	att	gcg	tac	aag	tac	cct	ccg	gag	gag	gtc	acc	acc	aag	ctg	ctt	595	
Ala	Ile	Ala	Tyr	Lys	Tyr	Pro	Pro	Glu	Glu	Val	Thr	Thr	Lys	Leu	Leu		
150					155					160					165		
gat	att	cag	gtt	ggc	gtt	ggg	cgc	acc	ggc	cgt	gtc	acc	cca	ttc	gcg	643	
Asp	Ile	Gln	Val	Gly	Val	Gly	Arg	Thr	Gly	Arg	Val	Thr	Pro	Phe	Ala		
				170					175					180			
gtc	atg	gag	ccg	gtt	ctt	gtt	gca	gga	tca	acg	gtg	tct	atg	gcg	acg	691	
Val	Met	Glu	Pro	Val	Leu	Val	Ala	Gly	Ser	Thr	Val	Ser	Met	Ala	Thr		
			185					190						195			
ctg	cat	aac	cag	agc	gaa	gtc	aag	cgt	aaa	ggc	gtg	ctc	atc	ggg	gac	739	
Leu	His	Asn	Gln	Ser	Glu	Val	Lys	Arg	Lys	Gly	Val	Leu	Ile	Gly	Asp		
		200					205					210					
acc	gtg	gtt	atc	cgc	aag	gcg	ggc	gag	gtt	atc	cca	gag	gtg	ctt	ggc	787	
Thr	Val	Val	Ile	Arg	Lys	Ala	Gly	Glu	Val	Ile	Pro	Glu	Val	Leu	Gly		
	215					220					225						
cct	gtc	gta	gag	ctt	cgt	gac	ggc	aca	gag	cgc	gag	tac	atc	ttc	cca	835	
Pro	Val	Val	Glu	Leu	Arg	Asp	Gly	Thr	Glu	Arg	Glu	Tyr	Ile	Phe	Pro		
230					235					240					245		
acg	ctg	tgc	cct	gaa	tgc	ggg	acc	cgt	ctg	gcg	ccc	gcg	aag	gcc	gat	883	
Thr	Leu	Cys	Pro	Glu	Cys	Gly	Thr	Arg	Leu	Ala	Pro	Ala	Lys	Ala	Asp		
				250					255					260			
gac	gtg	gat	tgg	cgt	tgc	ccc	aac	atg	caa	agc	tgt	cca	ggg	cag	ctg	931	
Asp	Val	Asp	Trp	Arg	Cys	Pro	Asn	Met	Gln	Ser	Cys	Pro	Gly	Gln	Leu		
			265				270						275				
tcc	acg	cgt	ttg	acc	tac	ctt	gct	ggg	cgt	ggc	gct	ttt	gat	att	gaa	979	
Ser	Thr	Arg	Leu	Thr	Tyr	Leu	Ala	Gly	Arg	Gly	Ala	Phe	Asp	Ile	Glu		
		280					285					290					
gca	ttg	ggc	gaa	aag	ggc	gct	gaa	gac	ctc	att	cgc	acc	ggc	att	ttg	1027	
Ala	Leu	Gly	Glu	Lys	Gly	Ala	Glu	Asp	Leu	Ile	Arg	Thr	Gly	Ile	Leu		
	295					300					305						
ctt	gac	gag	tct	ggc	ctg	ttc	gac	ctc	aca	gag	gac	gat	ctg	ctg	agc	1075	
Leu	Asp	Glu	Ser	Gly	Leu	Phe	Asp	Leu	Thr	Glu	Asp	Asp	Leu	Leu	Ser		
310					315					320					325		
tcc	aat	gtc	tac	acc	acc	aac	gcc	ggc	aaa	gta	aat	gcc	agc	ggc	aag	1123	
Ser	Asn	Val	Tyr	Thr	Thr	Asn	Ala	Gly	Lys	Val	Asn	Ala	Ser	Gly	Lys		
				330					335					340			
aaa	ctg	ctg	gac	aac	ctg	caa	aaa	tcc	aag	cag	acc	gac	ctc	tgg	cga	1171	
Lys	Leu	Leu	Asp	Asn	Leu	Gln	Lys	Ser	Lys	Gln	Thr	Asp	Leu	Trp	Arg		
			345					350					355				
gtc	ctc	gtg	gca	tta	tct	atc	agg	cac	gta	ggc	ccc	acc	gca	gcg	cgc	1219	
Val	Leu	Val	Ala	Leu	Ser	Ile	Arg	His	Val	Gly	Pro	Thr	Ala	Ala	Arg		
		360					365					370					
gcc	ctt	gca	ggg	cgc	tac	cac	tcc	atc	cag	gcg	ctt	atc	gac	gcc	ccc	1267	
Ala	Leu	Ala	Gly	Arg	Tyr	His	Ser	Ile	Gln	Ala	Leu	Ile	Asp	Ala	Pro		

375	380	385	
ctc gag gaa ctc tcc gaa acc gat gga gta ggt acc atc att gcc caa			1315
Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly Thr Ile Ile Ala Gln			
390	395	400	405
tcc ttc aag gac tgg ttc gag gtt gat tgg cac aag gcc atc gtg gac			1363
Ser Phe Lys Asp Trp Phe Glu Val Asp Trp His Lys Ala Ile Val Asp			
	410	415	420
aag tgg gca gcc gct ggt gtg act atg gag gaa gaa gta ggg gag gtc			1411
Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu Glu Val Gly Glu Val			
	425	430	435
gct gaa caa acc ctt gaa ggc cta acc atc gtg gtc acc gga ggg ttg			1459
Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val Val Thr Gly Gly Leu			
	440	445	450
gaa ggc ttc acc aga gat tcc gtg aag gaa gcc atc atc tcc cgt ggc			1507
Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala Ile Ile Ser Arg Gly			
	455	460	465
gga aaa gcc tct gga tct gtc tcc aag aaa act gac tac gtg gtg att			1555
Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr Asp Tyr Val Val Ile			
	470	475	480
ggt gaa aac gca ggt tcc aag gcc acc aag gca gaa gaa cta ggg ctg			1603
Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala Glu Glu Leu Gly Leu			
	490	495	500
cgc att ctg gat gag gca gga ttc gtc cgt ttg ctc aat acc ggc tca			1651
Arg Ile Leu Asp Glu Ala Gly Phe Val Arg Leu Leu Asn Thr Gly Ser			
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gct gac gaa tagtcgcaca tgaaaatgcc cca			1683
Ala Asp Glu			
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<213> Corynebacterium glutamicum			
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Ser Leu Trp Arg Ile Ser Gln Glu Val Asn Ala Gln Arg Ile Ala Asp			
	20	25	30
Gly Gly Lys Pro Phe Ala Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu			
	35	40	45
Arg Gln Lys Asn Ile Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile			
	50	55	60
Ser His Gly Ile Gly Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His			
	65	70	75
Asp Ala Tyr Leu Ala Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr			

85										90					95				
Thr	Glu	Ala	Val	Thr	Asp	Pro	Glu	Asp	Val	Val	Lys	Lys	Val	Ser	Tyr				
			100					105						110					
Trp	Ala	Asp	His	Arg	His	Asp	Ala	Leu	His	Glu	Met	Asp	Gly	Leu	Val				
		115					120					125							
Ile	Lys	Val	Asp	Asp	Ile	Ala	Ser	Gln	Arg	Ala	Leu	Gly	Ser	Thr	Ser				
	130					135					140								
Arg	Ala	Pro	Arg	Trp	Ala	Ile	Ala	Tyr	Lys	Tyr	Pro	Pro	Glu	Glu	Val				
145					150					155					160				
Thr	Thr	Lys	Leu	Leu	Asp	Ile	Gln	Val	Gly	Val	Gly	Arg	Thr	Gly	Arg				
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Val	Thr	Pro	Phe	Ala	Val	Met	Glu	Pro	Val	Leu	Val	Ala	Gly	Ser	Thr				
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Val	Ser	Met	Ala	Thr	Leu	His	Asn	Gln	Ser	Glu	Val	Lys	Arg	Lys	Gly				
		195					200					205							
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Pro	Glu	Val	Leu	Gly	Pro	Val	Val	Glu	Leu	Arg	Asp	Gly	Thr	Glu	Arg				
225					230					235					240				
Glu	Tyr	Ile	Phe	Pro	Thr	Leu	Cys	Pro	Glu	Cys	Gly	Thr	Arg	Leu	Ala				
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Pro	Ala	Lys	Ala	Asp	Asp	Val	Asp	Trp	Arg	Cys	Pro	Asn	Met	Gln	Ser				
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Cys	Pro	Gly	Gln	Leu	Ser	Thr	Arg	Leu	Thr	Tyr	Leu	Ala	Gly	Arg	Gly				
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Ala	Phe	Asp	Ile	Glu	Ala	Leu	Gly	Glu	Lys	Gly	Ala	Glu	Asp	Leu	Ile				
	290					295					300								
Arg	Thr	Gly	Ile	Leu	Leu	Asp	Glu	Ser	Gly	Leu	Phe	Asp	Leu	Thr	Glu				
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Asp	Asp	Leu	Leu	Ser	Ser	Asn	Val	Tyr	Thr	Thr	Asn	Ala	Gly	Lys	Val				
				325					330					335					
Asn	Ala	Ser	Gly	Lys	Lys	Leu	Leu	Asp	Asn	Leu	Gln	Lys	Ser	Lys	Gln				
			340					345					350						
Thr	Asp	Leu	Trp	Arg	Val	Leu	Val	Ala	Leu	Ser	Ile	Arg	His	Val	Gly				
		355				360						365							
Pro	Thr	Ala	Ala	Arg	Ala	Leu	Ala	Gly	Arg	Tyr	His	Ser	Ile	Gln	Ala				
		370				375					380								
Leu	Ile	Asp	Ala	Pro	Leu	Glu	Glu	Leu	Ser	Glu	Thr	Asp	Gly	Val	Gly				
385					390					395					400				
Thr	Ile	Ile	Ala	Gln	Ser	Phe	Lys	Asp	Trp	Phe	Glu	Val	Asp	Trp	His				
				405					410					415					

Lys Ala Ile Val Asp Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu
 420 425 430
 Glu Val Gly Glu Val Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val
 435 440 445
 Val Thr Gly Gly Leu Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala
 450 455 460
 Ile Ile Ser Arg Gly Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr
 465 470 475 480
 Asp Tyr Val Val Ile Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala
 485 490 495
 Glu Glu Leu Gly Leu Arg Ile Leu Asp Glu Ala Gly Phe Val Arg Leu
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 Leu Asn Thr Gly Ser Ala Asp Glu
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<211> 696

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(673)

<223> RXA00213

<400> 199

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 Val Thr Glu Asp Asn
 1 5

gct caa ctg cgt aga acg tgg aac gac tta gcc gag aag gtt cgt tat 163
 Ala Gln Leu Arg Arg Thr Trp Asn Asp Leu Ala Glu Lys Val Arg Tyr
 10 15 20

cac cga gat cgt tat tac aac gaa cag cca gag atc cct gat gct gat 211
 His Arg Asp Arg Tyr Tyr Asn Glu Gln Pro Glu Ile Pro Asp Ala Asp
 25 30 35

ttt gat gcg ctt ttt aag cag ctt cag cag ttg gaa gaa gac cac ccg 259
 Phe Asp Ala Leu Phe Lys Gln Leu Gln Gln Leu Glu Glu Asp His Pro
 40 45 50

gag ctg gcc gtc cct gat agc ccc acc atg gtt gtg ggc gct ccg gtg 307
 Glu Leu Ala Val Pro Asp Ser Pro Thr Met Val Val Gly Ala Pro Val
 55 60 65

gca gag caa tca agc ttt gac aat gtt gag cac ttg gag cga atg ctg 355
 Ala Glu Gln Ser Ser Phe Asp Asn Val Glu His Leu Glu Arg Met Leu
 70 75 80 85

agc ttg gac aat gtt ttt gat gag cag gag ttg cgt gat tgg ttg ggc 403

Ser Leu Asp Asn Val Phe Asp Glu Gln Glu Leu Arg Asp Trp Leu Gly
 90 95 100

agg acg cca gcc aag cag tat ttg acg gag ttg aaa att gat ggc ttg 451
 Arg Thr Pro Ala Lys Gln Tyr Leu Thr Glu Leu Lys Ile Asp Gly Leu
 105 110 115

tcc atc gac ttg gtg tat cgc aat ggc cag tta gag cgt gcc gct act 499
 Ser Ile Asp Leu Val Tyr Arg Asn Gly Gln Leu Glu Arg Ala Ala Thr
 120 125 130

cgt ggt gat ggt cgc gtg ggc gag gac atc acg gcc aat gct cgc gtg 547
 Arg Gly Asp Gly Arg Val Gly Glu Asp Ile Thr Ala Asn Ala Arg Val
 135 140 145

atc gaa gat atc ccg cac cag ctt cag ggc act gat gaa tat cct gtg 595
 Ile Glu Asp Ile Pro His Gln Leu Gln Gly Thr Asp Glu Tyr Pro Val
 150 155 160 165

cct gct gtg ctg gaa att cgc ggt gag gtg ttc atc act gtg gag gat 643
 Pro Ala Val Leu Glu Ile Arg Gly Glu Val Phe Ile Thr Val Glu Asp
 170 175 180

ttc cca gga ggt caa cgc gca gcg cat tgc tgatgggtggc aagccgtttg 693
 Phe Pro Gly Gly Gln Arg Ala Ala His Cys
 185 190

cca 696

<210> 200

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<212> PRT

<213> Corynebacterium glutamicum

<400> 200

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Glu Lys Val Arg Tyr His Arg Asp Arg Tyr Tyr Asn Glu Gln Pro Glu
 20 25 30

Ile Pro Asp Ala Asp Phe Asp Ala Leu Phe Lys Gln Leu Gln Gln Leu
 35 40 45

Glu Glu Asp His Pro Glu Leu Ala Val Pro Asp Ser Pro Thr Met Val
 50 55 60

Val Gly Ala Pro Val Ala Glu Gln Ser Ser Phe Asp Asn Val Glu His
 65 70 75 80

Leu Glu Arg Met Leu Ser Leu Asp Asn Val Phe Asp Glu Gln Glu Leu
 85 90 95

Arg Asp Trp Leu Gly Arg Thr Pro Ala Lys Gln Tyr Leu Thr Glu Leu
 100 105 110

Lys Ile Asp Gly Leu Ser Ile Asp Leu Val Tyr Arg Asn Gly Gln Leu
 115 120 125

Glu Arg Ala Ala Thr Arg Gly Asp Gly Arg Val Gly Glu Asp Ile Thr

130	135	140
Ala Asn Ala Arg Val Ile Glu Asp Ile Pro His Gln Leu Gln Gly Thr		
145	150	155 160
Asp Glu Tyr Pro Val Pro Ala Val Leu Glu Ile Arg Gly Glu Val Phe		
	165	170 175
Ile Thr Val Glu Asp Phe Pro Gly Gly Gln Arg Ala Ala His Cys		
	180	185 190

<210> 201
 <211> 366
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(343)
 <223> RXA00789

<400> 201
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 gcacccagca agcaaaactaa aaacttagga gaatgaagaa atg acc aat cca gat 115
 Met Thr Asn Pro Asp
 1 5
 atc gtc ggt tcc ggc caa ggc aac gat tcc ttc gag cca gtc gcc caa 163
 Ile Val Gly Ser Gly Gln Gly Asn Asp Ser Phe Glu Pro Val Ala Gln
 10 15 20
 tta tcc tac gag cgt gca cgc gat gaa ctc gtt gaa att gta aaa att 211
 Leu Ser Tyr Glu Arg Ala Arg Asp Glu Leu Val Glu Ile Val Lys Ile
 25 30 35
 ttg gag ctc ggc caa atg ggc ctc gac gaa tcc ctc aaa tac tgg gag 259
 Leu Glu Leu Gly Gln Met Gly Leu Asp Glu Ser Leu Lys Tyr Trp Glu
 40 45 50
 cgc ggc gaa gcc cta gca aag cgc tgc gaa gag cac ctg gcc ggc gcc 307
 Arg Gly Glu Ala Leu Ala Lys Arg Cys Glu Glu His Leu Ala Gly Ala
 55 60 65
 tca gcg cgc gtc gag caa gca tta aac cag gca gaa taatgctttt 353
 Ser Ala Arg Val Glu Gln Ala Leu Asn Gln Ala Glu
 70 75 80
 cgacgcatcc ctc 366

<210> 202
 <211> 81
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 202
 Met Thr Asn Pro Asp Ile Val Gly Ser Gly Gln Gly Asn Asp Ser Phe
 1 5 10 15

<400> 203																
acggcttggc catttgtggg tggagggcca gtcgctcag attaatgtaa agcccaattg																60
aaagctgtcg aatttgacgc ttcgtgatgt ggagcaagaa atg tct gtg cag ctg																115
Met Ser Val Gln Leu																
1 5																
acc tgc ccg acg gac att atc cgc aat cgc ccc aca ccg ctc aag gat																163
Thr Cys Pro Thr Asp Ile Ile Arg Asn Arg Pro Thr Pro Leu Lys Asp																
10 15 20																
ggc gac cgc gtg att gtg tac ggc aag ccc gcg ttt tat gca ggc cgc																211
Gly Asp Arg Val Ile Val Tyr Gly Lys Pro Ala Phe Tyr Ala Gly Arg																
25 30 35																
ggc act ttt tcg ctg tgg gtg act gat atc cgt ccc gtg ggt att ggt																259
Gly Thr Phe Ser Leu Trp Val Thr Asp Ile Arg Pro Val Gly Ile Gly																
40 45 50																
gag ttg ctg gcg cgc att gag gag ctg cgt aaa agg ctt gcc gcg gag																307
Glu Leu Leu Ala Arg Ile Glu Glu Leu Arg Lys Arg Leu Ala Ala Glu																
55 60 65																
ggt ctt ttt gat cca gct cgg aag aag cga ctg cca ttt ctg ccc aac																355
Gly Leu Phe Asp Pro Ala Arg Lys Lys Arg Leu Pro Phe Leu Pro Asn																
70 75 80 85																
cgc gtt ggt ttg atc acg gga cgt ggt tca gcg gct gag cgc gat gtg																403
Arg Val Gly Leu Ile Thr Gly Arg Gly Ser Ala Ala Glu Arg Asp Val																
90 95 100																
ctg agc gtg gct aag gat cgc tgg ccg gaa gtg cag ttt gag gtg atc																451
Leu Ser Val Ala Lys Asp Arg Trp Pro Glu Val Gln Phe Glu Val Ile																
105 110 115																

aac acg gca gtt cag ggc gct tca gct gtt cct gaa atc atc gaa gcg	499
Asn Thr Ala Val Gln Gly Ala Ser Ala Val Pro Glu Ile Ile Glu Ala	
120 125 130	
ttg cgg gtt tta gat cag gac cct cgc gtg gat gtc atc atc att gcc	547
Leu Arg Val Leu Asp Gln Asp Pro Arg Val Asp Val Ile Ile Ile Ala	
135 140 145	
cgc ggc ggc ggt tct gtg gag gat ctg ctc ccc ttc tct gag gag gcc	595
Arg Gly Gly Gly Ser Val Glu Asp Leu Leu Pro Phe Ser Glu Glu Ala	
150 155 160 165	
ttg cag cgc gca gtc gcg gca gcg cag acg ccc gtg gtg tcc gcg att	643
Leu Gln Arg Ala Val Ala Ala Ala Gln Thr Pro Val Val Ser Ala Ile	
170 175 180	
ggc cac gaa cca gat acg ccg gtg ttg gac aat gtc gcc gac ctt cgc	691
Gly His Glu Pro Asp Thr Pro Val Leu Asp Asn Val Ala Asp Leu Arg	
185 190 195	
gcg gcg acc ccg acc gat gca gca aag cgc gtg gtg cct gat gtg gca	739
Ala Ala Thr Pro Thr Asp Ala Ala Lys Arg Val Val Pro Asp Val Ala	
200 205 210	
gaa gaa cgc atg ttg atc aat cag ctt cgc agt cgt agt gcc gcg gcg	787
Glu Glu Arg Met Leu Ile Asn Gln Leu Arg Ser Arg Ser Ala Ala Ala	
215 220 225	
ttg cgc ggt tgg gtg cag cgc gag cag cag gcg ttg gca gcg att cgc	835
Leu Arg Gly Trp Val Gln Arg Glu Gln Gln Ala Leu Ala Ala Ile Arg	
230 235 240 245	
acc agg ccg gtg ctg gct gat ccg atg acc ccg att aac cgc cga cgt	883
Thr Arg Pro Val Leu Ala Asp Pro Met Thr Pro Ile Asn Arg Arg Arg	
250 255 260	
gat gag att gcc cag gct gtg ggc ttg att agg cgc gat gtc acc cat	931
Asp Glu Ile Ala Gln Ala Val Gly Leu Ile Arg Arg Asp Val Thr His	
265 270 275	
ctc gtc cgc acc gag caa gca ctg gtg gcg tcg ttg cgc gca cag gtt	979
Leu Val Arg Thr Glu Gln Ala Leu Val Ala Ser Leu Arg Ala Gln Val	
280 285 290	
tcc gcg ctc ggc ccg tcc gca acc ttg gcg cgc ggt tat tcc gtg gtg	1027
Ser Ala Leu Gly Pro Ser Ala Thr Leu Ala Arg Gly Tyr Ser Val Val	
295 300 305	
cag gtt att cct cgc gac ggc agc gcc ccg gaa gtg gtc acc acc atc	1075
Gln Val Ile Pro Arg Asp Gly Ser Ala Pro Glu Val Val Thr Thr Ile	
310 315 320 325	
gag caa tca ccg ccc ggc agc cag ctg cgc atc cgc gtt gcc gac ggc	1123
Glu Gln Ser Pro Pro Gly Ser Gln Leu Arg Ile Arg Val Ala Asp Gly	
330 335 340	
tcc atc act gcg gca tcc atg ggc acc cag caa gca aac taaaaactta	1172
Ser Ile Thr Ala Ala Ser Met Gly Thr Gln Gln Ala Asn	
345 350	
ggagaatgaa gaa	1185

<210> 204
<211> 354
<212> PRT
<213> Corynebacterium glutamicum

<400> 204
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1 5 10 15
Thr Pro Leu Lys Asp Gly Asp Arg Val Ile Val Tyr Gly Lys Pro Ala
20 25 30
Phe Tyr Ala Gly Arg Gly Thr Phe Ser Leu Trp Val Thr Asp Ile Arg
35 40 45
Pro Val Gly Ile Gly Glu Leu Leu Ala Arg Ile Glu Glu Leu Arg Lys
50 55 60
Arg Leu Ala Ala Glu Gly Leu Phe Asp Pro Ala Arg Lys Lys Arg Leu
65 70 75 80
Pro Phe Leu Pro Asn Arg Val Gly Leu Ile Thr Gly Arg Gly Ser Ala
85 90 95
Ala Glu Arg Asp Val Leu Ser Val Ala Lys Asp Arg Trp Pro Glu Val
100 105 110
Gln Phe Glu Val Ile Asn Thr Ala Val Gln Gly Ala Ser Ala Val Pro
115 120 125
Glu Ile Ile Glu Ala Leu Arg Val Leu Asp Gln Asp Pro Arg Val Asp
130 135 140
Val Ile Ile Ile Ala Arg Gly Gly Gly Ser Val Glu Asp Leu Leu Pro
145 150 155 160
Phe Ser Glu Glu Ala Leu Gln Arg Ala Val Ala Ala Ala Gln Thr Pro
165 170 175
Val Val Ser Ala Ile Gly His Glu Pro Asp Thr Pro Val Leu Asp Asn
180 185 190
Val Ala Asp Leu Arg Ala Ala Thr Pro Thr Asp Ala Ala Lys Arg Val
195 200 205
Val Pro Asp Val Ala Glu Glu Arg Met Leu Ile Asn Gln Leu Arg Ser
210 215 220
Arg Ser Ala Ala Ala Leu Arg Gly Trp Val Gln Arg Glu Gln Gln Ala
225 230 235 240
Leu Ala Ala Ile Arg Thr Arg Pro Val Leu Ala Asp Pro Met Thr Pro
245 250 255
Ile Asn Arg Arg Arg Asp Glu Ile Ala Gln Ala Val Gly Leu Ile Arg
260 265 270
Arg Asp Val Thr His Leu Val Arg Thr Glu Gln Ala Leu Val Ala Ser
275 280 285

Leu Arg Ala Gln Val Ser Ala Leu Gly Pro Ser Ala Thr Leu Ala Arg
 290 295 300

Gly Tyr Ser Val Val Gln Val Ile Pro Arg Asp Gly Ser Ala Pro Glu
 305 310 315 320

Val Val Thr Thr Ile Glu Gln Ser Pro Pro Gly Ser Gln Leu Arg Ile
 325 330 335

Arg Val Ala Asp Gly Ser Ile Thr Ala Ala Ser Met Gly Thr Gln Gln
 340 345 350

Ala Asn

<210> 205

<211> 1049

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1026)

<223> FRXA00790

<400> 205

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 Arg Asn Arg Pro Thr Pro Leu Lys Asp Gly Asp Arg Val Ile Val Tyr
 1 5 10 15

ggc aag ccc gcg ttt tat gca ggc cgc ggc act ttt tcg ctg tgg gtg 96
 Gly Lys Pro Ala Phe Tyr Ala Gly Arg Gly Thr Phe Ser Leu Trp Val
 20 25 30

act gat atc cgt ccc gtg ggt att ggt gag ttg ctg gcg cgc att gag 144
 Thr Asp Ile Arg Pro Val Gly Ile Gly Glu Leu Leu Ala Arg Ile Glu
 35 40 45

gag ctg cgt aaa agg ctt gcc gcg gag ggt ctt ttt gat cca gct cgg 192
 Glu Leu Arg Lys Arg Leu Ala Ala Glu Gly Leu Phe Asp Pro Ala Arg
 50 55 60

aag aag cga ctg cca ttt ctg ccc aac cgc gtt ggt ttg atc acg gga 240
 Lys Lys Arg Leu Pro Phe Leu Pro Asn Arg Val Gly Leu Ile Thr Gly
 65 70 75 80

cgt ggt tca gcg gct gag cgc gat gtg ctg agc gtg gct aag gat cgc 288
 Arg Gly Ser Ala Ala Glu Arg Asp Val Leu Ser Val Ala Lys Asp Arg
 85 90 95

tgg ccg gaa gtg cag ttt gag gtg atc aac acg gca gtt cag ggc gct 336
 Trp Pro Glu Val Gln Phe Glu Val Ile Asn Thr Ala Val Gln Gly Ala
 100 105 110

tca gct gtt cct gaa atc atc gaa gcg ttg cgg gtt tta gat cag gac 384
 Ser Ala Val Pro Glu Ile Ile Glu Ala Leu Arg Val Leu Asp Gln Asp
 115 120 125

cct cgc gtg gat gtc atc atc att gcc cgc ggc ggc ggt tct gtg gag 432

Pro	Arg	Val	Asp	Val	Ile	Ile	Ile	Ala	Arg	Gly	Gly	Gly	Ser	Val	Glu		
130							135					140					
gat	ctg	ctc	ccc	ttc	tct	gag	gag	gcc	ttg	cag	cgc	gca	gtc	gcg	gca	480	
Asp	Leu	Leu	Pro	Phe	Ser	Glu	Glu	Ala	Leu	Gln	Arg	Ala	Val	Ala	Ala	160	
145					150					155							
gcg	cag	acg	ccc	gtg	gtg	tcc	gcg	att	ggc	cac	gaa	cca	gat	acg	ccg	528	
Ala	Gln	Thr	Pro	Val	Val	Ser	Ala	Ile	Gly	His	Glu	Pro	Asp	Thr	Pro	175	
				165					170								
gtg	ttg	gac	aat	gtc	gcc	gac	ctt	cgc	gcg	gcg	acc	ccg	acc	gat	gca	576	
Val	Leu	Asp	Asn	Val	Ala	Asp	Leu	Arg	Ala	Ala	Thr	Pro	Thr	Asp	Ala	190	
			180					185									
gca	aag	cgc	gtg	gtg	cct	gat	gtg	gca	gaa	gaa	cgc	atg	ttg	atc	aat	624	
Ala	Lys	Arg	Val	Val	Pro	Asp	Val	Ala	Glu	Glu	Arg	Met	Leu	Ile	Asn	205	
		195					200										
cag	ctt	cgc	agt	cgt	agt	gcc	gcg	gcg	ttg	cgc	ggt	tgg	gtg	cag	cgc	672	
Gln	Leu	Arg	Ser	Arg	Ser	Ala	Ala	Ala	Leu	Arg	Gly	Trp	Val	Gln	Arg	220	
	210					215											
gag	cag	cag	gcg	ttg	gca	gcg	att	cgc	acc	agg	ccg	gtg	ctg	gct	gat	720	
Glu	Gln	Gln	Ala	Leu	Ala	Ala	Ile	Arg	Thr	Arg	Pro	Val	Leu	Ala	Asp	240	
225					230					235							
ccg	atg	acc	ccg	att	aac	cgc	cga	cgt	gat	gag	att	gcc	cag	gct	gtg	768	
Pro	Met	Thr	Pro	Ile	Asn	Arg	Arg	Arg	Asp	Glu	Ile	Ala	Gln	Ala	Val	255	
				245					250								
ggc	ttg	att	agg	cgc	gat	gtc	acc	cat	ctc	gtc	cgc	acc	gag	caa	gca	816	
Gly	Leu	Ile	Arg	Arg	Asp	Val	Thr	His	Leu	Val	Arg	Thr	Glu	Gln	Ala	270	
			260					265									
ctg	gtg	gcg	tgc	ttg	cgc	gca	cag	gtt	tcc	gcg	ctc	ggc	ccg	tcc	gca	864	
Leu	Val	Ala	Ser	Leu	Arg	Ala	Gln	Val	Ser	Ala	Leu	Gly	Pro	Ser	Ala	285	
		275					280										
acc	ttg	gcg	cgc	ggt	tat	tcc	gtg	gtg	cag	gtt	att	cct	cgc	gac	ggc	912	
Thr	Leu	Ala	Arg	Gly	Tyr	Ser	Val	Val	Gln	Val	Ile	Pro	Arg	Asp	Gly	300	
	290					295											
agc	gcc	ccg	gaa	gtg	gtc	acc	acc	atc	gag	caa	tca	ccg	ccc	ggc	agc	960	
Ser	Ala	Pro	Glu	Val	Val	Thr	Thr	Ile	Glu	Gln	Ser	Pro	Pro	Gly	Ser	320	
305					310					315							
cag	ctg	cgc	atc	cgc	gtt	gcc	gac	ggc	tcc	atc	act	gcg	gca	tcc	atg	1008	
Gln	Leu	Arg	Ile	Arg	Val	Ala	Asp	Gly	Ser	Ile	Thr	Ala	Ala	Ser	Met	335	
				325					330								
ggc	acc	cag	caa	gca	aac	taaaaactta	ggagaatgaa	gaa								1049	
Gly	Thr	Gln	Gln	Ala	Asn												
				340													

<210> 206

<211> 342

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

Arg Asn Arg Pro Thr Pro Leu Lys Asp Gly Asp Arg Val Ile Val Tyr
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Gly Lys Pro Ala Phe Tyr Ala Gly Arg Gly Thr Phe Ser Leu Trp Val
20 25 30

Thr Asp Ile Arg Pro Val Gly Ile Gly Glu Leu Leu Ala Arg Ile Glu
35 40 45

Glu Leu Arg Lys Arg Leu Ala Ala Glu Gly Leu Phe Asp Pro Ala Arg
50 55 60

Lys Lys Arg Leu Pro Phe Leu Pro Asn Arg Val Gly Leu Ile Thr Gly
65 70 75 80

Arg Gly Ser Ala Ala Glu Arg Asp Val Leu Ser Val Ala Lys Asp Arg
85 90 95

Trp Pro Glu Val Gln Phe Glu Val Ile Asn Thr Ala Val Gln Gly Ala
100 105 110

Ser Ala Val Pro Glu Ile Ile Glu Ala Leu Arg Val Leu Asp Gln Asp
115 120 125

Pro Arg Val Asp Val Ile Ile Ile Ala Arg Gly Gly Gly Ser Val Glu
130 135 140

Asp Leu Leu Pro Phe Ser Glu Glu Ala Leu Gln Arg Ala Val Ala Ala
145 150 155 160

Ala Gln Thr Pro Val Val Ser Ala Ile Gly His Glu Pro Asp Thr Pro
165 170 175

Val Leu Asp Asn Val Ala Asp Leu Arg Ala Ala Thr Pro Thr Asp Ala
180 185 190

Ala Lys Arg Val Val Pro Asp Val Ala Glu Glu Arg Met Leu Ile Asn
195 200 205

Gln Leu Arg Ser Arg Ser Ala Ala Ala Leu Arg Gly Trp Val Gln Arg
210 215 220

Glu Gln Gln Ala Leu Ala Ala Ile Arg Thr Arg Pro Val Leu Ala Asp
225 230 235 240

Pro Met Thr Pro Ile Asn Arg Arg Arg Asp Glu Ile Ala Gln Ala Val
245 250 255

Gly Leu Ile Arg Arg Asp Val Thr His Leu Val Arg Thr Glu Gln Ala
260 265 270

Leu Val Ala Ser Leu Arg Ala Gln Val Ser Ala Leu Gly Pro Ser Ala
275 280 285

Thr Leu Ala Arg Gly Tyr Ser Val Val Gln Val Ile Pro Arg Asp Gly
290 295 300

Ser Ala Pro Glu Val Val Thr Thr Ile Glu Gln Ser Pro Pro Gly Ser
305 310 315 320

<400> 207																
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aacggaaatt ctaaaatcca aaacagctag ggtataagtc atg cgc atc gtt aat 115																
Met Arg Ile Val Asn 5																
1																
tgg aac gtc aac tct gct cgc act cgt gtg gac cgg atg gtc gat ttt 163																
Trp Asn Val Asn Ser Ala Arg Thr Arg Val Asp Arg Met Val Asp Phe 20																
10 15																
ttg ctt cgc cat gat gtt gat gta tta gcg gtg cag gaa acc aag tgt 211																
Leu Leu Arg His Asp Val Asp Val Leu Ala Val Gln Glu Thr Lys Cys 35																
25 30																
aaa gat gag caa ttt ccc acc gag cgt ttc acc gaa atc ggc tat gag 259																
Lys Asp Glu Gln Phe Pro Thr Glu Arg Phe Thr Glu Ile Gly Tyr Glu 50																
40 45																
gta gcc cat ttc ggc ctt aac cag tgg aat ggt gtc gcc att att tcc 307																
Val Ala His Phe Gly Leu Asn Gln Trp Asn Gly Val Ala Ile Ile Ser 65																
55 60																
cgc gtt ggc att gaa aat gtg gaa acc cac ttc cct gcc caa ccg gga 355																
Arg Val Gly Ile Glu Asn Val Glu Thr His Phe Pro Ala Gln Pro Gly 85																
70 75 80																
ttc aac aaa gac atc acc aag gaa caa tcc atc gaa gcc cgc gcc atc 403																
Phe Asn Lys Asp Ile Thr Lys Glu Gln Ser Ile Glu Ala Arg Ala Ile 100																
90 95																
ggc gcc cgc tgc ggt ggt gtc cag gtg tgg agc ctc tat gtt ccc aac 451																
Gly Ala Arg Cys Gly Gly Val Gln Val Trp Ser Leu Tyr Val Pro Asn 115																
105 110																
ggc cgc gaa atc gca gat cct cac tac gac tac aaa ctg cgc tgg cta 499																
Gly Arg Glu Ile Ala Asp Pro His Tyr Asp Tyr Lys Leu Arg Trp Leu 130																
120 125																
ttc tcc ctg cgc aac tac gtg atc gac acc ttg gaa tac cgc ccc gag 547																
Phe Ser Leu Arg Asn Tyr Val Ile Asp Thr Leu Glu Tyr Arg Pro Glu 145																
135 140 145																
gaa aaa ctg gtg ttg ctc ggc gac ttc aac atc gcg ccc aca gac atc 595																

Glu Lys Leu Val Leu Leu Gly Asp Phe Asn Ile Ala Pro Thr Asp Ile
 150 155 160 165
 gac gtc tgg gac atc gca gcc ttc gaa gga aaa acc cac gtc acc gaa 643
 Asp Val Trp Asp Ile Ala Ala Phe Glu Gly Lys Thr His Val Thr Glu
 170 175 180
 cca gaa cgt gca gct ttc gac ggc ctc atc gaa gcc gga ctc aaa gaa 691
 Pro Glu Arg Ala Ala Phe Asp Gly Leu Ile Glu Ala Gly Leu Lys Glu
 185 190 195
 acc acc ccc gga cct ggt acc tac acc tac tgg gat tac aaa ggc gca 739
 Thr Thr Pro Gly Pro Gly Thr Tyr Thr Tyr Trp Asp Tyr Lys Gly Ala
 200 205 210
 cgc ttc ctc aaa ggc gaa ggc atg cgc atc gat ttc cag ctc gca tcc 787
 Arg Phe Leu Lys Gly Glu Gly Met Arg Ile Asp Phe Gln Leu Ala Ser
 215 220 225
 ccg gcc ctt gct gca acc gcg ggt gaa acc ttt gtg gac gtt gaa gaa 835
 Pro Ala Leu Ala Ala Thr Ala Gly Glu Thr Phe Val Asp Val Glu Glu
 230 235 240 245
 cgc agc gga acc ggc gcc tct gac cac gca cca gtc atc gtt gat tac 883
 Arg Ser Gly Thr Gly Ala Ser Asp His Ala Pro Val Ile Val Asp Tyr
 250 255 260
 aag gtg taactgcgta tgatctttca gat 912
 Lys Val

<210> 208

<211> 263

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

Met Arg Ile Val Asn Trp Asn Val Asn Ser Ala Arg Thr Arg Val Asp
 1 5 10 15

Arg Met Val Asp Phe Leu Leu Arg His Asp Val Asp Val Leu Ala Val
 20 25 30

Gln Glu Thr Lys Cys Lys Asp Glu Gln Phe Pro Thr Glu Arg Phe Thr
 35 40 45

Glu Ile Gly Tyr Glu Val Ala His Phe Gly Leu Asn Gln Trp Asn Gly
 50 55 60

Val Ala Ile Ile Ser Arg Val Gly Ile Glu Asn Val Glu Thr His Phe
 65 70 75 80

Pro Ala Gln Pro Gly Phe Asn Lys Asp Ile Thr Lys Glu Gln Ser Ile
 85 90 95

Glu Ala Arg Ala Ile Gly Ala Arg Cys Gly Gly Val Gln Val Trp Ser
 100 105 110

Leu Tyr Val Pro Asn Gly Arg Glu Ile Ala Asp Pro His Tyr Asp Tyr
 115 120 125

Lys Leu Arg Trp Leu Phe Ser Leu Arg Asn Tyr Val Ile Asp Thr Leu
 130 135 140
 Glu Tyr Arg Pro Glu Glu Lys Leu Val Leu Leu Gly Asp Phe Asn Ile
 145 150 155 160
 Ala Pro Thr Asp Ile Asp Val Trp Asp Ile Ala Ala Phe Glu Gly Lys
 165 170 175
 Thr His Val Thr Glu Pro Glu Arg Ala Ala Phe Asp Gly Leu Ile Glu
 180 185 190
 Ala Gly Leu Lys Glu Thr Thr Pro Gly Pro Gly Thr Tyr Thr Tyr Trp
 195 200 205
 Asp Tyr Lys Gly Ala Arg Phe Leu Lys Gly Glu Gly Met Arg Ile Asp
 210 215 220
 Phe Gln Leu Ala Ser Pro Ala Leu Ala Ala Thr Ala Gly Glu Thr Phe
 225 230 235 240
 Val Asp Val Glu Glu Arg Ser Gly Thr Gly Ala Ser Asp His Ala Pro
 245 250 255
 Val Ile Val Asp Tyr Lys Val
 260

<210> 209

<211> 806

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(783)

<223> .RXN03175

<400> 209

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 Val Arg Ala Ser Glu Lys Asp Thr Ala Thr Ala Leu Gln Pro Ala Leu
 1 5 10 15

gat aac gga tgg cac tac att ggt gcc cca gca gct gcc aag gga cgt 96
 Asp Asn Gly Trp His Tyr Ile Gly Ala Pro Ala Ala Ala Lys Gly Arg
 20 25 30

gcc ggt gtc ggc att ttg tct agg cat gaa ctt gaa gat gtg aac atc 144
 Ala Gly Val Gly Ile Leu Ser Arg His Glu Leu Glu Asp Val Asn Ile
 35 40 45

ggt ttt gga tct ttc ctt gac tcc ggc cgc tac att gaa gca acc atc 192
 Gly Phe Gly Ser Phe Leu Asp Ser Gly Arg Tyr Ile Glu Ala Thr Ile
 50 55 60

aaa gac acc acc ctg gat gtg cca gta acc gtg gca tct ctt tac ctc 240
 Lys Asp Thr Thr Leu Asp Val Pro Val Thr Val Ala Ser Leu Tyr Leu
 65 70 75 80

ccc tca ggt tca gcg ggc acc gac aag cag gat gaa aag tac cgc ttc 288

Pro Ser Gly Ser Ala Gly Thr Asp Lys Gln Asp Glu Lys Tyr Arg Phe
85 90 95

ctc gat gaa ttc gaa ggg ttc ctg gac cag cgc gct aaa gaa cgc tcc 336
Leu Asp Glu Phe Glu Gly Phe Leu Asp Gln Arg Ala Lys Glu Arg Ser
100 105 110

cac atg gtc atc ggt ggc gac tgg aac atc tgc cac cgc cgc gaa gac 384
His Met Val Ile Gly Gly Asp Trp Asn Ile Cys His Arg Arg Glu Asp
115 120 125

ctg aaa aac tgg aaa acc aac caa aag aaa tcc ggt ttc ctt ccc gac 432
Leu Lys Asn Trp Lys Thr Asn Gln Lys Lys Ser Gly Phe Leu Pro Asp
130 135 140

gaa cgc gca ttc atg gat tca gtc ttt ggc acc ttc cca gat gag gca 480
Glu Arg Ala Phe Met Asp Ser Val Phe Gly Thr Phe Pro Asp Glu Ala
145 150 155 160

acc cag gtt gca ggg gcc ggc gac ttc ttc ggt gcc gtg gac tat gaa 528
Thr Gln Val Ala Gly Ala Gly Asp Phe Phe Gly Ala Val Asp Tyr Glu
165 170 175

gga acg agg cgt cga gaa gca act acg gac cct gcg tgg ttc gac gtt 576
Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp Pro Ala Trp Phe Asp Val
180 185 190

gca cgt cgc ctg caa cct gaa ggc gac ggc ccc tac act tgg tgg acc 624
Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly Pro Tyr Thr Trp Trp Thr
195 200 205

tac cgc gga aaa gcc ttc gac acc ggc gcc gga tgg cgc atc gac tac 672
Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala Gly Trp Arg Ile Asp Tyr
210 215 220

caa gca gca acc gca gcg atg ctc gaa cgc gca gaa cgc tcc tgg gta 720
Gln Ala Ala Thr Ala Ala Met Leu Glu Arg Ala Glu Arg Ser Trp Val
225 230 235 240

gac aaa gcc gct gca tac gat ttg cgc tgg tca gat cac tca cca ctg 768
Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp Ser Asp His Ser Pro Leu
245 250 255

aac gtg atc tac tcc taaaatgctgctgacaattc tat 806
Asn Val Ile Tyr Ser
260

<210> 210

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

Val Arg Ala Ser Glu Lys Asp Thr Ala Thr Ala Leu Gln Pro Ala Leu
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Asp Asn Gly Trp His Tyr Ile Gly Ala Pro Ala Ala Ala Lys Gly Arg
20 25 30

Ala Gly Val Gly Ile Leu Ser Arg His Glu Leu Glu Asp Val Asn Ile

35 40 45
 Gly Phe Gly Ser Phe Leu Asp Ser Gly Arg Tyr Ile Glu Ala Thr Ile
 50 55 60
 Lys Asp Thr Thr Leu Asp Val Pro Val Thr Val Ala Ser Leu Tyr Leu
 65 70 75 80
 Pro Ser Gly Ser Ala Gly Thr Asp Lys Gln Asp Glu Lys Tyr Arg Phe
 85 90 95
 Leu Asp Glu Phe Glu Gly Phe Leu Asp Gln Arg Ala Lys Glu Arg Ser
 100 105 110
 His Met Val Ile Gly Gly Asp Trp Asn Ile Cys His Arg Arg Glu Asp
 115 120 125
 Leu Lys Asn Trp Lys Thr Asn Gln Lys Lys Ser Gly Phe Leu Pro Asp
 130 135 140
 Glu Arg Ala Phe Met Asp Ser Val Phe Gly Thr Phe Pro Asp Glu Ala
 145 150 155 160
 Thr Gln Val Ala Gly Ala Gly Asp Phe Phe Gly Ala Val Asp Tyr Glu
 165 170 175
 Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp Pro Ala Trp Phe Asp Val
 180 185 190
 Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly Pro Tyr Thr Trp Trp Thr
 195 200 205
 Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala Gly Trp Arg Ile Asp Tyr
 210 215 220
 Gln Ala Ala Thr Ala Ala Met Leu Glu Arg Ala Glu Arg Ser Trp Val
 225 230 235 240
 Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp Ser Asp His Ser Pro Leu
 245 250 255
 Asn Val Ile Tyr Ser
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<210> 211

<211> 1035

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1012)

<223> FRXA02883

<400> 211

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Met Ser Phe His Ile

1

5

aca tcc gtc aat gtc aac ggc att agg gca gcg gtc aaa cag cga agc	163
Thr Ser Val Asn Val Asn Gly Ile Arg Ala Ala Val Lys Gln Arg Ser	
10 15 20	
gaa aca aac cta ggt ttc ctt ccg tgg ctt gaa gaa act cgc ccg gac	211
Glu Thr Asn Leu Gly Phe Leu Pro Trp Leu Glu Glu Thr Arg Pro Asp	
25 30 35	
gtt gtc ctc ctc caa gaa gtc cgc gca agc gaa aaa gac acc gcc acc	259
Val Val Leu Leu Gln Glu Val Arg Ala Ser Glu Lys Asp Thr Ala Thr	
40 45 50	
gca ctg caa ccc gcc tta gat aac gga tgg cac tac att ggt gcc cca	307
Ala Leu Gln Pro Ala Leu Asp Asn Gly Trp His Tyr Ile Gly Ala Pro	
55 60 65	
gca gct gcc aag gga cgt gcc ggt gtc ggc att ttg tct agg cat gaa	355
Ala Ala Ala Lys Gly Arg Ala Gly Val Gly Ile Leu Ser Arg His Glu	
70 75 80 85	
ctt gaa gat gtg aac atc ggt ttt gga tct ttc ctt gac tcc ggc cgc	403
Leu Glu Asp Val Asn Ile Gly Phe Gly Ser Phe Leu Asp Ser Gly Arg	
90 95 100	
tac att gaa gca acc atc aaa gac acc acc ctg gat gtg cca gta acc	451
Tyr Ile Glu Ala Thr Ile Lys Asp Thr Thr Leu Asp Val Pro Val Thr	
105 110 115	
gtg gca tct ctt tac ctc ccc tca ggt tca gcg ggc acc gac aag cag	499
Val Ala Ser Leu Tyr Leu Pro Ser Gly Ser Ala Gly Thr Asp Lys Gln	
120 125 130	
gat gaa aag tac cgc ttc ctc gat gaa ttc gaa ggg ttc ctg gac cag	547
Asp Glu Lys Tyr Arg Phe Leu Asp Glu Phe Glu Phe Leu Asp Gln	
135 140 145	
cgc gct aaa gaa cgc tcc cac atg gtc atc ggt ggc gac tgg aac atc	595
Arg Ala Lys Glu Arg Ser His Met Val Ile Gly Gly Asp Trp Asn Ile	
150 155 160 165	
tgc cac cgc cgc gaa gac ctg aaa aac tgg aaa acc aac caa aag aaa	643
Cys His Arg Arg Glu Asp Leu Lys Asn Trp Lys Thr Asn Gln Lys Lys	
170 175 180	
tcc ggt ttc ctt ccc gac gaa cgc gca ttc atg gat tca gtc ttt ggc	691
Ser Gly Phe Leu Pro Asp Glu Arg Ala Phe Met Asp Ser Val Phe Gly	
185 190 195	
acc ttc cca gat gag gca acc cag gtt gca ggg gcc ggc gac ttc ttc	739
Thr Phe Pro Asp Glu Ala Thr Gln Val Ala Gly Ala Gly Asp Phe Phe	
200 205 210	
ggt gcc gtg gac tat gaa gga acg agg cgt cga gaa gca act acg gac	787
Gly Ala Val Asp Tyr Glu Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp	
215 220 225	
cct gcg tgg ttc gac gtt gca cgt cgc ctg caa cct gaa ggc gac ggc	835
Pro Ala Trp Phe Asp Val Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly	
230 235 240 245	

ccc tac act tgg tgg acc tac cgc gga aaa gcc ttc gac acc ggc gcc 883
 Pro Tyr Thr Trp Trp Thr Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala
 250 255 260

gga tgg cgc atc gac tac caa gca gca acc gca gcg atg ctc gaa cgc 931
 Gly Trp Arg Ile Asp Tyr Gln Ala Ala Thr Ala Ala Met Leu Glu Arg
 265 270 275

gca gaa cgc tcc tgg gta gac aaa gcc gct gca tac gat ttg cgc tgg 979
 Ala Glu Arg Ser Trp Val Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp
 280 285 290

tca gat cac tca cca ctg aac gtg atc tac tcc taaaatgctg ctgacaattc 1032
 Ser Asp His Ser Pro Leu Asn Val Ile Tyr Ser
 295 300

tat 1035

<210> 212
 <211> 304
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 212
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Val Lys Gln Arg Ser Glu Thr Asn Leu Gly Phe Leu Pro Trp Leu Glu
 20 25 30

Glu Thr Arg Pro Asp Val Val Leu Leu Gln Glu Val Arg Ala Ser Glu
 35 40 45

Lys Asp Thr Ala Thr Ala Leu Gln Pro Ala Leu Asp Asn Gly Trp His
 50 55 60

Tyr Ile Gly Ala Pro Ala Ala Ala Lys Gly Arg Ala Gly Val Gly Ile
 65 70 75 80

Leu Ser Arg His Glu Leu Glu Asp Val Asn Ile Gly Phe Gly Ser Phe
 85 90 95

Leu Asp Ser Gly Arg Tyr Ile Glu Ala Thr Ile Lys Asp Thr Thr Leu
 100 105 110

Asp Val Pro Val Thr Val Ala Ser Leu Tyr Leu Pro Ser Gly Ser Ala
 115 120 125

Gly Thr Asp Lys Gln Asp Glu Lys Tyr Arg Phe Leu Asp Glu Phe Glu
 130 135 140

Gly Phe Leu Asp Gln Arg Ala Lys Glu Arg Ser His Met Val Ile Gly
 145 150 155 160

Gly Asp Trp Asn Ile Cys His Arg Arg Glu Asp Leu Lys Asn Trp Lys
 165 170 175

Thr Asn Gln Lys Lys Ser Gly Phe Leu Pro Asp Glu Arg Ala Phe Met
 180 185 190

Asp Ser Val Phe Gly Thr Phe Pro Asp Glu Ala Thr Gln Val Ala Gly
 195 200 205

Ala Gly Asp Phe Phe Gly Ala Val Asp Tyr Glu Gly Thr Arg Arg Arg
 210 215 220

Glu Ala Thr Thr Asp Pro Ala Trp Phe Asp Val Ala Arg Arg Leu Gln
 225 230 235 240

Pro Glu Gly Asp Gly Pro Tyr Thr Trp Trp Thr Tyr Arg Gly Lys Ala
 245 250 255

Phe Asp Thr Gly Ala Gly Trp Arg Ile Asp Tyr Gln Ala Ala Thr Ala
 260 265 270

Ala Met Leu Glu Arg Ala Glu Arg Ser Trp Val Asp Lys Ala Ala Ala
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Tyr Asp Leu Arg Trp Ser Asp His Ser Pro Leu Asn Val Ile Tyr Ser
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<210> 213

<211> 1530

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1507)

<223> RXA00341

<400> 213

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cccctgcata tactttttccg ctgtggaaca atgggagcgc atg aag ctc tat gca 115
 Met Lys Leu Tyr Ala
 1 5

gca gtc ctc gac ttt gaa cca gtg gca caa gag ttc ggt gtg gag cga 163
 Ala Val Leu Asp Phe Glu Pro Val Ala Gln Glu Phe Gly Val Glu Arg
 10 15 20

ggt ttt gac cct cat atc cac gac gaa gcc gcg tca agt gtc gat agg 211
 Gly Phe Asp Pro His Ile His Asp Glu Ala Ala Ser Ser Val Asp Arg
 25 30 35

tat gcg caa gag cgg gaa gat ctc ctg cac atg ccc ttt gtc acc atc 259
 Tyr Ala Gln Glu Arg Glu Asp Leu Leu His Met Pro Phe Val Thr Ile
 40 45 50

gat ccc gta ggt tcc aga gac ctc gat caa gct gtg ctg att gag gag 307
 Asp Pro Val Gly Ser Arg Asp Leu Asp Gln Ala Val Leu Ile Glu Glu
 55 60 65

atc gac agc gga ttt cgg gtg cat tac gcg att gca gat gtc gca gcc 355
 Ile Asp Ser Gly Phe Arg Val His Tyr Ala Ile Ala Asp Val Ala Ala
 70 75 80 85

ttc gtg gag ccg ggc agt gaa ttg gaa aag att tcc ctt cac cgc ggg	403
Phe Val Glu Pro Gly Ser Glu Leu Glu Lys Ile Ser Leu His Arg Gly	
90 95 100	
cag act att tat ctg ccg gat tcc cca gcg cga ctg cac cct gag gaa	451
Gln Thr Ile Tyr Leu Pro Asp Ser Pro Ala Arg Leu His Pro Glu Glu	
105 110 115	
tta tcc gaa gat gcg gca agc ctg ctg gag gga caa acg aga cca gcg	499
Leu Ser Glu Asp Ala Ala Ser Leu Leu Glu Gly Gln Thr Arg Pro Ala	
120 125 130	
gtt gtg tgg tcg att gat cta gat gaa cgt ggc gaa gtc aca gcc acc	547
Val Val Trp Ser Ile Asp Leu Asp Glu Arg Gly Glu Val Thr Ala Thr	
135 140 145	
aag gtg cgt cgc ggg ttg gtg aaa tcc ccg gcg cgt ttg gat tat gat	595
Lys Val Arg Arg Gly Leu Val Lys Ser Arg Ala Arg Leu Asp Tyr Asp	
150 155 160 165	
cag gct caa ata gat gcc gag aat ggt ccg ttg cat ccg tcg ata agc	643
Gln Ala Gln Ile Asp Ala Glu Asn Gly Arg Leu His Pro Ser Ile Ser	
170 175 180	
tta ttg ccc aag gtc ggg cag ctg agg cag gaa agc gcg cta ccg cgc	691
Leu Leu Pro Lys Val Gly Gln Leu Arg Gln Glu Ser Ala Leu Arg Arg	
185 190 195	
gaa gcc gtg aat ctt tct att ccc agc cag cga gtg gtg aaa gtg ccc	739
Glu Ala Val Asn Leu Ser Ile Pro Ser Gln Arg Val Val Lys Val Pro	
200 205 210	
aat gat gac gcc ggt gaa cac tat gaa att gtc atc gag cca cgc ccg	787
Asn Asp Asp Ala Gly Glu His Tyr Glu Ile Val Ile Glu Pro Arg Pro	
215 220 225	
cac atc atg gat tac aat tcc gag att tcc ctg ctc aca ggc atg gta	835
His Ile Met Asp Tyr Asn Ser Glu Ile Ser Leu Leu Thr Gly Met Val	
230 235 240 245	
gcg ggg gag atg atg gtg aaa gcg ggg cac ggt ttg ctg cgt aca ctc	883
Ala Gly Glu Met Met Val Lys Ala Gly His Gly Leu Leu Arg Thr Leu	
250 255 260	
gcc ccg gcg acc aaa gaa tcc gaa gct act ttc aga tca gag gcg caa	931
Ala Pro Ala Thr Lys Glu Ser Glu Ala Thr Phe Arg Ser Glu Ala Gln	
265 270 275	
gcc ctt ggt ttt gag atc gcg ccc gaa caa ccc atc ggt gag ttt ctt	979
Ala Leu Gly Phe Glu Ile Ala Pro Glu Gln Pro Ile Gly Glu Phe Leu	
280 285 290	
caa agt gtg gat ccc aat acg ccc aaa ggg atg gcc att cag agg gaa	1027
Gln Ser Val Asp Pro Asn Thr Pro Lys Gly Met Ala Ile Gln Arg Glu	
295 300 305	
gca cag aaa ctc ttg ccg ggc tcc ggc tac gcc agc gtg aaa aat ggg	1075
Ala Gln Lys Leu Leu Arg Gly Ser Gly Tyr Ala Ser Val Lys Asn Gly	
310 315 320 325	

gac tcg gaa gtg cat tcc ggt gtt ggt ggt tac tat gct cac gtc acc 1123
 Asp Ser Glu Val His Ser Gly Val Gly Gly Tyr Tyr Ala His Val Thr
 330 335 340

gca ccg ctg cgc cga ctt atc gac cgt ttc gcc acc gaa cat tgc ctt 1171
 Ala Pro Leu Arg Arg Leu Ile Asp Arg Phe Ala Thr Glu His Cys Leu
 345 350 355

gcg att gcc tcc gga acg gac gtt cct gaa tgg gtg acc agg gtg gaa 1219
 Ala Ile Ala Ser Gly Thr Asp Val Pro Glu Trp Val Thr Arg Val Glu
 360 365 370

gag caa gtt ctc gac acc atg aaa tac tcc tcc att ttg gcc agc caa 1267
 Glu Gln Val Leu Asp Thr Met Lys Tyr Ser Ser Ile Leu Ala Ser Gln
 375 380 385

gtg gat aat gcc tgc ctc gac ctc aca gaa gcc acc gtg ttg aaa tac 1315
 Val Asp Asn Ala Cys Leu Asp Leu Thr Glu Ala Thr Val Leu Lys Tyr
 390 395 400 405

tgg gag ggc caa aac ttc aac gcg gtg gtt gta gcg agc gaa cct gaa 1363
 Trp Glu Gly Gln Asn Phe Asn Ala Val Val Val Ala Ser Glu Pro Glu
 410 415 420

aag aac tct gct cga ctt ttt gtg tac aaa ccg cca gtg ttg gca aag 1411
 Lys Asn Ser Ala Arg Leu Phe Val Tyr Lys Pro Pro Val Leu Ala Lys
 425 430 435

tgt att ggc gcc cca gaa cag gga aca aac caa gat gtc aca ctg gtg 1459
 Cys Ile Gly Ala Pro Glu Gln Gly Thr Asn Gln Asp Val Thr Leu Val
 440 445 450

act gcg aac ttg aag aag cgt gaa gtt ttg ttt gcg tgg ccg gct gac 1507
 Thr Ala Asn Leu Lys Lys Arg Glu Val Leu Phe Ala Trp Pro Ala Asp
 455 460 465

taagcatgca ggctgggttaa gta 1530

<210> 214

<211> 469

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

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Phe Gly Val Glu Arg Gly Phe Asp Pro His Ile His Asp Glu Ala Ala
 20 25 30

Ser Ser Val Asp Arg Tyr Ala Gln Glu Arg Glu Asp Leu Leu His Met
 35 40 45

Pro Phe Val Thr Ile Asp Pro Val Gly Ser Arg Asp Leu Asp Gln Ala
 50 55 60

Val Leu Ile Glu Glu Ile Asp Ser Gly Phe Arg Val His Tyr Ala Ile
 65 70 75 80

Ala Asp Val Ala Ala Phe Val Glu Pro Gly Ser Glu Leu Glu Lys Ile

85										90					95				
Ser	Leu	His	Arg	Gly	Gln	Thr	Ile	Tyr	Leu	Pro	Asp	Ser	Pro	Ala	Arg				
			100					105					110						
Leu	His	Pro	Glu	Glu	Leu	Ser	Glu	Asp	Ala	Ala	Ser	Leu	Leu	Glu	Gly				
		115					120					125							
Gln	Thr	Arg	Pro	Ala	Val	Val	Trp	Ser	Ile	Asp	Leu	Asp	Glu	Arg	Gly				
	130						135				140								
Glu	Val	Thr	Ala	Thr	Lys	Val	Arg	Arg	Gly	Leu	Val	Lys	Ser	Arg	Ala				
145					150					155					160				
Arg	Leu	Asp	Tyr	Asp	Gln	Ala	Gln	Ile	Asp	Ala	Glu	Asn	Gly	Arg	Leu				
				165					170					175					
His	Pro	Ser	Ile	Ser	Leu	Leu	Pro	Lys	Val	Gly	Gln	Leu	Arg	Gln	Glu				
			180					185					190						
Ser	Ala	Leu	Arg	Arg	Glu	Ala	Val	Asn	Leu	Ser	Ile	Pro	Ser	Gln	Arg				
		195					200					205							
Val	Val	Lys	Val	Pro	Asn	Asp	Asp	Ala	Gly	Glu	His	Tyr	Glu	Ile	Val				
	210					215					220								
Ile	Glu	Pro	Arg	Pro	His	Ile	Met	Asp	Tyr	Asn	Ser	Glu	Ile	Ser	Leu				
225					230					235					240				
Leu	Thr	Gly	Met	Val	Ala	Gly	Glu	Met	Met	Val	Lys	Ala	Gly	His	Gly				
			245					250						255					
Leu	Leu	Arg	Thr	Leu	Ala	Pro	Ala	Thr	Lys	Glu	Ser	Glu	Ala	Thr	Phe				
			260					265					270						
Arg	Ser	Glu	Ala	Gln	Ala	Leu	Gly	Phe	Glu	Ile	Ala	Pro	Glu	Gln	Pro				
		275					280					285							
Ile	Gly	Glu	Phe	Leu	Gln	Ser	Val	Asp	Pro	Asn	Thr	Pro	Lys	Gly	Met				
	290					295					300								
Ala	Ile	Gln	Arg	Glu	Ala	Gln	Lys	Leu	Leu	Arg	Gly	Ser	Gly	Tyr	Ala				
305					310					315					320				
Ser	Val	Lys	Asn	Gly	Asp	Ser	Glu	Val	His	Ser	Gly	Val	Gly	Gly	Tyr				
				325					330				335						
Tyr	Ala	His	Val	Thr	Ala	Pro	Leu	Arg	Arg	Leu	Ile	Asp	Arg	Phe	Ala				
			340					345					350						
Thr	Glu	His	Cys	Leu	Ala	Ile	Ala	Ser	Gly	Thr	Asp	Val	Pro	Glu	Trp				
		355					360					365							
Val	Thr	Arg	Val	Glu	Glu	Gln	Val	Leu	Asp	Thr	Met	Lys	Tyr	Ser	Ser				
	370					375					380								
Ile	Leu	Ala	Ser	Gln	Val	Asp	Asn	Ala	Cys	Leu	Asp	Leu	Thr	Glu	Ala				
385					390					395					400				
Thr	Val	Leu	Lys	Tyr	Trp	Glu	Gly	Gln	Asn	Phe	Asn	Ala	Val	Val	Val				
				405					410					415					

Ala Ser Glu Pro Glu Lys Asn Ser Ala Arg Leu Phe Val Tyr Lys Pro
 420 425 430

Pro Val Leu Ala Lys Cys Ile Gly Ala Pro Glu Gln Gly Thr Asn Gln
 435 440 445

Asp Val Thr Leu Val Thr Ala Asn Leu Lys Lys Arg Glu Val Leu Phe
 450 455 460

Ala Trp Pro Ala Asp
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<210> 215

<211> 519

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(496)

<223> RXA02077

<400> 215

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tggcagatat cgctcgcgaa attgatcttg gcaaccacat atg ctg ggc aaa ggc 115
 Met Leu Gly Lys Gly
 1 5

gaa ttg ctc acc gaa ggt cgc agt aag gat tcc att ctt gcg gac acc 163
 Glu Leu Leu Thr Glu Gly Arg Ser Lys Asp Ser Ile Leu Ala Asp Thr
 10 15 20

aca gag gcg ttg ttc ggc gcg att ttc cgc cag cac ggt ttt gaa acc 211
 Thr Glu Ala Leu Phe Gly Ala Ile Phe Arg Gln His Gly Phe Glu Thr
 25 30 35

gcc cgc gac gta att ttg cgc ctg ttt gcc tac aag atc gat aac gca 259
 Ala Arg Asp Val Ile Leu Arg Leu Phe Ala Tyr Lys Ile Asp Asn Ala
 40 45 50

tcg gcc agg ggc att cac cag gac tgg aag acc acg ctg cag gag gaa 307
 Ser Ala Arg Gly Ile His Gln Asp Trp Lys Thr Thr Leu Gln Glu Glu
 55 60 65

ctt gct cag cgc aag cgc ccc atg gct gaa tat tcc gcc acc tca gtc 355
 Leu Ala Gln Arg Lys Arg Pro Met Ala Glu Tyr Ser Ala Thr Ser Val
 70 75 80 85

ggc ccg gat cac gat cta gtg ttc acc gcc atc gtg acg ctg gaa ggt 403
 Gly Pro Asp His Asp Leu Val Phe Thr Ala Ile Val Thr Leu Glu Gly
 90 95 100

gaa gaa atg ggt cgg gga gaa ggc ccg aac aag aag ctg gcc gag cag 451
 Glu Glu Met Gly Arg Gly Glu Gly Pro Asn Lys Lys Leu Ala Glu Gln
 105 110 115

gaa gca gcg cac cag gca ttc cga aag ctt cgg gag tcc cgt gcc 496
 Glu Ala Ala His Gln Ala Phe Arg Lys Leu Arg Glu Ser Arg Ala

120

125

130

tgaactgcct gaagttgagg tgg

519

<210> 216

<211> 132

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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Ile	Leu	Ala	Asp	Thr	Thr	Glu	Ala	Leu	Phe	Gly	Ala	Ile	Phe	Arg	Gln
			20					25					30		

His	Gly	Phe	Glu	Thr	Ala	Arg	Asp	Val	Ile	Leu	Arg	Leu	Phe	Ala	Tyr
		35					40					45			

Lys	Ile	Asp	Asn	Ala	Ser	Ala	Arg	Gly	Ile	His	Gln	Asp	Trp	Lys	Thr
	50					55					60				

Thr	Leu	Gln	Glu	Glu	Leu	Ala	Gln	Arg	Lys	Arg	Pro	Met	Ala	Glu	Tyr
65					70					75				80	

Ser	Ala	Thr	Ser	Val	Gly	Pro	Asp	His	Asp	Leu	Val	Phe	Thr	Ala	Ile
				85					90					95	

Val	Thr	Leu	Glu	Gly	Glu	Glu	Met	Gly	Arg	Gly	Glu	Gly	Pro	Asn	Lys
		100						105					110		

Lys	Leu	Ala	Glu	Gln	Glu	Ala	Ala	His	Gln	Ala	Phe	Arg	Lys	Leu	Arg
	115						120					125			

Glu	Ser	Arg	Ala
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<210> 217

<211> 1332

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1309)

<223> RXN01563

<400> 217

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				Met	Val	Ser	Asp	Leu	
				1				5	

ctt	caa	ccc	cgc	gac	ggc	att	ccg	cct	ttg	cta	tct	acc	cct	ggt	gag	163
Leu	Gln	Pro	Arg	Asp	Gly	Ile	Pro	Pro	Leu	Leu	Ser	Thr	Pro	Gly	Glu	
				10					15					20		

ttc	act	gct	gcg	gca	gat	ctc	ttg	gct	agc	gga	act	ggg	ccc	ttc	gcc	211
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Phe Thr Ala Ala Ala Asp Leu Leu Ala Ser Gly Thr Gly Pro Phe Ala	
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Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr Asp Asp Arg Ala Phe	
40 45 50	
ttg att cag atc cgg cgc cgt ggc agc gga act ctc cta ttc gac ccg	307
Leu Ile Gln Ile Arg Arg Arg Gly Ser Gly Thr Leu Leu Phe Asp Pro	
55 60 65	
gag cag ttc cgt cct gaa tta act cag gcg tta aag ccg gtg ctc aat	355
Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu Lys Pro Val Leu Asn	
70 75 80 85	
ggt caa gag tgg atc att cac gca gca agc acc gat ttg ccg agc ctt	403
Gly Gln Glu Trp Ile Ile His Ala Ala Ser Thr Asp Leu Pro Ser Leu	
90 95 100	
gcg tgg ctt gat ctt cac ccc gga tta ctc ttt gat aca gaa ctt gct	451
Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe Asp Thr Glu Leu Ala	
105 110 115	
ggc cgc tta gcc gga ttt gat cac gtt aat ctc gct gcc atg gtg gaa	499
Gly Arg Leu Ala Gly Phe Asp His Val Asn Leu Ala Ala Met Val Glu	
120 125 130	
cag att ttt gat ctc cac ttg ctc aaa ggc cac cgt tcg gaa gat tgg	547
Gln Ile Phe Asp Leu His Leu Leu Lys Gly His Arg Ser Glu Asp Trp	
135 140 145	
tcc aag cgt cct ctg ccg gaa tct tgg ctc aac tac gca gca ctc gat	595
Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn Tyr Ala Ala Leu Asp	
150 155 160 165	
gtg gag atg ctg ctg gag ctt gcc gat gtc atg gct gaa atc ctg gat	643
Val Glu Met Leu Leu Glu Leu Ala Asp Val Met Ala Glu Ile Leu Asp	
170 175 180	
cag cag gga aaa ctc ccc tgg gct gaa cag gaa ttt gtc cat att gtg	691
Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu Phe Val His Ile Val	
185 190 195	
gat caa ttc gcc acg atg acc gaa cct tcc gaa acg tcc tgg cag gac	739
Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu Thr Ser Trp Gln Asp	
200 205 210	
ctt aaa ggg ctg tcc act ctc aaa cga cca gac caa tta gtt gtg gcc	787
Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp Gln Leu Val Val Ala	
215 220 225	
cgt gaa atg tgg ttg gaa cgc gac tct ttc gca gcc tcc cgc gac ctg	835
Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala Ala Ser Arg Asp Leu	
230 235 240 245	
gcg ccc ggt aaa gtg ctg tcc aac aaa gtc atc gtg gaa gtc gcc cgt	883
Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile Val Glu Val Ala Arg	
250 255 260	
gtt ctc ccc cgc acc ccg gca gaa tta gcg cag gtc aag gga ttc ccc	931
Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln Val Lys Gly Phe Pro	

265	270	275	
ggt cga tcc cag ggt gcc acc aaa cgc tgg ttc cgc atc atc acc cgg Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe Arg Ile Ile Thr Arg 280 285 290			979
gcg ctc aaa tcc cct cgc agg aac tgg cca aag cct cag cag cgc aag Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys Pro Gln Gln Arg Lys 295 300 305			1027
gac ggc atc ccc gat cgt cgc gcg tgg gcg tcc tac tac cca gaa gag Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser Tyr Tyr Pro Glu Glu 310 315 320 325			1075
cac gaa gtg ctc caa gag att aga gcg ctt atc gac gac ctc gcc gcc His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile Asp Asp Leu Ala Ala 330 335 340			1123
gat atc aac gtt ccc ggc gag aat atc ctt cag cct tca act ctg cga Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln Pro Ser Thr Leu Arg 345 350 355			1171
gta gct gtg tgg atg gct aaa cac acc ggc gag atc cat aat gct gaa Val Ala Val Trp Met Ala Lys His Thr Gly Glu Ile His Asn Ala Glu 360 365 370			1219
aca ctc aac gct gta ctt cgc gat tat ggt gcc cgc cag tgg caa att Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala Arg Gln Trp Gln Ile 375 380 385			1267
gac cag act ttt ccg att ctg tcc gcc aac ttg ctg aag ctc Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu Leu Lys Leu 390 395 400			1309
taaacctaaa gcccgcggt aag			1332

<210> 218

<211> 403

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

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Ser	Thr	Pro	Gly	Glu	Phe	Thr	Ala	Ala	Ala	Asp	Leu	Leu	Ala	Ser	Gly
			20					25					30		

Thr	Gly	Pro	Phe	Ala	Ile	Asp	Thr	Glu	Arg	Ala	Ser	Gly	Phe	Arg	Tyr
		35					40					45			

Asp	Asp	Arg	Ala	Phe	Leu	Ile	Gln	Ile	Arg	Arg	Arg	Gly	Ser	Gly	Thr
	50					55					60				

Leu	Leu	Phe	Asp	Pro	Glu	Gln	Phe	Arg	Pro	Glu	Leu	Thr	Gln	Ala	Leu
65						70				75					80

Lys	Pro	Val	Leu	Asn	Gly	Gln	Glu	Trp	Ile	Ile	His	Ala	Ala	Ser	Thr
				85					90					95	

Asp Leu Pro Ser Leu Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe
100 105 110

Asp Thr Glu Leu Ala Gly Arg Leu Ala Gly Phe Asp His Val Asn Leu
115 120 125

Ala Ala Met Val Glu Gln Ile Phe Asp Leu His Leu Leu Lys Gly His
130 135 140

Arg Ser Glu Asp Trp Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn
145 150 155 160

Tyr Ala Ala Leu Asp Val Glu Met Leu Leu Glu Leu Ala Asp Val Met
165 170 175

Ala Glu Ile Leu Asp Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu
180 185 190

Phe Val His Ile Val Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu
195 200 205

Thr Ser Trp Gln Asp Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp
210 215 220

Gln Leu Val Val Ala Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala
225 230 235 240

Ala Ser Arg Asp Leu Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile
245 250 255

Val Glu Val Ala Arg Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln
260 265 270

Val Lys Gly Phe Pro Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe
275 280 285

Arg Ile Ile Thr Arg Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys
290 295 300

Pro Gln Gln Arg Lys Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser
305 310 315 320

Tyr Tyr Pro Glu Glu His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile
325 330 335

Asp Asp Leu Ala Ala Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln
340 345 350

Pro Ser Thr Leu Arg Val Ala Val Trp Met Ala Lys His Thr Gly Glu
355 360 365

Ile His Asn Ala Glu Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala
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Arg Gln Trp Gln Ile Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu
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Leu Lys Leu

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<211> 833
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (1)..(810)
<223> FRXA01563

<400> 219
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tcc aag cgt cct ctg ccg gaa tct tgg ctc aac tac gca gca ctc gat 96
Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn Tyr Ala Ala Leu Asp
20 25 30
gtg gag atg ctg ctg gag ctt gcc gat gtc atg gct gaa atc ctg gat 144
Val Glu Met Leu Leu Glu Leu Ala Asp Val Met Ala Glu Ile Leu Asp
35 40 45
cag cag gga aaa ctc ccc tgg gct gaa cag gaa ttt gtc cat att gtg 192
Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu Phe Val His Ile Val
50 55 60
gat caa ttc gcc acg atg acc gaa cct tcc gaa acg tcc tgg cag gac 240
Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu Thr Ser Trp Gln Asp
65 70 75 80
ctt aaa ggg ctg tcc act ctc aaa cga cca gac caa tta gtt gtg gcc 288
Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp Gln Leu Val Val Ala
85 90 95
cgt gaa atg tgg ttg gaa cgc gac tct ttc gca gcc tcc cgc gac ctg 336
Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala Ala Ser Arg Asp Leu
100 105 110
gcg ccc ggt aaa gtg ctg tcc aac aaa gtc atc gtg gaa gtc gcc cgt 384
Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile Val Glu Val Ala Arg
115 120 125
gtt ctc ccc cgc acc ccg gca gaa tta gcg cag gtc aag gga ttc ccc 432
Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln Val Lys Gly Phe Pro
130 135 140
ggt cga tcc cag ggt gcc acc aaa cgc tgg ttc cgc atc atc acc cgg 480
Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe Arg Ile Ile Thr Arg
145 150 155 160
gcg ctc aaa tcc cct cgc agg aac tgg cca aag cct cag cag cgc aag 528
Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys Pro Gln Gln Arg Lys
165 170 175
gac ggc atc ccc gat cgt cgc gcg tgg gcg tcc tac tac cca gaa gag 576
Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser Tyr Tyr Pro Glu Glu
180 185 190
cac gaa gtg ctc caa gag att aga gcg ctt atc gac gac ctc gcc gcc 624
His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile Asp Asp Leu Ala Ala

195	200	205	
gat atc aac gtt ccc ggc gag aat atc ctt cag cct tca act ctg cga			672
Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln Pro Ser Thr Leu Arg			
210	215	220	
gta gct gtg tgg atg gct aaa cac acc ggc gag atc cat aat gct gaa			720
Val Ala Val Trp Met Ala Lys His Thr Gly Glu Ile His Asn Ala Glu			
225	230	235	240
aca ctc aac gct gta ctt cgc gat tat ggt gcc cgc cag tgg caa att			768
Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala Arg Gln Trp Gln Ile			
245	250		255
gac cag act ttt ccg att ctg tcc gcc aac ttg ctg aag ctc			810
Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu Leu Lys Leu			
260	265		270
taaacctaaa gcccgcggt aag			833

<210> 220

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

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Val Glu Met Leu Leu Glu Leu Ala Asp Val Met Ala Glu Ile Leu Asp	
35 40 45	

Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu Phe Val His Ile Val	
50 55 60	

Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu Thr Ser Trp Gln Asp	
65 70 75 80	

Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp Gln Leu Val Val Ala	
85 90 95	

Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala Ala Ser Arg Asp Leu	
100 105 110	

Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile Val Glu Val Ala Arg	
115 120 125	

Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln Val Lys Gly Phe Pro	
130 135 140	

Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe Arg Ile Ile Thr Arg	
145 150 155 160	

Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys Pro Gln Gln Arg Lys	
165 170 175	

Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser Tyr Tyr Pro Glu Glu	
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180	185	190
His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile Asp Asp Leu Ala Ala		
195	200	205
Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln Pro Ser Thr Leu Arg		
210	215	220
Val Ala Val Trp Met Ala Lys His Thr Gly Glu Ile His Asn Ala Glu		
225	230	235
Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala Arg Gln Trp Gln Ile		
245	250	255
Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu Leu Lys Leu		
260	265	270

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(454)
 <223> FRXA01713

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 ccagagggcg tcaccgaact acgaaggtag attggacacc atg gtt tcc gat .ctc 115
 Met Val Ser Asp Leu
 1 5
 ctt caa ccc cgc gac ggc att ccg cct ttg cta tct acc cct ggt gag 163
 Leu Gln Pro Arg Asp Gly Ile Pro Pro Leu Leu Ser Thr Pro Gly Glu
 10 15 20
 ttc act gct gcg gca gat ctc ttg gct agc gga act ggg ccc ttc gcc 211
 Phe Thr Ala Ala Ala Asp Leu Leu Ala Ser Gly Thr Gly Pro Phe Ala
 25 30 35
 att gat acg gaa cgc gcg tcc ggt ttt aga tac gat gac cgc gca ttt 259
 Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr Asp Asp Arg Ala Phe
 40 45 50
 ttg att cag atc cgg cgc cgt ggc agc gga act ctc cta ttc gac ccg 307
 Leu Ile Gln Ile Arg Arg Arg Gly Ser Gly Thr Leu Leu Phe Asp Pro
 55 60 65
 gag cag ttc cgt cct gaa tta act cag gcg tta aag ccg gtg ctc aat 355
 Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu Lys Pro Val Leu Asn
 70 75 80 85
 ggt caa gag tgg atc att cac gca gca agc acc gat ttg ccg agc ctt 403
 Gly Gln Glu Trp Ile Ile His Ala Ala Ser Thr Asp Leu Pro Ser Leu
 90 95 100
 gcg tgg ctt gat ctt cac ccc gga tta ctc ttt gat aca gaa ctt gct 451
 Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe Asp Thr Glu Leu Ala

105

110

115

ggc
Gly

454

<210> 222
 <211> 118
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 222
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 Ser Thr Pro Gly Glu Phe Thr Ala Ala Ala Asp Leu Leu Ala Ser Gly
 20 25 30
 Thr Gly Pro Phe Ala Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr
 35 40 45
 Asp Asp Arg Ala Phe Leu Ile Gln Ile Arg Arg Arg Gly Ser Gly Thr
 50 55 60
 Leu Leu Phe Asp Pro Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu
 65 70 75 80
 Lys Pro Val Leu Asn Gly Gln Glu Trp Ile Ile His Ala Ala Ser Thr
 85 90 95
 Asp Leu Pro Ser Leu Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe
 100 105 110
 Asp Thr Glu Leu Ala Gly
 115

<210> 223
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(2389)
 <223> RXA02369

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 cattgctcaa tcgtggagat aagaaaatag gagtgtcgct gtg cca aat aac aag 115
 Val Pro Asn Asn Lys
 1 5
 gca gta gaa gca gaa atc tct ccc tcg gct gtg ctg gcc gcg gaa ttt 163
 Ala Val Glu Ala Glu Ile Ser Pro Ser Ala Val Leu Ala Ala Glu Phe
 10 15 20
 gat cga gat tca ttg agc gaa aaa acc cgc gta cat caa ctg gcc aaa 211
 Asp Arg Asp Ser Leu Ser Glu Lys Thr Arg Val His Gln Leu Ala Lys

25										30					35					
cga	ctt	gga	atg	gtt	tcc	aag	gac	gtc	gtt	gtt	gcg	ctc	gat	ggc	atc	259				
Arg	Leu	Gly	Met	Val	Ser	Lys	Asp	Val	Val	Val	Ala	Leu	Asp	Gly	Ile					
		40					45					50								
ggc	ctg	gtc	aag	gtt	gcg	cag	tca	aac	ctg	agc	aaa	gaa	gaa	gta	gaa	307				
Gly	Leu	Val	Lys	Val	Ala	Gln	Ser	Asn	Leu	Ser	Lys	Glu	Glu	Val	Glu					
	55					60					65									
aag	ctt	ctc	gac	gcc	ctg	tct	cag	ccc	gta	ctc	aac	gct	gcc	cca	gct	355				
Lys	Leu	Leu	Asp	Ala	Leu	Ser	Gln	Pro	Val	Leu	Asn	Ala	Ala	Pro	Ala					
	70				75					80					85					
gcc	gtc	ccc	gac	gtt	gaa	ccg	gtg	gag	aag	att	cgt	cga	cgc	gtt	gag	403				
Ala	Val	Pro	Asp	Val	Glu	Pro	Val	Glu	Lys	Ile	Arg	Arg	Arg	Val	Glu					
				90					95					100						
aag	aat	gtg	gaa	aat	gaa	atc	cac	caa	atc	gaa	gaa	aaa	gta	gag	cgc	451				
Lys	Asn	Val	Glu	Asn	Glu	Ile	His	Gln	Ile	Glu	Glu	Lys	Val	Glu	Arg					
			105					110					115							
gaa	ctc	gcg	gca	gtc	gcg	caa	cct	act	gac	ttc	gag	gcg	gca	gcc	cgc	499				
Glu	Leu	Ala	Ala	Val	Ala	Gln	Pro	Thr	Asp	Phe	Glu	Ala	Ala	Ala	Arg					
		120				125						130								
gaa	gaa	gcc	act	gca	gaa	ctg	ctg	gaa	gat	atc	gtc	cca	gag	atc	acc	547				
Glu	Glu	Ala	Thr	Ala	Glu	Leu	Leu	Glu	Asp	Ile	Val	Pro	Glu	Ile	Thr					
	135					140					145									
ccg	gcg	ccg	gtg	gaa	gca	tct	gtg	tac	acg	ccg	atc	ttt	gtg	gca	cct	595				
Pro	Ala	Pro	Val	Glu	Ala	Ser	Val	Tyr	Thr	Pro	Ile	Phe	Val	Ala	Pro					
	150				155					160					165					
gca	gtt	gta	cct	act	gaa	aac	gtc	caa	gac	acc	gac	gat	gaa	cag	gtc	643				
Ala	Val	Val	Pro	Thr	Glu	Asn	Val	Gln	Asp	Thr	Asp	Asp	Glu	Gln	Val					
				170					175					180						
cgc	gaa	cgc	acg	gcg	cgg	aag	cgc	cgt	ggg	cgt	cgt	ggc	acc	ggc	cgc	691				
Arg	Glu	Arg	Thr	Ala	Arg	Lys	Arg	Arg	Gly	Arg	Arg	Gly	Thr	Gly	Arg					
			185					190					195							
gga	cgt	gga	gct	gaa	gct	gaa	acc	gtc	acc	gaa	gtg	agt	gag	gag	gcg	739				
Gly	Arg	Gly	Ala	Glu	Ala	Glu	Thr	Val	Thr	Glu	Val	Ser	Glu	Glu	Ala					
		200					205					210								
tcg	aca	agc	gaa	gta	gaa	gag	gta	aac	gag	cca	atc	gga	att	aag	ggc	787				
Ser	Thr	Ser	Glu	Val	Glu	Glu	Val	Asn	Glu	Pro	Ile	Gly	Ile	Lys	Gly					
	215					220					225									
tcc	act	cgc	ttg	gag	gcg	caa	cgc	cgc	cgt	cgc	acg	gaa	atg	cgc	gaa	835				
Ser	Thr	Arg	Leu	Glu	Ala	Gln	Arg	Arg	Arg	Arg	Thr	Glu	Met	Arg	Glu					
	230				235					240					245					
gaa	aac	aaa	aaa	cgc	cgc	cat	gtg	gtc	agc	acc	cag	gag	ttc	atg	gaa	883				
Glu	Asn	Lys	Lys	Arg	Arg	His	Val	Val	Ser	Thr	Gln	Glu	Phe	Met	Glu					
				250					255					260						
cgc	cgt	gaa	tcg	atg	gaa	cgt	cgc	atg	att	gtg	cgc	gag	cgc	caa	cgc	931				
Arg	Arg	Glu	Ser	Met	Glu	Arg	Arg	Met	Ile	Val	Arg	Glu	Arg	Gln	Arg					
		265						270					275							

cac gat cac cca ggt ctg gtc act cag gtt ggt gtg ctg gaa gac gat His Asp His Pro Gly Leu Val Thr Gln Val Gly Val Leu Glu Asp Asp 280 285 290	979
cag ctg gtt gag cag ttt gtt acc tct gat gcg cag atg tct atg gtg Gln Leu Val Glu Gln Phe Val Thr Ser Asp Ala Gln Met Ser Met Val 295 300 305	1027
ggc aat att tat ctg ggg cgc gtt caa aat gtg ctg cca agc atg gaa Gly Asn Ile Tyr Leu Gly Arg Val Gln Asn Val Leu Pro Ser Met Glu 310 315 320 325	1075
gct gcc ttc att gac att gga aaa ggt cgc aac ggt gtg ttg tat gcc Ala Ala Phe Ile Asp Ile Gly Lys Gly Arg Asn Gly Val Leu Tyr Ala 330 335 340	1123
ggc gaa gtc gac tgg aaa gct gct gga ctt ggc gga cgt gga cgt cgc Gly Glu Val Asp Trp Lys Ala Ala Gly Leu Gly Gly Arg Gly Arg Arg 345 350 355	1171
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aag gat cca ttg ggc cat aag ggt gcg cgt ttg acc acc caa att tcc Lys Asp Pro Leu Gly His Lys Gly Ala Arg Leu Thr Thr Gln Ile Ser 375 380 385	1267
ctg gcg gga cgt tac ctg gtg tac gtt cca ggt ggt cgc agc gct ggc Leu Ala Gly Arg Tyr Leu Val Tyr Val Pro Gly Gly Arg Ser Ala Gly 390 395 400 405	1315
att tcc cgc aaa ctg cct gga cct gag cgc aag cgt ctg aag gaa atc Ile Ser Arg Lys Leu Pro Gly Pro Glu Arg Lys Arg Leu Lys Glu Ile 410 415 420	1363
ctt ggc cgc gtt gtc cca gcg cag ggt gga acc atc atc cga act gct Leu Gly Arg Val Val Pro Ala Gln Gly Gly Thr Ile Ile Arg Thr Ala 425 430 435	1411
gct gaa ggt gtg tcg gaa gaa aac atc gca gct gac gtg aac cgt ctg Ala Glu Gly Val Ser Glu Glu Asn Ile Ala Ala Asp Val Asn Arg Leu 440 445 450	1459
cac acc ctg tgg gag cag atc aag gaa cgc act gcg gag gaa aag aag His Thr Leu Trp Glu Gln Ile Lys Glu Arg Thr Ala Glu Glu Lys Lys 455 460 465	1507
tcc cgc ggt tct aag ccg atc acc atg tat gaa gag cca gac atg ctg Ser Arg Gly Ser Lys Pro Ile Thr Met Tyr Glu Glu Pro Asp Met Leu 470 475 480 485	1555
gtg aag gtg atc cgt gac ctc ttc aat gaa gat ttc acc tca ctg atc Val Lys Val Ile Arg Asp Leu Phe Asn Glu Asp Phe Thr Ser Leu Ile 490 495 500	1603
gtt gac ggc gac cgt gcc tgg aac acc gtg cgt gcc tac atc caa tca Val Asp Gly Asp Arg Ala Trp Asn Thr Val Arg Ala Tyr Ile Gln Ser 505 510 515	1651

gtc gct cct gat ttg gtg tcc cgc gtg gaa cac ttc aat cgc gca gac	1699
Val Ala Pro Asp Leu Val Ser Arg Val Glu His Phe Asn Arg Ala Asp	
520 525 530	
ttt gac ggc aag gat gct ttc gaa gca ttc gac ctg aac acc cag ctt	1747
Phe Asp Gly Lys Asp Ala Phe Glu Ala Phe Asp Leu Asn Thr Gln Leu	
535 540 545	
gag gaa gcg ctg tcc cga aag gtg aac ctg cca tcg ggt gga tcg ctg	1795
Glu Glu Ala Leu Ser Arg Lys Val Asn Leu Pro Ser Gly Gly Ser Leu	
550 555 560 565	
atc atc gac cgc acc gaa gcc atg acg gtg atc gat gtg aac acc gga	1843
Ile Ile Asp Arg Thr Glu Ala Met Thr Val Ile Asp Val Asn Thr Gly	
570 575 580	
cgc tac acc ggc aag ggt ggt ggc aac ttg gaa gaa acc gtc acg ctc	1891
Arg Tyr Thr Gly Lys Gly Gly Gly Asn Leu Glu Glu Thr Val Thr Leu	
585 590 595	
aac aac att gaa gct gcc gaa gaa atc gtg cgc caa atg cgc ctg cgg	1939
Asn Asn Ile Glu Ala Ala Glu Glu Ile Val Arg Gln Met Arg Leu Arg	
600 605 610	
gat ctc ggt ggc atg atc gtt gtc gac ttc atc gat atg gtg ctg cca	1987
Asp Leu Gly Gly Met Ile Val Val Asp Phe Ile Asp Met Val Leu Pro	
615 620 625	
gaa aac caa gaa ttg gtc ctg cgc cga ctc aat gaa gcg cta gaa aac	2035
Glu Asn Gln Glu Leu Val Leu Arg Arg Leu Asn Glu Ala Leu Glu Asn	
630 635 640 645	
gat cgc acc cgc cac caa gtc tct gag gta acc tca ctg gga ctt gtt	2083
Asp Arg Thr Arg His Gln Val Ser Glu Val Thr Ser Leu Gly Leu Val	
650 655 660	
cag atg acc cgc aaa cgc atc ggc gcg ggc ctg ctg gaa acc ttc tct	2131
Gln Met Thr Arg Lys Arg Ile Gly Ala Gly Leu Leu Glu Thr Phe Ser	
665 670 675	
tca ccg tgt gag cac tgt gaa ggc cga ggc atc atc gtt cat gtt gat	2179
Ser Pro Cys Glu His Cys Glu Gly Arg Gly Ile Ile Val His Val Asp	
680 685 690	
cca gta gac acc gtt gac gag cgc gtt gag gcg aaa gcg gaa gag cgt	2227
Pro Val Asp Thr Val Asp Glu Arg Val Glu Ala Lys Ala Glu Glu Arg	
695 700 705	
agc cgt cgt cac cag cgt tcc aat agc act aac aag gca gct gcg gag	2275
Ser Arg Arg His Gln Arg Ser Asn Ser Thr Asn Lys Ala Ala Ala Glu	
710 715 720 725	
cac ccg atg gtt gtt gcc atg cgt gat ctc gtg gaa agc gat gaa cac	2323
His Pro Met Val Val Ala Met Arg Asp Leu Val Glu Ser Asp Glu His	
730 735 740	
gat ctg gat caa gaa ttt gag gaa ctc gct gca tca atg atc gtt ctc	2371
Asp Leu Asp Gln Glu Phe Glu Glu Leu Ala Ala Ser Met Ile Val Leu	
745 750 755	
gat gac tcc gat cta tta tgatgtggac aacgacaagc tcg	2412

Asp Asp Ser Asp Leu Leu
760

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<211> 763

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

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Leu Ala Ala Glu Phe Asp Arg Asp Ser Leu Ser Glu Lys Thr Arg Val
20 25 30

His Gln Leu Ala Lys Arg Leu Gly Met Val Ser Lys Asp Val Val Val
35 40 45

Ala Leu Asp Gly Ile Gly Leu Val Lys Val Ala Gln Ser Asn Leu Ser
50 55 60

Lys Glu Glu Val Glu Lys Leu Leu Asp Ala Leu Ser Gln Pro Val Leu
65 70 75 80

Asn Ala Ala Pro Ala Ala Val Pro Asp Val Glu Pro Val Glu Lys Ile
85 90 95

Arg Arg Arg Val Glu Lys Asn Val Glu Asn Glu Ile His Gln Ile Glu
100 105 110

Glu Lys Val Glu Arg Glu Leu Ala Val Ala Gln Pro Thr Asp Phe
115 120 125

Glu Ala Ala Ala Arg Glu Glu Ala Thr Ala Glu Leu Leu Glu Asp Ile
130 135 140

Val Pro Glu Ile Thr Pro Ala Pro Val Glu Ala Ser Val Tyr Thr Pro
145 150 155 160

Ile Phe Val Ala Pro Ala Val Val Pro Thr Glu Asn Val Gln Asp Thr
165 170 175

Asp Asp Glu Gln Val Arg Glu Arg Thr Ala Arg Lys Arg Arg Gly Arg
180 185 190

Arg Gly Thr Gly Arg Gly Arg Gly Ala Glu Ala Glu Thr Val Thr Glu
195 200 205

Val Ser Glu Glu Ala Ser Thr Ser Glu Val Glu Glu Val Asn Glu Pro
210 215 220

Ile Gly Ile Lys Gly Ser Thr Arg Leu Glu Ala Gln Arg Arg Arg Arg
225 230 235 240

Thr Glu Met Arg Glu Glu Asn Lys Lys Arg Arg His Val Val Ser Thr
245 250 255

Gln Glu Phe Met Glu Arg Arg Glu Ser Met Glu Arg Arg Met Ile Val
260 265 270

Arg Glu Arg Gln Arg His Asp His Pro Gly Leu Val Thr Gln Val Gly
275 280 285

Val Leu Glu Asp Asp Gln Leu Val Glu Gln Phe Val Thr Ser Asp Ala
290 295 300

Gln Met Ser Met Val Gly Asn Ile Tyr Leu Gly Arg Val Gln Asn Val
305 310 315 320

Leu Pro Ser Met Glu Ala Ala Phe Ile Asp Ile Gly Lys Gly Arg Asn
325 330 335

Gly Val Leu Tyr Ala Gly Glu Val Asp Trp Lys Ala Ala Gly Leu Gly
340 345 350

Gly Arg Gly Arg Arg Ile Glu Gln Ala Leu Lys Ala Gly Asp Gln Val
355 360 365

Leu Val Gln Val Ser Lys Asp Pro Leu Gly His Lys Gly Ala Arg Leu
370 375 380

Thr Thr Gln Ile Ser Leu Ala Gly Arg Tyr Leu Val Tyr Val Pro Gly
385 390 395 400

Gly Arg Ser Ala Gly Ile Ser Arg Lys Leu Pro Gly Pro Glu Arg Lys
405 410 415

Arg Leu Lys Glu Ile Leu Gly Arg Val Val Pro Ala Gln Gly Gly Thr
420 425 430

Ile Ile Arg Thr Ala Ala Glu Gly Val Ser Glu Glu Asn Ile Ala Ala
435 440 445

Asp Val Asn Arg Leu His Thr Leu Trp Glu Gln Ile Lys Glu Arg Thr
450 455 460

Ala Glu Glu Lys Lys Ser Arg Gly Ser Lys Pro Ile Thr Met Tyr Glu
465 470 475 480

Glu Pro Asp Met Leu Val Lys Val Ile Arg Asp Leu Phe Asn Glu Asp
485 490 495

Phe Thr Ser Leu Ile Val Asp Gly Asp Arg Ala Trp Asn Thr Val Arg
500 505 510

Ala Tyr Ile Gln Ser Val Ala Pro Asp Leu Val Ser Arg Val Glu His
515 520 525

Phe Asn Arg Ala Asp Phe Asp Gly Lys Asp Ala Phe Glu Ala Phe Asp
530 535 540

Leu Asn Thr Gln Leu Glu Glu Ala Leu Ser Arg Lys Val Asn Leu Pro
545 550 555 560

Ser Gly Gly Ser Leu Ile Ile Asp Arg Thr Glu Ala Met Thr Val Ile
565 570 575

Asp Val Asn Thr Gly Arg Tyr Thr Gly Lys Gly Gly Gly Asn Leu Glu
580 585 590

Glu Thr Val Thr Leu Asn Asn Ile Glu Ala Ala Glu Glu Ile Val Arg

595					600					605				
Gln Met Arg Leu Arg Asp	Leu Gly Gly Met Ile Val Val Asp Phe Ile													
610	615				620									
Asp Met Val Leu Pro Glu Asn Gln Glu Leu Val Leu Arg Arg Leu Asn														
625	630				635								640	
Glu Ala Leu Glu Asn Asp Arg Thr Arg His Gln Val Ser Glu Val Thr														
	645				650								655	
Ser Leu Gly Leu Val Gln Met Thr Arg Lys Arg Ile Gly Ala Gly Leu														
	660				665								670	
Leu Glu Thr Phe Ser Ser Pro Cys Glu His Cys Glu Gly Arg Gly Ile														
	675				680								685	
Ile Val His Val Asp Pro Val Asp Thr Val Asp Glu Arg Val Glu Ala														
	690				695								700	
Lys Ala Glu Glu Arg Ser Arg Arg His Gln Arg Ser Asn Ser Thr Asn														
	705				710								720	
Lys Ala Ala Ala Glu His Pro Met Val Val Ala Met Arg Asp Leu Val														
	725				730								735	
Glu Ser Asp Glu His Asp Leu Asp Gln Glu Phe Glu Glu Leu Ala Ala														
	740				745								750	
Ser Met Ile Val Leu Asp Asp Ser Asp Leu Leu														
	755				760									

<210> 225

<211> 915

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(892)

<223> RXN02370

<400> 225

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caagaatttg aggaactcgc tgcataatg atcgttctcg	atg act ccg atc tat	115
	Met Thr Pro Ile Tyr	
	1	5

gat gat gtg gac aac gac aag ctc gac gag cct gag cgc att ctt gct	163
Asp Asp Val Asp Asn Asp Lys Leu Asp Glu Pro Glu Arg Ile Leu Ala	
	10 15 20

gaa tcc acc gtg gaa ccg gag gaa gga cca cgc atg agg gcc cgc cgt	211
Glu Ser Thr Val Glu Pro Glu Glu Gly Pro Arg Met Arg Ala Arg Arg	
	25 30 35

caa cgt cag gaa tct gct gcg gat gat att gcc gcg att gca gct gct	259
Gln Arg Gln Glu Ser Ala Ala Asp Asp Ile Ala Ala Ala Ala Ala Ala	
	40 45 50

gcc gtg gac att gct tct gaa gaa gac cct gat gag cct tcg gga tcg	307
Ala Val Asp Ile Ala Ser Glu Glu Asp Pro Asp Glu Pro Ser Gly Ser	
55 60 65	
tcg tat gtg tct gac ttt gag gca gag cct att gca cct gta gtt gag	355
Ser Tyr Val Ser Asp Phe Glu Ala Glu Pro Ile Ala Pro Val Val Glu	
70 75 80 85	
aag gct gct gaa cct gtg gct gag cca acc gct gat tat gaa aag gca	403
Lys Ala Ala Glu Pro Val Ala Glu Pro Thr Ala Asp Tyr Glu Lys Ala	
90 95 100	
cgt gcc gaa ttt gag gca agc cca cgc agg cgc cgc aag act cgt ggc	451
Arg Ala Glu Phe Glu Ala Ser Pro Arg Arg Arg Arg Lys Thr Arg Gly	
105 110 115	
aat tca cgt tcg gat cat gct cca aag cca gag gat ttc gca cct gta	499
Asn Ser Arg Ser Asp His Ala Pro Lys Pro Glu Asp Phe Ala Pro Val	
120 125 130	
gtt gaa gag gtt gct gag act cca gtg aag aca cct gcg cgg aag gct	547
Val Glu Glu Val Ala Glu Thr Pro Val Lys Thr Pro Ala Arg Lys Ala	
135 140 145	
cca cgc cgt aac cgt cca agt gag ctc agt tcc ggt gcg ccg tcc tct	595
Pro Arg Arg Asn Arg Pro Ser Glu Leu Ser Ser Gly Ala Pro Ser Ser	
150 155 160 165	
gca cca tcg acc agg aac cgt cgc cgc gca gtg cgc cgt caa ctg gtg	643
Ala Pro Ser Thr Arg Asn Arg Arg Arg Ala Val Arg Arg Gln Leu Val	
170 175 180	
gaa gct cct gag acc gtc gtt gag ata gca cct gaa gca gca cca gaa	691
Glu Ala Pro Glu Thr Val Val Glu Ile Ala Pro Glu Ala Ala Pro Glu	
185 190 195	
cag gtt gca gag cct cag gtt gaa ttc gac cag cca gac aac cgc cga	739
Gln Val Ala Glu Pro Gln Val Glu Phe Asp Gln Pro Asp Asn Arg Arg	
200 205 210	
aag cgt cgt cgt gct gtg cgc gtg aca gcg gcg ccg gtg gag aag aag	787
Lys Arg Arg Arg Ala Val Arg Val Thr Ala Ala Pro Val Glu Lys Lys	
215 220 225	
gtg gcg tcg aca agc aat gcg cgg gcg ccg aag aag gaa cct cag gcg	835
Val Ala Ser Thr Ser Asn Ala Arg Ala Pro Lys Lys Glu Pro Gln Ala	
230 235 240 245	
gcg agc acc acc aac cca ggc cgc cgt agg cgg gct acc cga cga ggc	883
Ala Ser Thr Thr Asn Pro Gly Arg Arg Arg Arg Ala Thr Arg Arg Gly	
250 255 260	
cca cga agc taggggtataa gggcggtttg tgt	915
Pro Arg Ser	

<210> 226

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

Met Thr Pro Ile Tyr Asp Asp Val Asp Asn Asp Lys Leu Asp Glu Pro
1 5 10 15
Glu Arg Ile Leu Ala Glu Ser Thr Val Glu Pro Glu Glu Gly Pro Arg
20 25 30
Met Arg Ala Arg Arg Gln Arg Gln Glu Ser Ala Ala Asp Asp Ile Ala
35 40 45
Ala Ile Ala Ala Ala Val Asp Ile Ala Ser Glu Glu Asp Pro Asp
50 55 60
Glu Pro Ser Gly Ser Ser Tyr Val Ser Asp Phe Glu Ala Glu Pro Ile
65 70 75 80
Ala Pro Val Val Glu Lys Ala Ala Glu Pro Val Ala Glu Pro Thr Ala
85 90 95
Asp Tyr Glu Lys Ala Arg Ala Glu Phe Glu Ala Ser Pro Arg Arg Arg
100 105 110
Arg Lys Thr Arg Gly Asn Ser Arg Ser Asp His Ala Pro Lys Pro Glu
115 120 125
Asp Phe Ala Pro Val Val Glu Glu Val Ala Glu Thr Pro Val Lys Thr
130 135 140
Pro Ala Arg Lys Ala Pro Arg Arg Asn Arg Pro Ser Glu Leu Ser Ser
145 150 155 160
Gly Ala Pro Ser Ser Ala Pro Ser Thr Arg Asn Arg Arg Arg Ala Val
165 170 175
Arg Arg Gln Leu Val Glu Ala Pro Glu Thr Val Val Glu Ile Ala Pro
180 185 190
Glu Ala Ala Pro Glu Gln Val Ala Glu Pro Gln Val Glu Phe Asp Gln
195 200 205
Pro Asp Asn Arg Arg Lys Arg Arg Arg Ala Val Arg Val Thr Ala Ala
210 215 220
Pro Val Glu Lys Lys Val Ala Ser Thr Ser Asn Ala Arg Ala Pro Lys
225 230 235 240
Lys Glu Pro Gln Ala Ala Ser Thr Thr Asn Pro Gly Arg Arg Arg Arg
245 250 255
Ala Thr Arg Arg Gly Pro Arg Ser
260

<210> 227

<211> 915

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(892)

<223> FRXA02370

<400> 227

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caagaatttg	aggaactcgc	tgcatcaatg	atcggttctcg	atg	act	ccg	atc	tat	115
				Met	Thr	Pro	Ile	Tyr	
				1				5	

tat	gat	gtg	gac	aac	gac	aag	ctc	gac	gag	cct	gag	cgc	att	ctt	gct	163
Tyr	Asp	Val	Asp	Asn	Asp	Lys	Leu	Asp	Glu	Pro	Glu	Arg	Ile	Leu	Ala	
				10					15					20		

gaa	tcc	acc	gtg	gaa	ccg	gag	gaa	gga	cca	cgc	atg	agg	gcc	cgc	cgt	211
Glu	Ser	Thr	Val	Glu	Pro	Glu	Glu	Gly	Pro	Arg	Met	Arg	Ala	Arg	Arg	
			25					30					35			

caa	cgt	cag	gaa	tct	gct	gcg	gat	gat	att	gcc	gcg	att	gca	gct	gct	259
Gln	Arg	Gln	Glu	Ser	Ala	Ala	Asp	Asp	Ile	Ala	Ala	Ile	Ala	Ala	Ala	
			40				45					50				

gcc	gtg	gac	att	gct	tct	gaa	gaa	gac	cct	gat	gag	cct	tcg	gga	tcg	307
Ala	Val	Asp	Ile	Ala	Ser	Glu	Glu	Asp	Pro	Asp	Glu	Pro	Ser	Gly	Ser	
	55					60					65					

tcg	tat	gtg	tct	gac	ttt	gag	gca	gag	cct	att	gca	cct	gta	gtt	gag	355
Ser	Tyr	Val	Ser	Asp	Phe	Glu	Ala	Glu	Pro	Ile	Ala	Pro	Val	Val	Glu	
	70				75					80					85	

aag	gct	gct	gaa	cct	gtg	gct	gag	cca	acc	gct	gat	tat	gaa	aag	gca	403
Lys	Ala	Ala	Glu	Pro	Val	Ala	Glu	Pro	Thr	Ala	Asp	Tyr	Glu	Lys	Ala	
			90						95					100		

cgt	gcc	gaa	ttt	gag	gca	agc	cca	cgc	agg	cgc	cgc	aag	act	cgt	ggc	451
Arg	Ala	Glu	Phe	Glu	Ala	Ser	Pro	Arg	Arg	Arg	Arg	Lys	Thr	Arg	Gly	
			105					110					115			

aat	tca	cgt	tcg	gat	cat	gct	cca	aag	cca	gag	gat	ttc	gca	cct	gta	499
Asn	Ser	Arg	Ser	Asp	His	Ala	Pro	Lys	Pro	Glu	Asp	Phe	Ala	Pro	Val	
		120					125					130				

gtt	gaa	gag	gtt	gct	gag	act	cca	gtg	aag	aca	cct	gcg	cgg	aag	gct	547
Val	Glu	Glu	Val	Ala	Glu	Thr	Pro	Val	Lys	Thr	Pro	Ala	Arg	Lys	Ala	
	135					140					145					

cca	cgc	cgt	aac	cgt	cca	agt	gag	ctc	agt	tcc	ggt	gcg	ccg	tcc	tct	595
Pro	Arg	Arg	Asn	Arg	Pro	Ser	Glu	Leu	Ser	Ser	Gly	Ala	Pro	Ser	Ser	
150					155					160					165	

gca	cca	tcg	acc	agg	aac	cgt	cgc	cgc	gca	gtg	cgc	cgt	caa	ctg	gtg	643
Ala	Pro	Ser	Thr	Arg	Asn	Arg	Arg	Arg	Ala	Val	Arg	Arg	Gln	Leu	Val	
				170					175					180		

gaa	gct	cct	gag	acc	gtc	gtt	gag	ata	gca	cct	gaa	gca	gca	cca	gaa	691
Glu	Ala	Pro	Glu	Thr	Val	Val	Glu	Ile	Ala	Pro	Glu	Ala	Ala	Pro	Glu	
			185					190					195			

cag	gtt	gca	gag	cct	cag	gtt	gaa	ttc	gac	cag	cca	gac	aac	cgc	cga	739
Gln	Val	Ala	Glu	Pro	Gln	Val	Glu	Phe	Asp	Gln	Pro	Asp	Asn	Arg	Arg	

200	205	210	
aag cgt cgt cgt gct gtg cgc	gtg aca gcg gcg ccg	gtg gag aag aag	787
Lys Arg Arg Arg Ala Val Arg	Val Thr Ala Ala Pro	Val Glu Lys Lys	
215	220	225	
gtg gcg tcg aca agc aat gcg	cgg gcg ccg aag aag gaa	cct cag gcg	835
Val Ala Ser Thr Ser Asn Ala	Arg Ala Pro Lys Lys	Glu Pro Gln Ala	
230	235	240	245
gcg agc acc acc aac cca ggc	cgc cgt agg cgg gct acc	cga cga ggc	883
Ala Ser Thr Thr Asn Pro Gly	Arg Arg Arg Arg Ala Thr	Arg Arg Gly	
250	255	260	
cca cga agc tagggataaa	gggcgggttg tgt		915
Pro Arg Ser			

<210> 228

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

Met Thr Pro Ile Tyr Tyr Asp Val Asp Asn Asp Lys Leu Asp Glu Pro	
1 5 10 15	
Glu Arg Ile Leu Ala Glu Ser Thr Val Glu Pro Glu Glu Gly Pro Arg	
20 25 30	
Met Arg Ala Arg Arg Gln Arg Gln Glu Ser Ala Ala Asp Asp Ile Ala	
35 40 45	
Ala Ile Ala Ala Ala Ala Val Asp Ile Ala Ser Glu Glu Asp Pro Asp	
50 55 60	
Glu Pro Ser Gly Ser Ser Tyr Val Ser Asp Phe Glu Ala Glu Pro Ile	
65 70 75 80	
Ala Pro Val Val Glu Lys Ala Ala Glu Pro Val Ala Glu Pro Thr Ala	
85 90 95	
Asp Tyr Glu Lys Ala Arg Ala Glu Phe Glu Ala Ser Pro Arg Arg Arg	
100 105 110	
Arg Lys Thr Arg Gly Asn Ser Arg Ser Asp His Ala Pro Lys Pro Glu	
115 120 125	
Asp Phe Ala Pro Val Val Glu Glu Val Ala Glu Thr Pro Val Lys Thr	
130 135 140	
Pro Ala Arg Lys Ala Pro Arg Arg Asn Arg Pro Ser Glu Leu Ser Ser	
145 150 155 160	
Gly Ala Pro Ser Ser Ala Pro Ser Thr Arg Asn Arg Arg Arg Ala Val	
165 170 175	
Arg Arg Gln Leu Val Glu Ala Pro Glu Thr Val Val Glu Ile Ala Pro	
180 185 190	

Ala Thr Arg Arg Gly Pro Arg Ser
260

ggc tac gta ctt acc gac gcc atg aaa gtc ccc ggc ttc aca gtc cca 451
Gly Tyr Val Leu Thr Asp Ala Met Lys Val Pro Gly Phe Thr Val Pro
105 110 115

tac cta ccc atc atc ggc gga gac gcc tcc gcc cga tgc atc gcc gcc 499
Tyr Leu Pro Ile Ile Gly Gly Asp Ala Ser Ala Arg Cys Ile Ala Ala
120 125 130

gca agt gta tta gcc aaa caa acc cgc gac gac atc atg acc gac atg 547
Ala Ser Val Leu Ala Lys Gln Thr Arg Asp Asp Ile Met Thr Asp Met
135 140 145

gcc aac gac tac ccg cac tac ggt ctc gaa att cac aaa ggc tac agt 595
Ala Asn Asp Tyr Pro His Tyr Gly Leu Glu Ile His Lys Gly Tyr Ser
150 155 160 165

acg aag atc cac atg gat gcg gtg cgc cac cac ggc gca agt ccc gag 643
Thr Lys Ile His Met Asp Ala Val Arg His His Gly Ala Ser Pro Glu
170 175 180

cac aga tat agt tat gca aat gtg gcc aag gca cac caa gaa tgg cta 691
His Arg Tyr Ser Tyr Ala Asn Val Ala Lys Ala His Gln Glu Trp Leu
185 190 195

cac gct gca gat aat gac acg acg gaa ggt gga gca tgagcgctga 737
His Ala Ala Asp Asn Asp Thr Thr Glu Gly Gly Ala
200 205

agaactcgac aac 750

<210> 230

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 230

Leu Ser Arg Asn Gly Leu Gly Pro Val Ala Gly Val Asp Glu Ala Gly
1 5 10 15

Arg Gly Ala Cys Cys Gly Pro Ile Ser Ile Ala Ala Cys Ile Leu Pro
20 25 30

Asp Lys Pro Ile Gln Glu Leu Ala Ala Leu Thr Asp Ser Lys Lys Leu
35 40 45

Ser Ala Ser Thr Arg Glu Lys Leu Met Pro Leu Ile Lys Lys His Ala
50 55 60

Leu Ala Trp Ser Val Ile Val Ile Ser Ala Gln Asp Ile Asp Arg Phe
65 70 75 80

Gly Ile Gln His Ala Asn Ile Ser Gly Met Arg Arg Ala Val Ala Ala
85 90 95

Leu Gly Thr Gln Pro Gly Tyr Val Leu Thr Asp Ala Met Lys Val Pro
100 105 110

Gly Phe Thr Val Pro Tyr Leu Pro Ile Ile Gly Gly Asp Ala Ser Ala
115 120 125

Arg Cys Ile Ala Ala Ala Ser Val Leu Ala Lys Gln Thr Arg Asp Asp
130 135 140

Ile Met Thr Asp Met Ala Asn Asp Tyr Pro His Tyr Gly Leu Glu Ile

<400> 231																	
aagcatcttg gtgcgcgggg gtgttgggct ggaaggtacc ctgtatttca tgacttcttc																	60
ttccagcttt tctcgttttg atggccgcgc acaggatcag																	
												atg	cgt	gcc	gcc	aaa	115
												Met	Arg	Ala	Ala	Lys	
												1				5	
atc acc cgt gga ttt act tcc aac cct gca ggc agc gtg ctt gta gaa																	163
Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly Ser Val Leu Val Glu																	
												10				20	
ttc ggc aat act cgt gtc atg tgc acc gct tct gtg gaa ttg ggt gtg																	211
Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser Val Glu Leu Gly Val																	
												25				35	
cct cgt ttc aag cgt gat tca ggt gaa ggc tgg ttg acc gca gag tac																	259
Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp Leu Thr Ala Glu Tyr																	
												40				50	
gcg atg ctt cct gct gcg act gcg gag cgt aac cgt cgt gaa tcc atg																	307
Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn Arg Arg Glu Ser Met																	
												55				65	
gcc ggc aag gtc aag gga cgc act cat gaa att tct cgt ctg att ggt																	355
Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile Ser Arg Leu Ile Gly																	
												70				80	85
cgt tct ttg cgt gca gct gtg gat ctt tcc cag ctg ggt gag aac acc																	403
Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln Leu Gly Glu Asn Thr																	
												90				100	
att gcg att gac tgc gat gtt ctg caa gct gac ggc ggt act cgt act																	451
Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp Gly Gly Thr Arg Thr																	
												105				115	
gca tcg atc acc ggt gcg tat gtg gcg ctg gct gat gcc atc aag gtt																	499

Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala Asp Ala Ile Lys Val
120 125 130

ctg cag gag cgc ggg gtt gtt cca ggc agc cca ctt ctt gca cca gtt 547
Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro Leu Leu Ala Pro Val
135 140 145

gct gct gtt tcc gtt ggt ctg gtc gac ggt aat gta tgc ctt gac ttg 595
Ala Ala Val Ser Val Gly Leu Val Asp Gly Asn Val Cys Leu Asp Leu
150 155 160 165

cca tat gaa gaa gat tcc cgc gcc gat gtt gac ctc aac gtt gtt atg 643
Pro Tyr Glu Glu Asp Ser Arg Ala Asp Val Asp Leu Asn Val Val Met
170 175 180

acc gaa cac ggt gaa ttc gtg gaa att cag ggc acc ggc gaa gaa act 691
Thr Glu His Gly Glu Phe Val Glu Ile Gln Gly Thr Gly Glu Glu Thr
185 190 195

acc ttc acc cgc gcg cag ctc aac gac atg ctt gac cac gct gaa aag 739
Thr Phe Thr Arg Ala Gln Leu Asn Asp Met Leu Asp His Ala Glu Lys
200 205 210

ggc tgc cgc gaa ttg gtt gct gcc caa aaa gct gca ctg gga atc 784
Gly Cys Arg Glu Leu Val Ala Ala Gln Lys Ala Ala Leu Gly Ile
215 220 225

taaaaccaca acagagttaa gga 807

<210> 232
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 232
Met Arg Ala Ala Lys Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly
1 5 10 15

Ser Val Leu Val Glu Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser
20 25 30

Val Glu Leu Gly Val Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp
35 40 45

Leu Thr Ala Glu Tyr Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn
50 55 60

Arg Arg Glu Ser Met Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile
65 70 75 80

Ser Arg Leu Ile Gly Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln
85 90 95

Leu Gly Glu Asn Thr Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp
100 105 110

Gly Gly Thr Arg Thr Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala
115 120 125

Asp Ala Ile Lys Val Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro

130	135	140
Leu Leu Ala Pro Val Ala Ala Val Ser Val Gly Leu Val Asp Gly Asn		
145	150	155 160
Val Cys Leu Asp Leu Pro Tyr Glu Glu Asp Ser Arg Ala Asp Val Asp		
	165 170	175
Leu Asn Val Val Met Thr Glu His Gly Glu Phe Val Glu Ile Gln Gly		
	180 185	190
Thr Gly Glu Glu Thr Thr Phe Thr Arg Ala Gln Leu Asn Asp Met Leu		
	195 200	205
Asp His Ala Glu Lys Gly Cys Arg Glu Leu Val Ala Ala Gln Lys Ala		
	210 215	220
Ala Leu Gly Ile		
225		

<210> 233
 <211> 541
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(541)
 <223> FRXA01786

<400> 233
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 ttccagcttt tctcgttttg atggccgcgc acaggatcag atg cgt gcc gcc aaa 115
 Met Arg Ala Ala Lys
 1 5
 atc acc cgt gga ttt act tcc aac cct gca ggc agc gtg ctt gta gaa 163
 Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly Ser Val Leu Val Glu
 10 15 20
 ttc ggc aat act cgt gtc atg tgc acc gct tct gtg gaa ttg ggt gtg 211
 Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser Val Glu Leu Gly Val
 25 30 35
 cct cgt ttc aag cgt gat tca ggt gaa ggc tgg ttg acc gca gag tac 259
 Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp Leu Thr Ala Glu Tyr
 40 45 50
 gcg atg ctt cct gct gcg act gcg gag cgt aac cgt cgt gaa tcc atg 307
 Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn Arg Arg Glu Ser Met
 55 60 65
 gcc ggc aag gtc aag gga cgc act cat gaa att tct cgt ctg att ggt 355
 Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile Ser Arg Leu Ile Gly
 70 75 80 85
 cgt tct ttg cgt gca gct gtg gat ctt tcc cag ctg ggt gag aac acc 403
 Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln Leu Gly Glu Asn Thr
 90 95 100

att gcg att gac tgc gat gtt ctg caa gct gac ggc ggt act cgt act 451
Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp Gly Gly Thr Arg Thr
105 110 115

gca tcg atc acc ggt gcg tat gtg gcg ctg gct gat gcc atc aag gtt 499
Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala Asp Ala Ile Lys Val
120 125 130

ctg cag gag cgc ggg gtt gtt cca ggc agc cca ctt ctt gca 541
Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro Leu Leu Ala
135 140 145

<210> 234

<211> 147

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 234

Met Arg Ala Ala Lys Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly
1 5 10 15

Ser Val Leu Val Glu Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser
20 25 30

Val Glu Leu Gly Val Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp
35 40 45

Leu Thr Ala Glu Tyr Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn
50 55 60

Arg Arg Glu Ser Met Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile
65 70 75 80

Ser Arg Leu Ile Gly Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln
85 90 95

Leu Gly Glu Asn Thr Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp
100 105 110

Gly Gly Thr Arg Thr Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala
115 120 125

Asp Ala Ile Lys Val Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro
130 135 140

Leu Leu Ala
145

<210> 235

<211> 741

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(718)

<223> RXN00163

<400> 235

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cactgggaat ctaaaaccac aacagagtta aggacaccgg atg aaa ctt ctt ctt 115
Met Lys Leu Leu Leu
1 5

gca tcc aac aac gca aag aaa ctc aaa gaa ctc cag cgg att ttg gat 163
Ala Ser Asn Asn Ala Lys Lys Leu Lys Glu Leu Gln Arg Ile Leu Asp
10 15 20

caa gca ggc ctg gat tcc gtt gaa ttg ctt gcg ctg cgt gat gtc gag 211
Gln Ala Gly Leu Asp Ser Val Glu Leu Leu Ala Leu Arg Asp Val Glu
25 30 35

gca tac gac gag ccg atc gaa gac ggc cgc act ttt gcc gac aac gca 259
Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr Phe Ala Asp Asn Ala
40 45 50

cag atc aaa gcg cgc gcc ggg gta acc cac aca ggc atc gcc acg atc 307
Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr Gly Ile Ala Thr Ile
55 60 65

gcc gat gat tcc ggc atc gct gtc gaa gaa ctc aac gga atg ccc ggc 355
Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu Asn Gly Met Pro Gly
70 75 80 85

gtt ttg tcc gca cgc tgg tcc ggc gca cac ggc aac gac acc gcc aac 403
Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly Asn Asp Thr Ala Asn
90 95 100

aac gag ctg ctt ctt gcc caa atg gaa cat gtt ccc gac gag cgc cgc 451
Asn Glu Leu Leu Leu Ala Gln Met Glu His Val Pro Asp Glu Arg Arg
105 110 115

aac gca gcc ttc gtg tcc gta tgc gtg ctt gca ctt ccg gac ggc caa 499
Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala Leu Pro Asp Gly Gln
120 125 130

gaa ttt gtt cag gaa ggc cgt tgg gaa ggc caa ctc cta cgc gga cct 547
Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln Leu Leu Arg Gly Pro
135 140 145

aag ggc gaa aac ggt ttc gga tac gat cca ctg ttc att cca gca gag 595
Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu Phe Ile Pro Ala Glu
150 155 160 165

gaa atc gat gga caa gga cgc agc tcc gct gaa ctt tcc gca gag gaa 643
Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu Leu Ser Ala Glu Glu
170 175 180

aag gac gct ttg tcc cac cga ggt caa gcg ctg cgc gga ttg gtt gag 691
Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu Arg Gly Leu Val Glu
185 190 195

aag atc gca cag gta gct gcg gct agc taaggcctta aggaaaacta 738
Lys Ile Ala Gln Val Ala Ala Ala Ser
200 205

aaa 741

<210> 236
<211> 206
<212> PRT
<213> Corynebacterium glutamicum

<400> 236
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Gln Arg Ile Leu Asp Gln Ala Gly Leu Asp Ser Val Glu Leu Leu Ala
20 25 30
Leu Arg Asp Val Glu Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr
35 40 45
Phe Ala Asp Asn Ala Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr
50 55 60
Gly Ile Ala Thr Ile Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu
65 70 75 80
Asn Gly Met Pro Gly Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly
85 90 95
Asn Asp Thr Ala Asn Asn Glu Leu Leu Leu Ala Gln Met Glu His Val
100 105 110
Pro Asp Glu Arg Arg Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala
115 120 125
Leu Pro Asp Gly Gln Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln
130 135 140
Leu Leu Arg Gly Pro Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu
145 150 155 160
Phe Ile Pro Ala Glu Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu
165 170 175
Leu Ser Ala Glu Glu Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu
180 185 190
Arg Gly Leu Val Glu Lys Ile Ala Gln Val Ala Ala Ala Ser
195 200 205

<210> 237
<211> 641
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (58)..(618)
<223> FRXA00163

<400> 237
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Leu
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Asp Gln Ala Gly Leu Asp Ser Val Glu Leu Leu Ala Leu Arg Asp Val
5 10 15

gag gca tac gac gag ccg atc gaa gac ggc cgc act ttt gcc gac aac 156
Glu Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr Phe Ala Asp Asn
20 25 30

gca cag atc aaa gcg cgc gcc ggg gta acc cac aca ggc atc gcc acg 204
Ala Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr Gly Ile Ala Thr
35 40 45

atc gcc gat gat tcc ggc atc gct gtc gaa gaa ctc aac gga atg ccc 252
Ile Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu Asn Gly Met Pro
50 55 60 65

ggc gtt ttg tcc gca cgc tgg tcc ggc gca cac ggc aac gac acc gcc 300
Gly Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly Asn Asp Thr Ala
70 75 80

aac aac gag ctg ctt ctt gcc caa atg gaa cat gtt ccc gac gag cgc 348
Asn Asn Glu Leu Leu Leu Ala Gln Met Glu His Val Pro Asp Glu Arg
85 90 95

cgc aac gca gcc ttc gtg tcc gta tgc gtg ctt gca ctt ccg gac ggc 396
Arg Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala Leu Pro Asp Gly
100 105 110

caa gaa ttt gtt cag gaa ggc cgt tgg gaa ggc caa ctc cta cgc gga 444
Gln Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln Leu Leu Arg Gly
115 120 125

cct aag ggc gaa aac ggt ttc gga tac gat cca ctg ttc att cca gca 492
Pro Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu Phe Ile Pro Ala
130 135 140 145

gag gaa atc gat gga caa gga cgc agc tcc gct gaa ctt tcc gca gag 540
Glu Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu Leu Ser Ala Glu
150 155 160

gaa aag gac gct ttg tcc cac cga ggt caa gcg ctg cgc gga ttg gtt 588
Glu Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu Arg Gly Leu Val
165 170 175

gag aag atc gca cag gta gct gcg gct agc taaggcctta aggaaaacta 638
Glu Lys Ile Ala Gln Val Ala Ala Ala Ser
180 185

aaa 641

<210> 238

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

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<400> 239															
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gatgaggaaa gggcgctcgcg ctggcagtaa aactgtcggt gtg cac ctg tgg gat															115
Val His Leu Trp Asp															
1 5															
agt gcc gaa tcg ttg gat ggc acc gaa aaa cag ggc gaa gtc gcc tca															163
Ser Ala Glu Ser Leu Asp Gly Thr Glu Lys Gln Gly Glu Val Ala Ser															
10 15 20															
ttc ggt ggt ccg cgg ttc ggc ctt gtc gtt tct aag gcc gtc gga aat															211
Phe Gly Gly Pro Arg Phe Gly Leu Val Val Ser Lys Ala Val Gly Asn															
25 30 35															
gcg gtg gtt cgt cac cgc acc tcc cga cgg ctt cgt cat atc tgt gca															259
Ala Val Val Arg His Arg Thr Ser Arg Arg Leu Arg His Ile Cys Ala															

40 45 50
agc att gca gaa aaa tca cca gag cta ctc tcc ccc act cat cac gtg 307
Ser Ile Ala Glu Lys Ser Pro Glu Leu Leu Ser Pro Thr His His Val
55 60 65
gtg atc cgc gcg ttg gcg ggg gct ggg aat gca acc tcg gcg gaa ctt 355
Val Ile Arg Ala Leu Ala Gly Ala Gly Asn Ala Thr Ser Ala Glu Leu
70 75 80 85
gaa cga gac atc cgc tac ggg ttg ggg aaa gct agc cgt gtg cgc acc 403
Glu Arg Asp Ile Arg Tyr Gly Leu Gly Lys Ala Ser Arg Val Arg Thr
90 95 100
aac aag tgatgaccc ttcgacatcc cag 432
Asn Lys

<210> 240
<211> 103
<212> PRT
<213> Corynebacterium glutamicum

<400> 240
Val His Leu Trp Asp Ser Ala Glu Ser Leu Asp Gly Thr Glu Lys Gln
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Gly Glu Val Ala Ser Phe Gly Gly Pro Arg Phe Gly Leu Val Val Ser
20 25 30
Lys Ala Val Gly Asn Ala Val Val Arg His Arg Thr Ser Arg Arg Leu
35 40 45
Arg His Ile Cys Ala Ser Ile Ala Glu Lys Ser Pro Glu Leu Leu Ser
50 55 60
Pro Thr His His Val Val Ile Arg Ala Leu Ala Gly Ala Gly Asn Ala
65 70 75 80
Thr Ser Ala Glu Leu Glu Arg Asp Ile Arg Tyr Gly Leu Gly Lys Ala
85 90 95
Ser Arg Val Arg Thr Asn Lys
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<210> 241
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(592)
<223> RXA01481

<400> 241
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tcacttttagc ccgtcccttt agtgtgccta tattggttgt atg caa aac agc aag 115

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<210> 242
<211> 164
<212> PRT
<213> Corynebacterium glutamicum
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<400> 242
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Val Leu Ala Ala Ala Trp Phe Gly Ile Asp Leu Ser Thr Ser Gly Glu
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Ala Thr Ser Gln Ala Ser Ser Ser Ala Thr Thr Thr Ile Thr Ser
  35             40             45

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Ser Asn Thr Pro Thr Ser Glu Ser Ile Ser Ser Asn Ser Asp Leu Asp
 50 55 60

Gly Asp Ser Cys Ser Met Ser Glu Leu Pro Gln Glu Ala Asp Glu Val
 65 70 75 80

Val Asp Asp Ile Leu Ala Gly Gly Pro Phe Asp Tyr Pro Asp Asn Asp
 85 90 95

Gly Val Arg Phe Gly Asn Tyr Glu Gly Val Leu Pro Lys Glu Ser Ser
 100 105 110

Asn Tyr Tyr Arg Glu Tyr Thr Val Glu Thr Pro Gly Leu Ser His Arg
 115 120 125

Gly Pro Leu Arg Ile Val Thr Gly Gly Ser Asn Pro Thr Asp Pro Glu
 130 135 140

Val Trp Tyr Tyr Thr Ser Asp His Tyr Glu Thr Phe Cys Ala Ile Thr
 145 150 155 160

Asp Ala Glu Asn

<210> 243
 <211> 2100
 <212> DNA
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<220>
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 <222> (101)..(2077)
 <223> RXN00724

<400> 243
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tccgccacca tgtgcgcaaa tactccacca cggctctggc gtg gga att ggt gat 115
 Val Gly Ile Gly Asp
 1 5

gcc act gag ggc gat ctt gtt acc atc gtg ggt cag gtc gcc ttt gcc 163
 Ala Thr Glu Gly Asp Leu Val Thr Ile Val Gly Gln Val Ala Phe Ala
 10 15 20

aag cag tcc tat acc cag tcc ggc aag atg ctg tac aag gtt aca gtc 211
 Lys Gln Ser Tyr Thr Gln Ser Gly Lys Met Leu Tyr Lys Val Thr Val
 25 30 35

ttg act gag acg gaa cgc atc ggc att tcc ttc ttc gga gcc aag cac 259
 Leu Thr Glu Thr Glu Arg Ile Gly Ile Ser Phe Phe Gly Ala Lys His
 40 45 50

att ccg cgt ctt ctc cca gaa ggc act cgt gcg ctt ttt acc ggc aag 307
 Ile Pro Arg Leu Leu Pro Glu Gly Thr Arg Ala Leu Phe Thr Gly Lys
 55 60 65

gtg aag ttt ttt cgc aac gaa cct cag cta tct cat cca gag ttc att 355
 Val Lys Phe Phe Arg Asn Glu Pro Gln Leu Ser His Pro Glu Phe Ile
 70 75 80 85

gtg atc cca gat cct gga tca ggc cgc cga ctc acc gcc act ggc ggt	403
Val Ile Pro Asp Pro Gly Ser Gly Arg Arg Leu Thr Ala Thr Gly Gly	
90 95 100	
atg aaa tct ctg gct gcc tac ggc gat gtg gaa gaa gtg gca ctt cgt	451
Met Lys Ser Leu Ala Ala Tyr Gly Asp Val Glu Glu Val Ala Leu Arg	
105 110 115	
ttg gtg gat cgc gaa tac atc ccg atc tat gcc ggc acc gcc acc atg	499
Leu Val Asp Arg Glu Tyr Ile Pro Ile Tyr Ala Gly Thr Ala Thr Met	
120 125 130	
act acc tgg cgg atc atg gct gca gtg caa cgg gta ctg gaa acc atg	547
Thr Thr Trp Arg Ile Met Ala Ala Val Gln Arg Val Leu Glu Thr Met	
135 140 145	
ccg gtg atc aaa gaa cca ctg agc gtg gtg ccc gaa ggc atg ccc agt	595
Pro Val Ile Lys Glu Pro Leu Ser Val Val Pro Glu Gly Met Pro Ser	
150 155 160 165	
ttc gac gag gcc atc cgc ggc att cac gat cca ggc cat gaa tct ccc	643
Phe Asp Glu Ala Ile Arg Gly Ile His Asp Pro Gly His Glu Ser Pro	
170 175 180	
agc acg ttt atc aac cgt ctg aaa tac aac gaa gca cta tcg ctg gcc	691
Ser Thr Phe Ile Asn Arg Leu Lys Tyr Asn Glu Ala Leu Ser Leu Ala	
185 190 195	
acg gtg atg gcg atc cgg cgt gcc gat acc aag aac cgc aaa gca cca	739
Thr Val Met Ala Ile Arg Arg Ala Asp Thr Lys Asn Arg Lys Ala Pro	
200 205 210	
ccc atg ccg cgc gca ctc aaa ggg cat cag cac atg ctc atc gat gca	787
Pro Met Pro Arg Ala Leu Lys Gly His Gln His Met Leu Ile Asp Ala	
215 220 225	
ctc aac ttt cag ctc aca gtg gga cag aag caa gtg atc cgt gag atc	835
Leu Asn Phe Gln Leu Thr Val Gly Gln Lys Gln Val Ile Arg Glu Ile	
230 235 240 245	
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Ser Ala Asp Ile Glu Gln Arg Val Pro Met Ser Arg Leu Leu Gln Gly	
250 255 260	
gag gtt ggt tcg ggt aaa acc atc gtg tcg ttg atc gcg atg ctg cag	931
Glu Val Gly Ser Gly Lys Thr Ile Val Ser Leu Ile Ala Met Leu Gln	
265 270 275	
gca att gat tcc ggt agg cag tgc gcc atg ctc gcc ccg acg gaa gtg	979
Ala Ile Asp Ser Gly Arg Gln Cys Ala Met Leu Ala Pro Thr Glu Val	
280 285 290	
ttg gcc acc cag cat gcc cgc agc ctg agc aaa act ctc gac gac gca	1027
Leu Ala Thr Gln His Ala Arg Ser Leu Ser Lys Thr Leu Asp Asp Ala	
295 300 305	
ggc ctt gat atc aat gtt gtg ctc ttg act ggc tcg atg ccc acg gga	1075
Gly Leu Asp Ile Asn Val Val Leu Leu Thr Gly Ser Met Pro Thr Gly	
310 315 320 325	

gcc aag aag gag gct ctg ctg gaa atc atc tcc ggt gac gca gac att	1123
Ala Lys Lys Glu Ala Leu Leu Glu Ile Ile Ser Gly Asp Ala Asp Ile	
330 335 340	
gtg gtc ggc acg cat gcg ctg atc cag gac acc gtg gag ttc ttc gac	1171
Val Val Gly Thr His Ala Leu Ile Gln Asp Thr Val Glu Phe Phe Asp	
345 350 355	
ctt ggc ctc gtg gtg gtg gat gag cag cac cgt ttc ggc gtg gag caa	1219
Leu Gly Leu Val Val Val Asp Glu Gln His Arg Phe Gly Val Glu Gln	
360 365 370	
cgc gat caa ctg cgg acc aag ggc agg gaa ggc ctg acc ccg cac cta	1267
Arg Asp Gln Leu Arg Thr Lys Gly Arg Glu Gly Leu Thr Pro His Leu	
375 380 385	
ttg gtt atg act gcg acc cca att ccg cgc acc atc gcc atg acg gtg	1315
Leu Val Met Thr Ala Thr Pro Ile Pro Arg Thr Ile Ala Met Thr Val	
390 395 400 405	
ttc ggc gac ttg gcg gtg tcc acg ttg cgt gaa ctt cca ggc ggg cgc	1363
Phe Gly Asp Leu Ala Val Ser Thr Leu Arg Glu Leu Pro Gly Gly Arg	
410 415 420	
cgg ccg att caa acc tcg gtg ata ccc gat cac aaa cct ggc tgg gtt	1411
Arg Pro Ile Gln Thr Ser Val Ile Pro Asp His Lys Pro Gly Trp Val	
425 430 435	
aaa cgc ggt tgg gaa cgc atc ggt gag gaa gtc ctc gcc gga cgc caa	1459
Lys Arg Gly Trp Glu Arg Ile Gly Glu Glu Val Leu Ala Gly Arg Gln	
440 445 450	
gcc tat gtg gtg tgt ccg cgc att gaa ggc gaa ggc ggc gtg ctg gaa	1507
Ala Tyr Val Val Cys Pro Arg Ile Glu Gly Glu Gly Val Leu Glu	
455 460 465	
atc cac gcc tat ctt tcc gaa cag gta tat cca gga ttg aat gtt gga	1555
Ile His Ala Tyr Leu Ser Glu Gln Val Tyr Pro Gly Leu Asn Val Gly	
470 475 480 485	
atg ctg cac ggt cgc atg gac acg gat ctc aaa gat tcg gtc atg cag	1603
Met Leu His Gly Arg Met Asp Thr Asp Leu Lys Asp Ser Val Met Gln	
490 495 500	
gaa ttc gcc caa ggt gag atc gat att ttg gtc gcc acc acg gtc att	1651
Glu Phe Ala Gln Gly Glu Ile Asp Ile Leu Val Ala Thr Thr Val Ile	
505 510 515	
gag gtc ggt att gac gtt gcc aac gcc acc gtc atg ctc atc cgc gag	1699
Glu Val Gly Ile Asp Val Ala Asn Ala Thr Val Met Leu Ile Arg Glu	
520 525 530	
gcg gaa cgc ttc ggc gtt tcc cag atc cac cag ctg cgc ggc cgt gtt	1747
Ala Glu Arg Phe Gly Val Ser Gln Ile His Gln Leu Arg Gly Arg Val	
535 540 545	
ggc cgt ggg cag cac gat tcc ctc tgc ctg ctg cac acc acc ttc gac	1795
Gly Arg Gly Gln His Asp Ser Leu Cys Leu Leu His Thr Thr Phe Asp	
550 555 560 565	
gag gac tcc cca caa ggc caa cgc ctc gcc gca att tcc acc aca acc	1843

Glu Asp Ser Pro Gln Gly Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr
570 575 580

gac ggt ttt caa ctc tct gaa ctt gat ttg cag gta cgc caa gaa ggc 1891
Asp Gly Phe Gln Leu Ser Glu Leu Asp Leu Gln Val Arg Gln Glu Gly
585 590 595

gac gtg ttg ggc acc cgc cag tcc ggc agc gac acc aaa ctc cgt cac 1939
Asp Val Leu Gly Thr Arg Gln Ser Gly Ser Asp Thr Lys Leu Arg His
600 605 610

ctc tcg ttt atc agc gac caa aaa atc atc gag cgt gcg ctt atc gac 1987
Leu Ser Phe Ile Ser Asp Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp
615 620 625

gcc acc gag ctg gtt gcc gcc agc cgt tcc agg gcg ctt gag ctg gtc 2035
Ala Thr Glu Leu Val Ala Ala Ser Arg Ser Arg Ala Leu Glu Leu Val
630 635 640 645

agc gac atc gca atg atc aac cag gaa tac ctg gaa aag agc 2077
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<210> 244

<211> 659

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

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20 25 30

Tyr Lys Val Thr Val Leu Thr Glu Thr Glu Arg Ile Gly Ile Ser Phe
35 40 45

Phe Gly Ala Lys His Ile Pro Arg Leu Leu Pro Glu Gly Thr Arg Ala
50 55 60

Leu Phe Thr Gly Lys Val Lys Phe Phe Arg Asn Glu Pro Gln Leu Ser
65 70 75 80

His Pro Glu Phe Ile Val Ile Pro Asp Pro Gly Ser Gly Arg Arg Leu
85 90 95

Thr Ala Thr Gly Gly Met Lys Ser Leu Ala Ala Tyr Gly Asp Val Glu
100 105 110

Glu Val Ala Leu Arg Leu Val Asp Arg Glu Tyr Ile Pro Ile Tyr Ala
115 120 125

Gly Thr Ala Thr Met Thr Thr Trp Arg Ile Met Ala Ala Val Gln Arg
130 135 140

Val Leu Glu Thr Met Pro Val Ile Lys Glu Pro Leu Ser Val Val Pro
145 150 155 160

Glu Gly Met Pro Ser Phe Asp Glu Ala Ile Arg Gly Ile His Asp Pro
 165 170 175
 Gly His Glu Ser Pro Ser Thr Phe Ile Asn Arg Leu Lys Tyr Asn Glu
 180 185 190
 Ala Leu Ser Leu Ala Thr Val Met Ala Ile Arg Arg Ala Asp Thr Lys
 195 200 205
 Asn Arg Lys Ala Pro Pro Met Pro Arg Ala Leu Lys Gly His Gln His
 210 215 220
 Met Leu Ile Asp Ala Leu Asn Phe Gln Leu Thr Val Gly Gln Lys Gln
 225 230 235 240
 Val Ile Arg Glu Ile Ser Ala Asp Ile Glu Gln Arg Val Pro Met Ser
 245 250 255
 Arg Leu Leu Gln Gly Glu Val Gly Ser Gly Lys Thr Ile Val Ser Leu
 260 265 270
 Ile Ala Met Leu Gln Ala Ile Asp Ser Gly Arg Gln Cys Ala Met Leu
 275 280 285
 Ala Pro Thr Glu Val Leu Ala Thr Gln His Ala Arg Ser Leu Ser Lys
 290 295 300
 Thr Leu Asp Asp Ala Gly Leu Asp Ile Asn Val Val Leu Leu Thr Gly
 305 310 315 320
 Ser Met Pro Thr Gly Ala Lys Lys Glu Ala Leu Leu Glu Ile Ile Ser
 325 330 335
 Gly Asp Ala Asp Ile Val Val Gly Thr His Ala Leu Ile Gln Asp Thr
 340 345 350
 Val Glu Phe Phe Asp Leu Gly Leu Val Val Val Asp Glu Gln His Arg
 355 360 365
 Phe Gly Val Glu Gln Arg Asp Gln Leu Arg Thr Lys Gly Arg Glu Gly
 370 375 380
 Leu Thr Pro His Leu Leu Val Met Thr Ala Thr Pro Ile Pro Arg Thr
 385 390 395 400
 Ile Ala Met Thr Val Phe Gly Asp Leu Ala Val Ser Thr Leu Arg Glu
 405 410 415
 Leu Pro Gly Gly Arg Arg Pro Ile Gln Thr Ser Val Ile Pro Asp His
 420 425 430
 Lys Pro Gly Trp Val Lys Arg Gly Trp Glu Arg Ile Gly Glu Glu Val
 435 440 445
 Leu Ala Gly Arg Gln Ala Tyr Val Val Cys Pro Arg Ile Glu Gly Glu
 450 455 460
 Gly Gly Val Leu Glu Ile His Ala Tyr Leu Ser Glu Gln Val Tyr Pro
 465 470 475 480

Gly Leu Asn Val Gly Met Leu His Gly Arg Met Asp Thr Asp Leu Lys
 485 490 495
 Asp Ser Val Met Gln Glu Phe Ala Gln Gly Glu Ile Asp Ile Leu Val
 500 505 510
 Ala Thr Thr Val Ile Glu Val Gly Ile Asp Val Ala Asn Ala Thr Val
 515 520 525
 Met Leu Ile Arg Glu Ala Glu Arg Phe Gly Val Ser Gln Ile His Gln
 530 535 540
 Leu Arg Gly Arg Val Gly Arg Gly Gln His Asp Ser Leu Cys Leu Leu
 545 550 555 560
 His Thr Thr Phe Asp Glu Asp Ser Pro Gln Gly Gln Arg Leu Ala Ala
 565 570 575
 Ile Ser Thr Thr Thr Asp Gly Phe Gln Leu Ser Glu Leu Asp Leu Gln
 580 585 590
 Val Arg Gln Glu Gly Asp Val Leu Gly Thr Arg Gln Ser Gly Ser Asp
 595 600 605
 Thr Lys Leu Arg His Leu Ser Phe Ile Ser Asp Gln Lys Ile Ile Glu
 610 615 620
 Arg Ala Leu Ile Asp Ala Thr Glu Leu Val Ala Ala Ser Arg Ser Arg
 625 630 635 640
 Ala Leu Glu Leu Val Ser Asp Ile Ala Met Ile Asn Gln Glu Tyr Leu
 645 650 655
 Glu Lys Ser

<210> 245
 <211> 1604
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1581)
 <223> RXN01979

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 gcg gga ctt gcg ccc aat att ccc gtg cta gca acc aca gcc acc gcc 96
 Ala Gly Leu Ala Pro Asn Ile Pro Val Leu Ala Thr Thr Ala Thr Ala
 20 25 30
 aat gac cgc gtg gtt gaa gat gtc cgt gcc caa cta gaa gat ggc aca 144
 Asn Asp Arg Val Val Glu Asp Val Arg Ala Gln Leu Glu Asp Gly Thr
 35 40 45
 ggt ttg ttt cgt ggt ggg ata gac cgt gaa tcc ctt tac cta tca gtg 192

Gly	Leu	Phe	Arg	Gly	Gly	Ile	Asp	Arg	Glu	Ser	Leu	Tyr	Leu	Ser	Val		
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gtg	aac	ctg	ctc	aac	ccc	acc	gaa	cgc	cca	gct	tgg	ctt	gcc	acc	cac	240	
Val	Asn	Leu	Leu	Asn	Pro	Thr	Glu	Arg	Pro	Ala	Trp	Leu	Ala	Thr	His		
65					70				75						80		
ctc	aaa	gaa	ctg	acg	ggg	tcg	ggc	atc	att	tac	tgc	ctc	act	gtg	tca	288	
Leu	Lys	Glu	Leu	Thr	Gly	Ser	Gly	Ile	Ile	Tyr	Cys	Leu	Thr	Val	Ser		
				85					90					95			
gct	gca	cat	gat	ctt	gcc	gat	gca	ctt	aat	tct	gtt	gga	tgg	aat	gtt	336	
Ala	Ala	His	Asp	Leu	Ala	Asp	Ala	Leu	Asn	Ser	Val	Gly	Trp	Asn	Val		
			100					105					110				
gcc	gcg	tac	acc	ggg	cga	acc	gaa	gca	gga	gag	cgc	gaa	cgt	tta	gaa	384	
Ala	Ala	Tyr	Thr	Gly	Arg	Thr	Glu	Ala	Gly	Glu	Arg	Glu	Arg	Leu	Glu		
		115					120					125					
cat	gcc	ttg	atc	aac	aac	gag	atc	aaa	gca	cta	gta	gca	acc	tct	gca	432	
His	Ala	Leu	Ile	Asn	Asn	Glu	Ile	Lys	Ala	Leu	Val	Ala	Thr	Ser	Ala		
	130					135					140						
ctg	gga	atg	ggc	ttt	gac	aaa	cct	gac	ctt	gga	ttt	gtt	gtg	cac	atg	480	
Leu	Gly	Met	Gly	Phe	Asp	Lys	Pro	Asp	Leu	Gly	Phe	Val	Val	His	Met		
145					150				155						160		
ggc	agc	ccc	agc	tca	cgc	gtg	tct	tat	tac	cag	cag	att	ggg	cgc	gcc	528	
Gly	Ser	Pro	Ser	Ser	Pro	Val	Ser	Tyr	Tyr	Gln	Gln	Ile	Gly	Arg	Ala		
				165					170					175			
ggg	cgc	ggc	acc	gct	cgt	gcc	gat	gtc	atc	ctg	ctg	cca	gga	act	gaa	576	
Gly	Arg	Gly	Thr	Ala	Arg	Ala	Asp	Val	Ile	Leu	Leu	Pro	Gly	Thr	Glu		
			180					185					190				
gac	aaa	gag	atc	tgg	gag	tac	ttt	gca	tca	gta	tcg	ttc	cca	cgc	gaa	624	
Asp	Lys	Glu	Ile	Trp	Glu	Tyr	Phe	Ala	Ser	Val	Ser	Phe	Pro	Arg	Glu		
	195						200					205					
gag	gta	gtc	cgc	caa	ctg	ctt	gcg	gtg	tta	acc	gat	gag	gcg	caa	tcc	672	
Glu	Val	Val	Arg	Gln	Leu	Leu	Ala	Val	Leu	Thr	Asp	Glu	Ala	Gln	Ser		
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Thr	Val	Lys	Leu	Glu	Ser	Gln	Val	Asp	Leu	Ser	Arg	Ser	Arg	Leu	Glu		
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caa	gta	ctt	aaa	gtg	cta	gac	gta	gat	ggc	gca	gtc	aaa	cgt	gta	cgt	768	
Gln	Val	Leu	Lys	Val	Leu	Asp	Val	Asp	Gly	Ala	Val	Lys	Arg	Val	Arg		
				245					250					255			
ggc	gga	tgg	gtc	tcc	acc	ggg	caa	gag	tgg	atc	tac	gat	gcg	gaa	cgc	816	
Gly	Gly	Trp	Val	Ser	Thr	Gly	Gln	Glu	Trp	Ile	Tyr	Asp	Ala	Glu	Arg		
			260					265					270				
tac	gca	gga	ctt	gaa	caa	gca	agg	aaa	att	gaa	cag	caa	agc	atg	gtg	864	
Tyr	Ala	Gly	Leu	Glu	Gln	Ala	Arg	Lys	Ile	Glu	Gln	Gln	Ser	Met	Val		
		275					280					285					
aac	tac	cag	aac	acc	act	gag	tgc	cgc	atg	ctg	tac	ctc	cgc	aaa	gaa	912	
Asn	Tyr	Gln	Asn	Thr	Thr	Glu	Cys	Arg	Met	Leu	Tyr	Leu	Arg	Lys	Glu		

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Leu Asp Asp Val Glu Ala Thr Thr Pro Cys Gly Arg Cys Asp Asn Cys			
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acg ggc aaa acg tgg ggg ctc gac acc gat gcc tcg atc act ttg aaa			1008
Thr Gly Lys Thr Trp Gly Leu Asp Thr Asp Ala Ser Ile Thr Leu Lys			
	325	330	335
gtg gac caa cag ctt caa aca ccc gga gtg aaa ata gcc cca cga aaa			1056
Val Asp Gln Gln Leu Gln Thr Pro Gly Val Lys Ile Ala Pro Arg Lys			
	340	345	350
atg tgg ccg act ggc att agt gtc aga gga aaa atc gca ggg cta gaa			1104
Met Trp Pro Thr Gly Ile Ser Val Arg Gly Lys Ile Ala Gly Leu Glu			
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gaa gga cga gca ctg gga cga ctc aat gac att gcc cgt gga cct gca			1152
Glu Gly Arg Ala Leu Gly Arg Leu Asn Asp Ile Ala Arg Gly Pro Ala			
	370	375	380
cta aag gcc ctg ctg gac agc gga gct tat tct gat gat cca tgg atg			1200
Leu Lys Ala Leu Leu Asp Ser Gly Ala Tyr Ser Asp Asp Pro Trp Met			
	390	395	400
gca cgc atc atc gaa gtg ctg aaa aac tgg gat tgg acc aac cgg cct			1248
Ala Arg Ile Ile Glu Val Leu Lys Asn Trp Asp Trp Thr Asn Arg Pro			
	405	410	415
gcc aac gtg gtc gct ctc ggc aat acc aac ttt gga tca act gag atg			1296
Ala Asn Val Val Ala Leu Gly Asn Thr Asn Phe Gly Ser Thr Glu Met			
	420	425	430
atc atc cag gta gct caa tca atc gca gcg gtg gga cga atg aac ttt			1344
Ile Ile Gln Val Ala Gln Ser Ile Ala Ala Val Gly Arg Met Asn Phe			
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gcg ggt gta ctt ccc gcc gcg ccg ggt gct gaa gaa gtc atg gct cag			1392
Ala Gly Val Leu Pro Ala Ala Pro Gly Ala Glu Glu Val Met Ala Gln			
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aat tcc gca tac cga gta gaa gcc cta ttg aaa caa tgg gac tgg tcg			1440
Asn Ser Ala Tyr Arg Val Glu Ala Leu Leu Lys Gln Trp Asp Trp Ser			
	470	475	480
caa ggc ttg caa cta gtt ccc ggt ccc att ttg ctg gtg aca gac ctt			1488
Gln Gly Leu Gln Leu Val Pro Gly Pro Ile Leu Leu Val Thr Asp Leu			
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Ile Asp Thr Gly Trp Ser Val Thr Val Ala Gly Asn Gly Ile Ala Gln			
	500	505	510
cgg acc tca gag aag gtg ctg ccg ttc gct tta gcg agt agg gga			1581
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Gly Leu Phe Arg Gly Gly Ile Asp Arg Glu Ser Leu Tyr Leu Ser Val
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Val Asn Leu Leu Asn Pro Thr Glu Arg Pro Ala Trp Leu Ala Thr His
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Leu Lys Glu Leu Thr Gly Ser Gly Ile Ile Tyr Cys Leu Thr Val Ser
85 90 95

Ala Ala His Asp Leu Ala Asp Ala Leu Asn Ser Val Gly Trp Asn Val
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Ala Ala Tyr Thr Gly Arg Thr Glu Ala Gly Glu Arg Glu Arg Leu Glu
115 120 125

His Ala Leu Ile Asn Asn Glu Ile Lys Ala Leu Val Ala Thr Ser Ala
130 135 140

Leu Gly Met Gly Phe Asp Lys Pro Asp Leu Gly Phe Val Val His Met
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Gly Ser Pro Ser Ser Pro Val Ser Tyr Tyr Gln Gln Ile Gly Arg Ala
165 170 175

Gly Arg Gly Thr Ala Arg Ala Asp Val Ile Leu Leu Pro Gly Thr Glu
180 185 190

Asp Lys Glu Ile Trp Glu Tyr Phe Ala Ser Val Ser Phe Pro Arg Glu
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Glu Val Val Arg Gln Leu Leu Ala Val Leu Thr Asp Glu Ala Gln Ser
210 215 220

Thr Val Lys Leu Glu Ser Gln Val Asp Leu Ser Arg Ser Arg Leu Glu
225 230 235 240

Gln Val Leu Lys Val Leu Asp Val Asp Gly Ala Val Lys Arg Val Arg
245 250 255

Gly Gly Trp Val Ser Thr Gly Gln Glu Trp Ile Tyr Asp Ala Glu Arg
260 265 270

Tyr Ala Gly Leu Glu Gln Ala Arg Lys Ile Glu Gln Gln Ser Met Val
275 280 285

Asn Tyr Gln Asn Thr Thr Glu Cys Arg Met Leu Tyr Leu Arg Lys Glu

290	295	300
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Val Asp Gln Gln Leu Gln Thr Pro Gly Val Lys Ile Ala Pro Arg Lys 340 345 350		
Met Trp Pro Thr Gly Ile Ser Val Arg Gly Lys Ile Ala Gly Leu Glu 355 360 365		
Glu Gly Arg Ala Leu Gly Arg Leu Asn Asp Ile Ala Arg Gly Pro Ala 370 375 380		
Leu Lys Ala Leu Leu Asp Ser Gly Ala Tyr Ser Asp Asp Pro Trp Met 385 390 395 400		
Ala Arg Ile Ile Glu Val Leu Lys Asn Trp Asp Trp Thr Asn Arg Pro 405 410 415		
Ala Asn Val Val Ala Leu Gly Asn Thr Asn Phe Gly Ser Thr Glu Met 420 425 430		
Ile Ile Gln Val Ala Gln Ser Ile Ala Ala Val Gly Arg Met Asn Phe 435 440 445		
Ala Gly Val Leu Pro Ala Ala Pro Gly Ala Glu Glu Val Met Ala Gln 450 455 460		
Asn Ser Ala Tyr Arg Val Glu Ala Leu Leu Lys Gln Trp Asp Trp Ser 465 470 475 480		
Gln Gly Leu Gln Leu Val Pro Gly Pro Ile Leu Leu Val Thr Asp Leu 485 490 495		
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Met Pro Ile Ile Ile

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Tyr Asn Pro Asp Thr Asp Ala Asp Leu Leu Asp Ala Ile Asn Ala Asp	
25 30 35	
gct gac ctt gat ggc gac gcc acc atc agc act aac gcg aca gaa gaa	259
Ala Asp Leu Asp Gly Asp Ala Thr Ile Ser Thr Asn Ala Thr Glu Glu	
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Gly Val Asp Ala Ala Ala Glu Lys Pro Lys Lys Lys Arg Lys Ala Pro	
55 60 65	
gct ctg aag cct aaa gga ctc acg gca aag ttc ttc cac cgt gat ctt	355
Ala Leu Lys Pro Lys Gly Leu Thr Ala Lys Phe Phe His Arg Asp Leu	
70 75 80 85	
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Thr Gly Val Gly Gly Arg Thr Gly Arg Leu Asn Lys Asn Val His Pro	
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Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser Asp Val Tyr Thr Pro	
105 110 115	
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Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg Tyr Ile Leu Thr His	
120 125 130	
cca acc ccc gct gtt gtt ctc agt gag tcc atc agc aac gcg ttt cat	547
Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile Ser Asn Ala Phe His	
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Val Ser Thr Leu Arg Arg Asn Asn Asn Val Asn Asn Ser Asp Ser Glu	
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ttg gct gcc tgg ccg tac ctc tac caa ctc gat att ccg cag ctg gac	643
Leu Ala Ala Trp Pro Tyr Leu Tyr Gln Leu Asp Ile Pro Gln Leu Asp	
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Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr His Phe His Gly Tyr	
185 190 195	
aac ctg tgg gtg gat ttt acc ccg cag act atc gct cta cga tcc ggt	739
Asn Leu Trp Val Asp Phe Thr Pro Gln Thr Ile Ala Leu Arg Ser Gly	
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aag acg gta ctc gat gac ggt acc acc gcc tct gat aac acc act cat	787
Lys Thr Val Leu Asp Asp Gly Thr Thr Ala Ser Asp Asn Thr Thr His	
215 220 225	
gtc tat tac cgc gtc acc gtt cac gtt att gcc ggt caa gat cat gga	835
Val Tyr Tyr Arg Val Thr Val His Val Ile Ala Gly Gln Asp His Gly	
230 235 240 245	

tct act ctg ctt gat gac cag ggc aac cag gtg ctt gat agg gat gat	883
Ser Thr Leu Leu Asp Asp Gln Gly Asn Gln Val Leu Asp Arg Asp Asp	
250 255 260	
aat cct att tct acc cca agt atc aag cgt att ggc gct gtc act gat	931
Asn Pro Ile Ser Thr Pro Ser Ile Lys Arg Ile Gly Ala Val Thr Asp	
265 270 275	
ctt ttc gat cac aat cct ttt ggc ttc gct agt gta aac tct ttc gca	979
Leu Phe Asp His Asn Pro Phe Gly Phe Ala Ser Val Asn Ser Phe Ala	
280 285 290	
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Phe Val Asp Phe Ser Trp Asp Pro Ala Thr Thr Leu Val Asp Met Leu	
295 300 305	
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Asn Asn Leu Asp Ser Tyr Leu Ser Asn His Ile Asn Ile Ala Ser Ser	
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Pro Thr Pro Ile Ala Leu Asp Met Val Val Leu Asn Glu Trp Ser Glu	
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Lys Ser Tyr Gln Leu Cys Glu Arg Val Val Ala Gln Ala Lys Leu Ile	
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Asn Ser Asn Lys Ile Thr Ala His Val Ser Asp Val Ile Lys Gln Asn	
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Ala His Asn Ile Leu Trp Phe Thr Glu Gln Met Asn Pro Gly Thr Thr	
375 380 385	
aac ctc agc gag gta cct atc tcc aag aag tct atg ctg ccg atg tct	1315
Asn Leu Ser Glu Val Pro Ile Ser Lys Lys Ser Met Leu Pro Met Ser	
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Arg Gln Leu Arg Ile Leu Glu His Tyr Asp Val Pro Leu Thr Ala Tyr	
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Ser Ala Leu Phe Trp Thr Val Ser Ala Ile Lys Asn Glu Ser Met Val	
425 430 435	
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Gln Tyr Leu Val Arg Gln Asn Met Gln Leu Thr Leu Ser Ser Asn Leu	
440 445 450	
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Asp Ala Leu Asn Ser Ile Val Ser Gln Leu Pro Val Pro Asp Lys Asp	
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Val Val Ala Ala Ser Gly Tyr Gln Ile Gln Pro His Phe Ser Thr Gln	
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Gln	Arg	Glu	Ala	Ile	Thr	Thr	Asp	Asn	Pro	Leu	Ala	Ile	Ile	Gln	Ala		
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Gly	Ala	Gly	Thr	Gly	Lys	Ser	Thr	Val	Ile	Leu	Glu	Arg	Ile	Glu	Tyr		
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Ser	Met	Thr	Ile	Ser	Lys	Met	Val	His	Glu	Ile	Tyr	Ala	His	Asn	Phe		
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Pro	Asp	His	Glu	Ile	Ser	Thr	Ile	Asp	Thr	Ile	Ile	Asn	Thr	Leu	Asp		
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Ile	Glu	Tyr	Gly	Asp	Gln	Met	Val	Thr	Ser	Asp	Tyr	Met	Ile	Gln	Leu		
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Arg	Asp	Leu	Leu	Tyr	Lys	Val	Met	Thr	Gln	Gly	Gly	Asn	Ala	Asn	Leu		
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Val	Leu	Asp	Gln	Ile	Lys	Gln	Thr	Ser	Leu	Glu	Leu	Glu	Ile	Ile	Ile		
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Cys	Tyr	Leu	Leu	Leu	Asp	Lys	Leu	Ile	Glu	Pro	His	Ala	Ser	Pro	Lys		
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Tyr	Leu	Ile	Ile	Asp	Glu	Val	Gln	Asp	Asn	Ser	Val	Phe	Glu	Phe	Val		
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Phe	Ala	Leu	Arg	Phe	Ala	Ala	Lys	His	Asn	Thr	Ser	Leu	Tyr	Leu	Val		
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Ala	Leu	Asn	Ser	Leu	Glu	Ala	Ser	Gly	Val	Phe	Gly	Thr	Tyr	Arg	Leu		
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cgt	aac	ttg	cag	tcc	gat	aag	ggt	ttc	aac	aac	acg	gta	ttt	tcg	acc	2659				
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 Ser Ser Thr Ala Pro Val Thr Pro Val Val Ala Asp Leu Glu Val Thr
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 Thr Val Ala Ala Asp Pro Val Glu Pro Thr Ile Val Ala Ala Gln Pro
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 Asn Pro Val Leu Ser Asp Ile Glu Ala Leu Arg Ala Ile Phe Asn Asn
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Asn Ala Thr Glu Glu Gly Val Asp Ala Ala Ala Glu Lys Pro Lys Lys
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Lys Asn Val His Pro Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser
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Asp Val Tyr Thr Pro Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg
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Tyr Ile Leu Thr His Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile
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Ser Asn Ala Phe His Val Ser Thr Leu Arg Arg Asn Asn Asn Val Asn
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Asn Ser Asp Ser Glu Leu Ala Ala Trp Pro Tyr Leu Tyr Gln Leu Asp
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Ile Pro Gln Leu Asp Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr
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His Phe His Gly Tyr Asn Leu Trp Val Asp Phe Thr Pro Gln Thr Ile
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Ala Leu Arg Ser Gly Lys Thr Val Leu Asp Asp Gly Thr Thr Ala Ser
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Asp Asn Thr Thr His Val Tyr Tyr Arg Val Thr Val His Val Ile Ala
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Gly Gln Asp His Gly Ser Thr Leu Leu Asp Asp Gln Gly Asn Gln Val
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Gly Ala Val Thr Asp Leu Phe Asp His Asn Pro Phe Gly Phe Ala Ser
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Val Asn Ser Phe Ala Phe Val Asp Phe Ser Trp Asp Pro Ala Thr Thr
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Gln Ala Lys Leu Ile Asn Ser Asn Lys Ile Thr Ala His Val Ser Asp
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Val Ile Lys Gln Asn Ala His Asn Ile Leu Trp Phe Thr Glu Gln Met
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Asn Pro Gly Thr Thr Asn Leu Ser Glu Val Pro Ile Ser Lys Lys Ser
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Pro Leu Thr Ala Tyr Ser Ala Leu Phe Trp Thr Val Ser Ala Ile Lys
420 425 430

Asn Glu Ser Met Val Gln Tyr Leu Val Arg Gln Asn Met Gln Leu Thr
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Leu Ser Ser Asn Leu Asp Ala Leu Asn Ser Ile Val Ser Gln Leu Pro
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Val Pro Asp Lys Asp Val Val Ala Ala Ser Gly Tyr Gln Ile Gln Pro
465 470 475 480

His Phe Ser Thr Gln Gln Arg Glu Ala Ile Thr Thr Asp Asn Pro Leu
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Ala Ile Ile Gln Ala Gly Ala Gly Thr Gly Lys Ser Thr Val Ile Leu
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Glu Arg Ile Glu Tyr Leu Cys Ala Ala Gly Thr Asn Pro Glu Glu Ile
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His	Ala	Ser	Pro 660	Lys	Tyr	Leu	Ile	Ile 665	Asp	Glu	Val	Gln	Asp 670	Asn	Ser		
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Pro	Ser	Ile 835	Thr	Val	Arg	Asn	Leu 840	Gln	Ser	Asp	Lys	Gly 845	Phe	Asn	Asn		
Thr	Val 850	Phe	Ser	Thr	Phe	Ile 855	Lys	Asp	Phe	Trp	Phe 860	Glu	Val	Thr	Ala		
Val 865	Asp	Pro	Ala	His 870	Ala	Ala	Phe	Thr	Phe	Thr 875	Ser	Gln	Val	Thr	Ala 880		

His Leu Asp Lys Leu Val Arg Gly Lys Arg Glu Gln Met Glu Asp Arg
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Val Ile Arg Ser Met Ala Ala Trp Trp Arg Glu Asn Glu Arg Asp Ile
900 905 910

Gln Gly Trp Val Gln Gln Thr Gln Ser Gly Ala Ile Thr Asn Glu Glu
915 920 925

Phe Phe Tyr Arg Leu Arg Gln Cys Ile Leu Asp Tyr Glu Ile Arg Asn
930 935 940

Asn Arg Ala Arg Gln Ser Met Leu Asn Ala Arg Asn Asn Ala Asn Lys
945 950 955 960

Glu Ala Val Ala Gln Glu Lys Pro Leu Leu Met Val Ser Thr Ile His
965 970 975

Ser Ala Lys Gly Leu Glu Phe Asp Asn Val Ile Val Leu Gln Lys Pro
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Ser Ser Asp Ala Glu Met Thr Glu Glu Gly Lys Arg Ala Thr Tyr Val
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Lys Thr Asp Ser Pro Ile Arg Ile Met Ile Thr Gly Asp Val Ala Ser 120															

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Arg Tyr Gly Gln Thr His Asn Pro Ser Ile Val Thr Phe Leu Leu Asp	
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Pro Ala Glu Asp Ser Lys Val Gly Glu Val His Val Leu Glu Arg Leu	
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Met Glu Arg Glu His Glu Ala His Ser Leu Leu Gly Asp Ala Ala Ser	
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Leu Met Gly Lys His Ser Glu Arg Leu Glu Glu Glu Thr Ile Arg Glu	
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Val Leu Arg Gly Ala Gln Asn Phe Asn Asp Ala Val Ala Asp Pro Ala	
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Cys Leu Leu Glu Gly Phe Asn Asn Val Pro Glu Asp Ser Ile Asn Arg	
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Pro Thr Asp Asp Leu Arg Arg Arg Leu Asp Phe Leu Pro Gln Asp Tyr	
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 Gly Asp Val Ala Ser Glu Gly Val Asn Leu His Thr Leu Cys His Asn
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 Thr Phe Leu Leu Asp Pro Ala Glu Asp Ser Lys Val Gly Glu Val His
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 Val Leu Glu Arg Leu Met Glu Arg Glu His Glu Ala His Ser Leu Leu
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 Gly Asp Ala Ala Ser Leu Met Gly Lys His Ser Glu Arg Leu Glu Glu
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 Val Ala Asp Pro Ala Glu Val Leu Glu Asn Pro Ala Gly Leu Asp Asp
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Leu Pro Gln Asp Tyr Val Ala Ala Arg Lys Val Lys Glu Asp Leu Leu
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Leu Glu Arg Ala Pro Glu His Ile His Thr Tyr Arg Ile Thr Pro Leu
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Arg His Pro Ala His Gly Leu Ile Leu Glu Ser Gly Glu Pro Ala Ile
105 110 115

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120 125 130

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Gln Val Asp Pro Glu Thr Ile Val Val His Pro Ser Glu Arg Gly Arg
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Gly Tyr Val Asp Gly Glu Ser His Pro Ile Gly Leu Ser Thr Glu Phe
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185 190 195

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200 205 210

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Ile Leu Val Thr Asn Thr Val Ala Gly Arg Gln Trp Lys Asp Glu Leu	
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Pro Val Phe Arg Met Thr Ser Asp Leu Gln Ser Arg Arg Arg Leu Gly	
310 315 320 325	
ctg act gcc acc ctc gtg cgc gaa gac gga cga gaa ggc gat gtc ttc	1123
Leu Thr Ala Thr Leu Val Arg Glu Asp Gly Arg Glu Gly Asp Val Phe	
330 335 340	
agc ctg atc ggc ccc aag cgt tac gac gca cca tgg aaa gac ctc gag	1171
Ser Leu Ile Gly Pro Lys Arg Tyr Asp Ala Pro Trp Lys Asp Leu Glu	
345 350 355	
tcc caa ggg ttc atc gcc acc gcc gac tgc gta gaa atc cga tcc acc	1219
Ser Gln Gly Phe Ile Ala Thr Ala Asp Cys Val Glu Ile Arg Ser Thr	
360 365 370	
atg acc gat gct gag cgc atg gtg tac gcg act gcc gag tcg gca gat	1267
Met Thr Asp Ala Glu Arg Met Val Tyr Ala Thr Ala Glu Ser Ala Asp	
375 380 385	
cgt tac cgt cta gcc gcc act gcc cac act aag gtg gcc gtg gtg cgc	1315
Arg Tyr Arg Leu Ala Ala Thr Ala His Thr Lys Val Ala Val Val Arg	
390 395 400 405	
aaa ctc ctc gaa gag cac gct ggt aag ccc acg ctg atc atc ggc gca	1363
Lys Leu Leu Glu Glu His Ala Gly Lys Pro Thr Leu Ile Ile Gly Ala	
410 415 420	
tac ctc gat cag ttg gaa gaa cta ggt gca gaa ttc aac gca cca gtc	1411
Tyr Leu Asp Gln Leu Glu Glu Leu Gly Ala Glu Phe Asn Ala Pro Val	
425 430 435	
atc gac ggc aaa acg ccc aac aaa aag cgt gaa gcc ctc ttt gat caa	1459
Ile Asp Gly Lys Thr Pro Asn Lys Lys Arg Glu Ala Leu Phe Asp Gln	
440 445 450	
ttc cgt tcc ggc tcg ctt tcc gta ctg gtt gtc tcc aaa gtg gcg aac	1507

Phe Arg Ser Gly Ser Leu Ser Val Leu Val Val Ser Lys Val Ala Asn
 455 460 465

ttc tcc atc gac ctg ccc gaa gca tcc gta gcc atc cag gtc tct gga 1555
 Phe Ser Ile Asp Leu Pro Glu Ala Ser Val Ala Ile Gln Val Ser Gly
 470 475 480 485

aca ttc ggc agc cga caa gaa gaa gcc caa cgc tta ggc cgc ctc ctg 1603
 Thr Phe Gly Ser Arg Gln Glu Glu Ala Gln Arg Leu Gly Arg Leu Leu
 490 495 500

cga ccc aag cac gat ggc agc gaa gcc cac ttc tac tcc atc gtc agc 1651
 Arg Pro Lys His Asp Gly Ser Glu Ala His Phe Tyr Ser Ile Val Ser
 505 510 515

cgc gac acc ctc gac acc gaa tac gca gcc cac cgc cag cga ttc ctc 1699
 Arg Asp Thr Leu Asp Thr Glu Tyr Ala Ala His Arg Gln Arg Phe Leu
 520 525 530

gcc gaa caa ggc tac gca tac cgc atc ctc gac gcc gac gac atc ctc 1747
 Ala Glu Gln Gly Tyr Ala Tyr Arg Ile Leu Asp Ala Asp Asp Ile Leu
 535 540 545

ttc cca cta ccc aag aaa gag cta taacgtgcac aacttctcct tcg 1794
 Phe Pro Leu Pro Lys Lys Glu Leu
 550 555

<210> 252

<211> 557

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Val Ala Phe Gly Asp Gly Pro Leu Ile Val Gln Ser Asp Lys Thr Val
 1 5 10 15

Leu Leu Glu Ile Asp His Pro Gln Ala Gly Glu Ala Arg Ile Ala Leu
 20 25 30

Ala Pro Phe Ala Glu Leu Glu Arg Ala Pro Glu His Ile His Thr Tyr
 35 40 45

Arg Ile Thr Pro Leu Ala Leu Trp Asn Ala Arg Thr Ala Gly His Asp
 50 55 60

Ala Glu Gln Val Val Asp Met Leu Glu Arg Phe Ser Arg Phe Pro Val
 65 70 75 80

Pro Gln Ala Leu Leu Ile Asp Ile Ala Glu Thr Met Ser Arg Tyr Gly
 85 90 95

Arg Val Arg Leu His Arg His Pro Ala His Gly Leu Ile Leu Glu Ser
 100 105 110

Gly Glu Pro Ala Ile Leu Val Glu Ile Ser Arg His Lys Lys Ile Lys
 115 120 125

Pro Met Leu Gly Ala Gln Val Asp Pro Glu Thr Ile Val Val His Pro
 130 135 140

Ser Glu Arg Gly Arg Leu Lys Gln Glu Leu Leu Lys Val Gly Trp Pro
 145 150 155 160
 Ala Glu Asp Leu Ala Gly Tyr Val Asp Gly Glu Ser His Pro Ile Gly
 165 170 175
 Leu Ser Thr Glu Phe Glu Asp Trp Ser Leu Arg Asp Tyr Gln Gln Met
 180 185 190
 Ala Ala Asp Ser Phe Trp Glu Gly Gly Ser Gly Val Val Val Leu Pro
 195 200 205
 Cys Gly Ala Gly Lys Thr Met Val Gly Ala Ala Ser Met Ala Arg Ala
 210 215 220
 Gln Ala Thr Thr Leu Ile Leu Val Thr Asn Thr Val Ala Gly Arg Gln
 225 230 235 240
 Trp Lys Asp Glu Leu Leu Arg Arg Thr Thr Leu Thr Glu Asp Glu Ile
 245 250 255
 Gly Glu Tyr Ser Gly Glu Arg Lys Glu Ile Arg Pro Val Thr Ile Ala
 260 265 270
 Thr Tyr Gln Val Val Thr Arg Arg Thr Lys Gly Glu Tyr Lys Ala Leu
 275 280 285
 Glu Leu Phe Asp Ser Arg Asp Trp Gly Leu Ile Ile Tyr Asp Glu Val
 290 295 300
 His Leu Leu Pro Ala Pro Val Phe Arg Met Thr Ser Asp Leu Gln Ser
 305 310 315 320
 Arg Arg Arg Leu Gly Leu Thr Ala Thr Leu Val Arg Glu Asp Gly Arg
 325 330 335
 Glu Gly Asp Val Phe Ser Leu Ile Gly Pro Lys Arg Tyr Asp Ala Pro
 340 345 350
 Trp Lys Asp Leu Glu Ser Gln Gly Phe Ile Ala Thr Ala Asp Cys Val
 355 360 365
 Glu Ile Arg Ser Thr Met Thr Asp Ala Glu Arg Met Val Tyr Ala Thr
 370 375 380
 Ala Glu Ser Ala Asp Arg Tyr Arg Leu Ala Ala Thr Ala His Thr Lys
 385 390 395 400
 Val Ala Val Val Arg Lys Leu Leu Glu Glu His Ala Gly Lys Pro Thr
 405 410 415
 Leu Ile Ile Gly Ala Tyr Leu Asp Gln Leu Glu Glu Leu Gly Ala Glu
 420 425 430
 Phe Asn Ala Pro Val Ile Asp Gly Lys Thr Pro Asn Lys Lys Arg Glu
 435 440 445
 Ala Leu Phe Asp Gln Phe Arg Ser Gly Ser Leu Ser Val Leu Val Val
 450 455 460
 Ser Lys Val Ala Asn Phe Ser Ile Asp Leu Pro Glu Ala Ser Val Ala

465	470	475	480
Ile Gln Val Ser Gly Thr Phe Gly Ser Arg Gln Glu Glu Ala Gln Arg	485	490	495
Leu Gly Arg Leu Leu Arg Pro Lys His Asp Gly Ser Glu Ala His Phe	500	505	510
Tyr Ser Ile Val Ser Arg Asp Thr Leu Asp Thr Glu Tyr Ala Ala His	515	520	525
Arg Gln Arg Phe Leu Ala Glu Gln Gly Tyr Ala Tyr Arg Ile Leu Asp	530	535	540
Ala Asp Asp Ile Leu Phe Pro Leu Pro Lys Lys Glu Leu	545	550	555

<210> 253
 <211> 849
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(826)
 <223> RXN01066

<400> 253
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tttgaaccgc ctgggcttct agctttaagg ggggtgagttc atg cgt agg gac agt 115
 Met Arg Arg Asp Ser
 1 5

ttt cgg gac cgc gcg cta gta gtc aaa act tat gat ttt ggc gaa gcc 163
 Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr Asp Phe Gly Glu Ala
 10 15 20

gac cgc att att gtg ctg ctc acc cga gac cac ggc atc gtg cgc gga 211
 Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His Gly Ile Val Arg Gly
 25 30 35

gtt gcc aaa gga gta cgc cga tcc aaa tcc cgg ttt ggg tca agg ctg 259
 Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg Phe Gly Ser Arg Leu
 40 45 50

cag ctt ttt gtg gaa ctc gac gtg cag ctc tac cca ggt aga aaa ctg 307
 Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr Pro Gly Arg Lys Leu
 55 60 65

tcc acc atc tct ggc gcg gac acc gtc ggc tac tac gca tca ggc atc 355
 Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr Tyr Ala Ser Gly Ile
 70 75 80 85

atc gag gac ttc act cgg tat tcc tgt gcg tcc gcc atc ctg gaa atc 403
 Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser Ala Ile Leu Glu Ile
 90 95 100

gcc acc cac atc gca gga ctg gaa aac gat ccg cac ctg ttt gaa gaa 451
 Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro His Leu Phe Glu Glu

105	110	115	
acc acc cgg gcg ttg aaa aac att cag gac tcc cca gaa ccc atc ctc			499
Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser Pro Glu Pro Ile Leu			
120	125	130	
aac cta gac gag ttc atg ctc cgc gcc atg aac cac gcc ggc tgg gca			547
Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn His Ala Gly Trp Ala			
135	140	145	
cca agc ctt ttc gac tgc gca gcc tgc ggc cga cca gga cct cac aac			595
Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg Pro Gly Pro His Asn			
150	155	160	165
gca ttc cac cca ggc gtc ggc ggg gca gtg tgc ctg tac tgc cga ccg			643
Ala Phe His Pro Gly Val Gly Gly Ala Val Cys Leu Tyr Cys Arg Pro			
170	175		180
ccg gga agc gcc gaa gtc cca cca gaa gca cta cac atg atg tgg ttg			691
Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu His Met Met Trp Leu			
185	190		195
gtc gcc aac ggc caa gca gcc cgc att ccc cgg gaa cac cca gag cag			739
Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg Glu His Pro Glu Gln			
200	205		210
caa acc acc att cac caa ctg aca acc gcg cat ctg cag tgg cat att			787
Gln Thr Thr Ile His Gln Leu Thr Thr Ala His Leu Gln Trp His Ile			
215	220		225
gaa aga aag ctg ccc acg ctg gcg gtg ctg gat cag gcc tagtgcttag			836
Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp Gln Ala			
230	235		240
gcttaggcgt ccg			849

<210> 254

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Met	Arg	Arg	Asp	Ser	Phe	Arg	Asp	Arg	Ala	Leu	Val	Val	Lys	Thr	Tyr
1				5					10					15	

Asp	Phe	Gly	Glu	Ala	Asp	Arg	Ile	Ile	Val	Leu	Leu	Thr	Arg	Asp	His
		20					25					30			

Gly	Ile	Val	Arg	Gly	Val	Ala	Lys	Gly	Val	Arg	Arg	Ser	Lys	Ser	Arg
		35				40						45			

Phe	Gly	Ser	Arg	Leu	Gln	Leu	Phe	Val	Glu	Leu	Asp	Val	Gln	Leu	Tyr
50					55						60				

Pro	Gly	Arg	Lys	Leu	Ser	Thr	Ile	Ser	Gly	Ala	Asp	Thr	Val	Gly	Tyr
65					70				75					80	

Tyr	Ala	Ser	Gly	Ile	Ile	Glu	Asp	Phe	Thr	Arg	Tyr	Ser	Cys	Ala	Ser
				85					90					95	

Ala Ile Leu Glu Ile Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro
100 105 110

His Leu Phe Glu Glu Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser
115 120 125

Pro Glu Pro Ile Leu Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn
130 135 140

His Ala Gly Trp Ala Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg
145 150 155 160

Pro Gly Pro His Asn Ala Phe His Pro Gly Val Gly Gly Ala Val Cys
165 170 175

Leu Tyr Cys Arg Pro Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu
180 185 190

His Met Met Trp Leu Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg
195 200 205

Glu His Pro Glu Gln Gln Thr Thr Ile His Gln Leu Thr Thr Ala His
210 215 220

Leu Gln Trp His Ile Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp
225 230 235 240

Gln Ala

<210> 255
<211> 707
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(684)
<223> RXN01389

<220>
<221> misc_feature
<222> 638-668, 670-685, 688-694
<223> n = any nucleotide

<220>
<221> Variant
<222> 212
<223> Xaa = Thr or Pro

<220>
<221> Variant
<222> 213
<223> Xaa = Ile, Lys, Met, Asn, Arg, Ser, or Thr

<220>
<221> Variant
<222> 223
<223> Xaa = Cys, Asn, Ser, Thr, Phe, Leu, Pro, His, Arg, Ile,
Val, Ala, Asp, Gly or Tyr

<220>

<221> Variant

<222> 214-222,224-228

<223> Xaa = any amino acid

<400> 255

cag gac ggc gat aag ctc gct ggc cgc cac ggt aac aag ggt gtt gtc	48
Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val	
1 5 10 15	
ggt aaa att ttg cct cag aaa gat atg cca ttc ctt cca gac ggc act	96
Gly Lys Ile Leu Pro Gln Lys Asp Met Pro Phe Leu Pro Asp Gly Thr	
20 25 30	
cct gtt gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac	144
Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn	
35 40 45	
att ggt cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt	192
Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly	
50 55 60	
tgg tcc gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act	240
Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr	
65 70 75 80	
ctg cct gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act	288
Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr	
85 90 95	
cct gtg ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct	336
Pro Val Phe Asp Gly Ala Ser Asn Glu Leu Ala Gly Leu Leu Ala	
100 105 110	
aat tca cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt	384
Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly	
115 120 125	
aaa gca acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg	432
Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro	
130 135 140	
gtt tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac	480
Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp	
145 150 155 160	
gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc cag	528
Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr Gln	
165 170 175	
cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc ggc gaa	576
Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe Gly Glu	
180 185 190	
atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac aca ctt cag	624
Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr Thr Leu Gln	
195 200 205	
gag ctg ctg mcc ann nnn nnn nnn nnn nnn nnn nnn nnn nnt nnn	672

Glu Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
210 215 220

nnn nnn nnn nnn naannnnnnn tgcaccccg atc
Xaa Xaa Xaa Xaa
225

707

<210> 256
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<220>
<221> Variant
<222> 212
<223> Xaa = Thr or Pro

<220>
<221> Variant
<222> 213
<223> Xaa = Ile, Lys, Met, Asn, Arg, Ser, or Thr

<220>
<221> Variant
<222> 223
<223> Xaa = Cys, Asn, Ser, Thr, Phe, Leu, Pro, His, Arg, Ile,
Val, Ala, Asp, Gly or Tyr

<220>
<221> Variant
<222> 214-222, 224-228
<223> Xaa = any amino acid

<400> 256
Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val
1 5 10 15
Gly Lys Ile Leu Pro Gln Lys Asp Met Pro Phe Leu Pro Asp Gly Thr
20 25 30
Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn
35 40 45
Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly
50 55 60
Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr
65 70 75 80
Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr
85 90 95
Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala
100 105 110
Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly
115 120 125
Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro
130 135 140

Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp
 145 150 155 160

Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr Gln
 165 170 175

Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe Gly Glu
 180 185 190

Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr Thr Leu Gln
 195 200 205

Glu Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 210 215 220

Xaa Xaa Xaa Xaa
 225

<210> 257
 <211> 1245
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1222)
 <223> RXN02070

<400> 257
 agcacggatc aggacctcaa gatttgtctg accccactca gggatgatgtt gcagacgaat 60

tttagggagt atcaaaactt gggactacta tcgatacgtg atg act caa gta acc 115
 Met Thr Gln Val Thr 5

gaa tcc gct gtc cgc agc gcg cta tcc cgc gta gag gat cca gag atc 163
 Glu Ser Ala Val Arg Ser Ala Leu Ser Arg Val Glu Asp Pro Glu Ile 10 15 20

ggg aag ccc atc aca gag ctc ggc atg gtc aaa tca gtg tcc atc gac 211
 Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys Ser Val Ser Ile Asp 25 30 35

ggc tct gat gtc cag gtg gag gtc tac ctg acg atc gcg gct tgc ccg 259
 Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr Ile Ala Ala Cys Pro 40 45 50

atg aaa acc acc att gtc acc aac act gaa gca gct ctc aaa gac atc 307
 Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala Ala Leu Lys Asp Ile 55 60 65

gac ggg gtt ggc caa gtt cat gtc acc acc gat gtc atg agt gat gaa 355
 Asp Gly Val Gly Gln Val His Val Thr Thr Asp Val Met Ser Asp Glu 70 75 80 85

cag cgc cgt gcg ctc cgc gtc tcc ctg cgc ggt gaa act tct gag cca 403
 Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly Glu Thr Ser Glu Pro 90 95 100

gtg att cca ttc gct cag cct ggt tcc act acc cgc gtt tac gct gtt	451
Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr Arg Val Tyr Ala Val	
105 110 115	
gct tcc ggc aaa ggt ggc gta gga aaa tcc tcc atg acg gtg aac ttg	499
Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser Met Thr Val Asn Leu	
120 125 130	
gct gca gcc cta gcc aag cgc ggg ctg tct gtg gga att ttg gat gcc	547
Ala Ala Ala Leu Ala Lys Arg Gly Leu Ser Val Gly Ile Leu Asp Ala	
135 140 145	
gat att tac gga cac tca gtg ccc gga atg ctc ggc tcg gac caa cgc	595
Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu Gly Ser Asp Gln Arg	
150 155 160 165	
cca cac cag gtc gat gac atg atc atg cct ccc cag gcg cac ggc gtg	643
Pro His Gln Val Asp Asp Met Ile Met Pro Pro Gln Ala His Gly Val	
170 175 180	
aag atg ata tcc att gct cac ttc acc gaa gga aat gct cct gtg gtg	691
Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly Asn Ala Pro Val Val	
185 190 195	
tgg cgt gga cca atg ctg cac cgt gcc atc cag caa ttc ctc act gac	739
Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln Gln Phe Leu Thr Asp	
200 205 210	
gtg ttc tgg ggc gac ctg gat att ttg ctg ctg gat ctt cct cca gga	787
Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu Asp Leu Pro Pro Gly	
215 220 225	
act ggt gac atc gcc atc acc gtt gcc caa ttg atc ccg aat gct gag	835
Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu Ile Pro Asn Ala Glu	
230 235 240 245	
ttg ctc att gtg acc act cct cag gct gcc gca gct gag gtt gcc gag	883
Leu Leu Ile Val Thr Thr Pro Gln Ala Ala Ala Glu Val Ala Glu	
250 255 260	
cga gca gga acg atc tct gtg cag acc aac cag aag gtt gct ggc gtg	931
Arg Ala Gly Thr Ile Ser Val Gln Thr Asn Gln Lys Val Ala Gly Val	
265 270 275	
att gaa aac atg tct gcc atg gtg ctt cct gat ggc acc acc atg gat	979
Ile Glu Asn Met Ser Ala Met Val Leu Pro Asp Gly Thr Thr Met Asp	
280 285 290	
gtt ttc ggc acc ggc ggc ggt caa aag att gct gat cgt ctt acc gct	1027
Val Phe Gly Thr Gly Gly Gly Gln Lys Ile Ala Asp Arg Leu Thr Ala	
295 300 305	
gtg aca ggt gaa gag gtc aag gtt atc gga tct gtt cca ttg gat ccg	1075
Val Thr Gly Glu Glu Val Lys Val Ile Gly Ser Val Pro Leu Asp Pro	
310 315 320 325	
aac ctg cgt atc ggt ggc gat gtg gga aat cct att gcg att tct gaa	1123
Asn Leu Arg Ile Gly Gly Asp Val Gly Asn Pro Ile Ala Ile Ser Glu	
330 335 340	
cca cac tcc cca acc gct gca gcg atc aat gag atc gct gaa cac cta	1171

Pro His Ser Pro Thr Ala Ala Ala Ile Asn Glu Ile Ala Glu His Leu
 345 350 355

gct cac cgc aag gta tcg ctg gtg ggt aaa acg ctt ggg ctt ggc gtt 1219
 Ala His Arg Lys Val Ser Leu Val Gly Lys Thr Leu Gly Leu Gly Val
 360 365 370

aaa taaaagctaa ataatatcgg tcc 1245
 Lys

<210> 258

<211> 374

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

Met Thr Gln Val Thr Glu Ser Ala Val Arg Ser Ala Leu Ser Arg Val
 1 5 10 15

Glu Asp Pro Glu Ile Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys
 20 25 30

Ser Val Ser Ile Asp Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr
 35 40 45

Ile Ala Ala Cys Pro Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala
 50 55 60

Ala Leu Lys Asp Ile Asp Gly Val Gly Gln Val His Val Thr Thr Asp
 65 70 75 80

Val Met Ser Asp Glu Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly
 85 90 95

Glu Thr Ser Glu Pro Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr
 100 105 110

Arg Val Tyr Ala Val Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser
 115 120 125

Met Thr Val Asn Leu Ala Ala Ala Leu Ala Lys Arg Gly Leu Ser Val
 130 135 140

Gly Ile Leu Asp Ala Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu
 145 150 155 160

Gly Ser Asp Gln Arg Pro His Gln Val Asp Asp Met Ile Met Pro Pro
 165 170 175

Gln Ala His Gly Val Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly
 180 185 190

Asn Ala Pro Val Val Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln
 195 200 205

Gln Phe Leu Thr Asp Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu
 210 215 220

Asp Leu Pro Pro Gly Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu

<400> 259																		
gctcgtatcg cagaccaggt catgtggaca cagttattga gcaatggggc gagccgcgtg																		60
acgttgaagc ctttgtggag cgctagactt taaccccgtt																		
											atg	tat	ttg	aaa	tcg		115	
											Met	Tyr	Leu	Lys	Ser			
											1				5			
ttg acg ctc aag ggg ttt aag tct ttc gcg tct gcg acg acc ctg aaa																		163
Leu	Thr	Leu	Lys	Gly	Phe	Lys	Ser	Phe	Ala	Ser	Ala	Thr	Thr	Leu	Lys			
				10					15					20				
ttt gag cca ggc att tgt gcc gtg gtg ggt ccg aat ggt tca ggc aaa																		211
Phe	Glu	Pro	Gly	Ile	Cys	Ala	Val	Val	Gly	Pro	Asn	Gly	Ser	Gly	Lys			
			25					30					35					
tcc aat gtg gtt gat gcg ctg gcc tgg gtg atg ggt gaa ggt tct gcg																		259
Ser	Asn	Val	Val	Asp	Ala	Leu	Ala	Trp	Val	Met	Gly	Glu	Gly	Ser	Ala			
		40					45					50						
aag acc ttg cgt ggc ggc aaa atg gaa gat gtc att ttt gct ggc gcg																		307
Lys	Thr	Leu	Arg	Gly	Gly	Lys	Met	Glu	Asp	Val	Ile	Phe	Ala	Gly	Ala			

55	60	65	
ggc gat cgt aaa ccg ttg ggt cgc gca gaa gtc acg ctg acc att gat			355
Gly Asp Arg Lys Pro Leu Gly Arg Ala Glu Val Thr Leu Thr Ile Asp			
70	75	80	85
aac tct gat ggc gca ctg ccc att gag tac acc gaa gtg tcg gtg acc			403
Asn Ser Asp Gly Ala Leu Pro Ile Glu Tyr Thr Glu Val Ser Val Thr			
	90	95	100
aga cgg atg ttc cgt gat ggt gca agt gaa tat gag atc aat ggg gcg			451
Arg Arg Met Phe Arg Asp Gly Ala Ser Glu Tyr Glu Ile Asn Gly Ala			
	105	110	115
aaa gct cga ttg atg gat atc cag gag ctg ttg tcg gat acc ggt att			499
Lys Ala Arg Leu Met Asp Ile Gln Glu Leu Leu Ser Asp Thr Gly Ile			
	120	125	130
ggc cgt gaa atg cac atc atg gtg ggg cag gga aag ctc gca gag att			547
Gly Arg Glu Met His Ile Met Val Gly Gln Gly Lys Leu Ala Glu Ile			
	135	140	145
ttg gag tcc cgc ccc gaa gag cgc cga gcg tat atc gaa gaa gct gcg			595
Leu Glu Ser Arg Pro Glu Glu Arg Arg Ala Tyr Ile Glu Glu Ala Ala			
	150	155	160
ggc gtg ctc aag cac cgg cgc agg aaa gaa aag gcg cag cgc aaa ctt			643
Gly Val Leu Lys His Arg Arg Arg Lys Glu Lys Ala Gln Arg Lys Leu			
	170	175	180
cag ggc atg cag gtc aat ctt gat cgt ttg cag gat ctg acc cat gag			691
Gln Gly Met Gln Val Asn Leu Asp Arg Leu Gln Asp Leu Thr His Glu			
	185	190	195
ttg gcc aag cag ctc aag ccg ttg gct agg cag gcg gaa gca gcg cag			739
Leu Ala Lys Gln Leu Lys Pro Leu Ala Arg Gln Ala Glu Ala Ala Gln			
	200	205	210
cgt gcg gcg acg gtg cag gct gat ttg cgt gat gcg cgt ttc cag att			787
Arg Ala Ala Thr Val Gln Ala Asp Leu Arg Asp Ala Arg Phe Gln Ile			
	215	220	225
gct ggc ttt gag atc gtg aag ctc tcg gaa aag ctg gaa acc tct act			835
Ala Gly Phe Glu Ile Val Lys Leu Ser Glu Lys Leu Glu Thr Ser Thr			
	230	235	240
gag cgc gag aaa atg att cgt gag cag gcg gaa gca gca caa gag cag			883
Glu Arg Glu Lys Met Ile Arg Glu Gln Ala Glu Ala Ala Gln Glu Gln			
	250	255	260
ctg gaa gaa gcc acc aca act cag atg gaa gtg gag atg gag ttg gcg			931
Leu Glu Glu Ala Thr Thr Thr Gln Met Glu Val Glu Met Glu Leu Ala			
	265	270	275
gag atc act ccg cag gct gaa gct gcg caa cag ttg tgg ttt gat ttg			979
Glu Ile Thr Pro Gln Ala Glu Ala Ala Gln Gln Leu Trp Phe Asp Leu			
	280	285	290
tct tcg ctg gct gag cgg gtg tcg gca acg atg cgt att gct gca gac			1027
Ser Ser Leu Ala Glu Arg Val Ser Ala Thr Met Arg Ile Ala Ala Asp			
	295	300	305

cgt gcg agt tca ggt gcc gcg gat gtg ccg tat gcg ggc cag gat cct	1075
Arg Ala Ser Ser Gly Ala Ala Asp Val Pro Tyr Ala Gly Gln Asp Pro	
310 315 320 325	
gat gag ttg ctt ggt cgg gcc gaa act gct gac aaa gaa tta gaa gaa	1123
Asp Glu Leu Leu Gly Arg Ala Glu Thr Ala Asp Lys Glu Leu Glu Glu	
330 335 340	
ctc gag atg gcc gtg gaa atg acc acc gag cgt ttg acc tcc att caa	1171
Leu Glu Met Ala Val Glu Met Thr Thr Glu Arg Leu Thr Ser Ile Gln	
345 350 355	
gag gaa gcc gag gat aag gcc gcg cag gct cgt gag gct gag cgt gaa	1219
Glu Glu Ala Glu Asp Lys Ala Ala Gln Ala Arg Glu Ala Glu Arg Glu	
360 365 370	
cac ttg gcg cag gtc agg gcg att tct gat cgt cgt gaa ggt gtt gtg	1267
His Leu Ala Gln Val Arg Ala Ile Ser Asp Arg Arg Glu Gly Val Val	
375 380 385	
cgc ctg ctt gca tct gag gaa tct ttg cgc acc cag cac acg tca gca	1315
Arg Leu Leu Ala Ser Glu Glu Ser Leu Arg Thr Gln His Thr Ser Ala	
390 395 400 405	
gag gag gaa gct gag cga ctc agt gag cag ctt gag gag ttc atc ggc	1363
Glu Glu Glu Ala Glu Arg Leu Ser Glu Gln Leu Glu Glu Phe Ile Gly	
410 415 420	
cgc att ttg gat gtg gaa cgt gaa cgt cgc ctc acc gat gag cgt aaa	1411
Arg Ile Leu Asp Val Glu Arg Glu Arg Arg Leu Thr Asp Glu Arg Lys	
425 430 435	
cag ggc gtt gac acg gat cgt gcg ccc ttg gaa gaa gcc ctc aaa cag	1459
Gln Gly Val Asp Thr Asp Arg Ala Pro Leu Glu Glu Ala Leu Lys Gln	
440 445 450	
gca aaa cat gaa gcc gaa gca gca gag act cgt ctt gag gag ctt cgt	1507
Ala Lys His Glu Ala Glu Ala Ala Glu Thr Arg Leu Glu Glu Leu Arg	
455 460 465	
act aag cgc agc gat ctg gaa aaa gaa gta tcc agg ttg cag tcg cgc	1555
Thr Lys Arg Ser Asp Leu Glu Lys Glu Val Ser Arg Leu Gln Ser Arg	
470 475 480 485	
att gag acg ctt aac caa aat agg cca cgt tcc gat gct gct gat gtg	1603
Ile Glu Thr Leu Asn Gln Asn Arg Pro Arg Ser Asp Ala Ala Asp Val	
490 495 500	
gtg gat tac ccg cag ctg gcc acg ttg att cga ccg caa cga aac gtc	1651
Val Asp Tyr Pro Gln Leu Ala Thr Leu Ile Arg Pro Gln Arg Asn Val	
505 510 515	
gat aag gct ctc gct gcc gcc ctg ggt gcg cat gcc gag gcg ctg gct	1699
Asp Lys Ala Leu Ala Ala Ala Leu Gly Ala His Ala Glu Ala Leu Ala	
520 525 530	
ggc gag gct gcg gaa ggg ctc gtc gag aag ctt atc gac gcc ggc gtt	1747
Gly Glu Ala Ala Glu Gly Leu Val Glu Lys Leu Ile Asp Ala Gly Val	
535 540 545	

gca cgc acc atc atc gtt gat ggc acg cag gct ggc ggc gca tgg cgc Ala Arg Thr Ile Ile Val Asp Gly Thr Gln Ala Gly Gly Ala Trp Arg 550 555 560 565	1795
ctg gac gcg aac att ccg gcc ggg gcg agc tgg ctg ctc gac cat gtt Leu Asp Ala Asn Ile Pro Ala Gly Ala Ser Trp Leu Leu Asp His Val 570 575 580	1843
gat ctg gat ccg gcg att gcc ggc ccg gta aac cgg ctg ctt gcc gac Asp Leu Asp Pro Ala Ile Ala Gly Pro Val Asn Arg Leu Leu Ala Asp 585 590 595	1891
gtt gtg ctt gtc gac gac ccc tcc ctc ggc cgc caa gca atc gag gat Val Val Leu Val Asp Asp Pro Ser Leu Gly Arg Gln Ala Ile Glu Asp 600 605 610	1939
gat ccc cgt ctg cgt gcc gtt gac cgc aat ggt gtg ctc atc ggc gct Asp Pro Arg Leu Arg Ala Val Asp Arg Asn Gly Val Leu Ile Gly Ala 615 620 625	1987
ggg tgg att cag gtc ggc acc gaa acc tcg act gtg gaa atc aca gct Gly Trp Ile Gln Val Gly Thr Glu Thr Ser Thr Val Glu Ile Thr Ala 630 635 640 645	2035
cat att gag gaa gca gaa gct caa ctt gct gcg gcc tct gcc gcc ttg His Ile Glu Glu Ala Glu Ala Gln Leu Ala Ala Ser Ala Ala Leu 650 655 660	2083
gac gac att gcc ggc act ttt gat ggc gcc ctc cac gct gcc gac aac Asp Asp Ile Ala Gly Thr Phe Asp Gly Ala Leu His Ala Ala Asp Asn 665 670 675	2131
act cgc gtc gag gtg gct gcc cgc acc gca gcc ctg cgc gaa ctc gac Thr Arg Val Glu Val Ala Ala Arg Thr Ala Ala Leu Arg Glu Leu Asp 680 685 690	2179
atg acc agg gat tcc atc acc cgc gat ctc gcg cgc ttg gac aaa caa Met Thr Arg Asp Ser Ile Thr Arg Asp Leu Ala Arg Leu Asp Lys Gln 695 700 705	2227
cat gag gcc gcc gaa tcc gag cgc gtc cgc cat gtt gga cgc ctg cat His Glu Ala Ala Glu Ser Glu Arg Val Arg His Val Gly Arg Leu His 710 715 720 725	2275
gct gcg gaa aca cgc cgt gaa gag ctg cgc gaa cag tta gaa gac atc Ala Ala Glu Thr Arg Arg Glu Glu Leu Arg Glu Gln Leu Glu Asp Ile 730 735 740	2323
gtc gat cga ctc tcc cgc gtg gaa gac gaa gaa gac gct gac gaa ccc Val Asp Arg Leu Ser Arg Val Glu Asp Glu Glu Asp Ala Asp Glu Pro 745 750 755	2371
tca acc acc gcc cgc gac caa gca aat gcc gag ctg caa caa atc cgc Ser Thr Thr Ala Arg Asp Gln Ala Asn Ala Glu Leu Gln Gln Ile Arg 760 765 770	2419
gcc atg gaa atg gaa gca cgc ctt gcc caa cgc acc gcc gaa gag cgc Ala Met Glu Met Glu Ala Arg Leu Ala Gln Arg Thr Ala Glu Glu Arg 775 780 785	2467
gcc ggg cag cag cgg ggc aag ggc gat agt ctg cga cgc cag gcc gag	2515

Ala Gly Gln Gln Arg Gly Lys Gly Asp Ser Leu Arg Arg Gln Ala Glu
790 795 800 805

cat gag cgc caa gcc aaa atc cgg cat gaa caa gcc atg gaa gcc cgt 2563
His Glu Arg Gln Ala Lys Ile Arg His Glu Gln Ala Met Glu Ala Arg
810 815 820

cgc agg cgc acc caa ttg gct gca gcc gtg cat aat ggc gca cgc gat 2611
Arg Arg Arg Thr Gln Leu Ala Ala Val His Asn Gly Ala Arg Asp
825 830 835

gtg gcc gag cgt gtc tca agt gtc ctt gcc caa gca gcc atc gaa aga 2659
Val Ala Glu Arg Val Ser Ser Val Leu Ala Gln Ala Ala Ile Glu Arg
840 845 850

gat cag cac aac cgc gac aaa gcg ctg ctg acc tca cac tta gcg cgc 2707
Asp Gln His Asn Arg Asp Lys Ala Leu Leu Thr Ser His Leu Ala Arg
855 860 865

gcc aaa gat gct gtg agt gct gca cgc cag cac ctc aat cga ctc agc 2755
Ala Lys Asp Ala Val Ser Ala Ala Arg Gln His Leu Asn Arg Leu Ser
870 875 880 885

gac aac gcc cac tcc atg gaa ctt gcg cgc agc caa gct caa gtg cgc 2803
Asp Asn Ala His Ser Met Glu Leu Ala Arg Ser Gln Ala Gln Val Arg
890 895 900

atg gag gaa gcc gtt gcc aaa atc acc gag caa ctt ggc att ccg gtc 2851
Met Glu Glu Ala Val Ala Lys Ile Thr Glu Gln Leu Gly Ile Pro Val
905 910 915

gca gaa ttg ctg cgc gat tac acc cca gat gaa aac ttt gat gaa aag 2899
Ala Glu Leu Leu Arg Asp Tyr Thr Pro Asp Glu Asn Phe Asp Glu Lys
920 925 930

ttc caa cgc gca cgc ctc aaa caa gcc gaa aaa gac ctc gcc gca cta 2947
Phe Gln Arg Ala Arg Leu Lys Gln Ala Glu Lys Asp Leu Ala Ala Leu
935 940 945

ggc aaa gtc aac ccc ctg gcc ttg gaa gaa ttc aaa gcc ctt gga aga 2995
Gly Lys Val Asn Pro Leu Ala Leu Glu Glu Phe Lys Ala Leu Gly Arg
950 955 960 965

gcg cta cga gtt cct 3010
Ala Leu Arg Val Pro
970

<210> 260

<211> 970

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

Met Tyr Leu Lys Ser Leu Thr Leu Lys Gly Phe Lys Ser Phe Ala Ser
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Ala Thr Thr Leu Lys Phe Glu Pro Gly Ile Cys Ala Val Val Gly Pro
20 25 30

Asn Gly Ser Gly Lys Ser Asn Val Val Asp Ala Leu Ala Trp Val Met

35	40	45
Gly Glu Gly Ser Ala Lys Thr Leu Arg Gly Gly Lys Met Glu Asp Val		
50	55	60
Ile Phe Ala Gly Ala Gly Asp Arg Lys Pro Leu Gly Arg Ala Glu Val		
65	70	75
Thr Leu Thr Ile Asp Asn Ser Asp Gly Ala Leu Pro Ile Glu Tyr Thr		
	85	90
Glu Val Ser Val Thr Arg Arg Met Phe Arg Asp Gly Ala Ser Glu Tyr		
	100	110
Glu Ile Asn Gly Ala Lys Ala Arg Leu Met Asp Ile Gln Glu Leu Leu		
	115	120
Ser Asp Thr Gly Ile Gly Arg Glu Met His Ile Met Val Gly Gln Gly		
	130	135
Lys Leu Ala Glu Ile Leu Glu Ser Arg Pro Glu Glu Arg Arg Ala Tyr		
	145	150
Ile Glu Glu Ala Ala Gly Val Leu Lys His Arg Arg Arg Lys Glu Lys		
	165	170
Ala Gln Arg Lys Leu Gln Gly Met Gln Val Asn Leu Asp Arg Leu Gln		
	180	185
Asp Leu Thr His Glu Leu Ala Lys Gln Leu Lys Pro Leu Ala Arg Gln		
	195	200
Ala Glu Ala Ala Gln Arg Ala Ala Thr Val Gln Ala Asp Leu Arg Asp		
	210	215
Ala Arg Phe Gln Ile Ala Gly Phe Glu Ile Val Lys Leu Ser Glu Lys		
	225	230
Leu Glu Thr Ser Thr Glu Arg Glu Lys Met Ile Arg Glu Gln Ala Glu		
	245	250
Ala Ala Gln Glu Gln Leu Glu Glu Ala Thr Thr Thr Gln Met Glu Val		
	260	265
Glu Met Glu Leu Ala Glu Ile Thr Pro Gln Ala Glu Ala Ala Gln Gln		
	275	280
Leu Trp Phe Asp Leu Ser Ser Leu Ala Glu Arg Val Ser Ala Thr Met		
	290	295
Arg Ile Ala Ala Asp Arg Ala Ser Ser Gly Ala Ala Asp Val Pro Tyr		
	305	310
Ala Gly Gln Asp Pro Asp Glu Leu Leu Gly Arg Ala Glu Thr Ala Asp		
	325	330
Lys Glu Leu Glu Glu Leu Glu Met Ala Val Glu Met Thr Thr Glu Arg		
	340	345
Leu Thr Ser Ile Gln Glu Glu Ala Glu Asp Lys Ala Ala Gln Ala Arg		
	355	360
		365

Glu Ala Glu Arg Glu His Leu Ala Gln Val Arg Ala Ile Ser Asp Arg
370 375 380

Arg Glu Gly Val Val Arg Leu Leu Ala Ser Glu Glu Ser Leu Arg Thr
385 390 395 400

Gln His Thr Ser Ala Glu Glu Glu Ala Glu Arg Leu Ser Glu Gln Leu
405 410 415

Glu Glu Phe Ile Gly Arg Ile Leu Asp Val Glu Arg Glu Arg Arg Leu
420 425 430

Thr Asp Glu Arg Lys Gln Gly Val Asp Thr Asp Arg Ala Pro Leu Glu
435 440 445

Glu Ala Leu Lys Gln Ala Lys His Glu Ala Glu Ala Ala Glu Thr Arg
450 455 460

Leu Glu Glu Leu Arg Thr Lys Arg Ser Asp Leu Glu Lys Glu Val Ser
465 470 475 480

Arg Leu Gln Ser Arg Ile Glu Thr Leu Asn Gln Asn Arg Pro Arg Ser
485 490 495

Asp Ala Ala Asp Val Val Asp Tyr Pro Gln Leu Ala Thr Leu Ile Arg
500 505 510

Pro Gln Arg Asn Val Asp Lys Ala Leu Ala Ala Ala Leu Gly Ala His
515 520 525

Ala Glu Ala Leu Ala Gly Glu Ala Ala Glu Gly Leu Val Glu Lys Leu
530 535 540

Ile Asp Ala Gly Val Ala Arg Thr Ile Ile Val Asp Gly Thr Gln Ala
545 550 555 560

Gly Gly Ala Trp Arg Leu Asp Ala Asn Ile Pro Ala Gly Ala Ser Trp
565 570 575

Leu Leu Asp His Val Asp Leu Asp Pro Ala Ile Ala Gly Pro Val Asn
580 585 590

Arg Leu Leu Ala Asp Val Val Leu Val Asp Asp Pro Ser Leu Gly Arg
595 600 605

Gln Ala Ile Glu Asp Asp Pro Arg Leu Arg Ala Val Asp Arg Asn Gly
610 615 620

Val Leu Ile Gly Ala Gly Trp Ile Gln Val Gly Thr Glu Thr Ser Thr
625 630 635 640

Val Glu Ile Thr Ala His Ile Glu Glu Ala Glu Ala Gln Leu Ala Ala
645 650 655

Ala Ser Ala Ala Leu Asp Asp Ile Ala Gly Thr Phe Asp Gly Ala Leu
660 665 670

His Ala Ala Asp Asn Thr Arg Val Glu Val Ala Ala Arg Thr Ala Ala
675 680 685

Leu Arg Glu Leu Asp Met Thr Arg Asp Ser Ile Thr Arg Asp Leu Ala
690 695 700

Arg Leu Asp Lys Gln His Glu Ala Ala Glu Ser Glu Arg Val Arg His
705 710 715 720

Val Gly Arg Leu His Ala Ala Glu Thr Arg Arg Glu Glu Leu Arg Glu
725 730 735

Gln Leu Glu Asp Ile Val Asp Arg Leu Ser Arg Val Glu Asp Glu Glu
740 745 750

Asp Ala Asp Glu Pro Ser Thr Thr Ala Arg Asp Gln Ala Asn Ala Glu
755 760 765

Leu Gln Gln Ile Arg Ala Met Glu Met Glu Ala Arg Leu Ala Gln Arg
770 775 780

Thr Ala Glu Glu Arg Ala Gly Gln Gln Arg Gly Lys Gly Asp Ser Leu
785 790 795 800

Arg Arg Gln Ala Glu His Glu Arg Gln Ala Lys Ile Arg His Glu Gln
805 810 815

Ala Met Glu Ala Arg Arg Arg Arg Thr Gln Leu Ala Ala Val His
820 825 830

Asn Gly Ala Arg Asp Val Ala Glu Arg Val Ser Ser Val Leu Ala Gln
835 840 845

Ala Ala Ile Glu Arg Asp Gln His Asn Arg Asp Lys Ala Leu Leu Thr
850 855 860

Ser His Leu Ala Arg Ala Lys Asp Ala Val Ser Ala Ala Arg Gln His
865 870 875 880

Leu Asn Arg Leu Ser Asp Asn Ala His Ser Met Glu Leu Ala Arg Ser
885 890 895

Gln Ala Gln Val Arg Met Glu Glu Ala Val Ala Lys Ile Thr Glu Gln
900 905 910

Leu Gly Ile Pro Val Ala Glu Leu Leu Arg Asp Tyr Thr Pro Asp Glu
915 920 925

Asn Phe Asp Glu Lys Phe Gln Arg Ala Arg Leu Lys Gln Ala Glu Lys
930 935 940

Asp Leu Ala Ala Leu Gly Lys Val Asn Pro Leu Ala Leu Glu Glu Phe
945 950 955 960

Lys Ala Leu Gly Arg Ala Leu Arg Val Pro
965 970

<210> 261

<211> 570

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(547)

<223> RXA01495

<400> 261

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agaattattt cgactctgtg aagatgagga gtgggtccacc atg gct gac aac gcc 115
Met Ala Asp Asn Ala
1 5
cgc gcg gct cgt atg gca aag cgc att caa act atc gtg gcc agc gcc 163
Arg Ala Ala Arg Met Ala Lys Arg Ile Gln Thr Ile Val Ala Ser Ala
10 15 20
att gaa cgc gat atc aag gac cgc cga ctt gag ttc gtc aca att act 211
Ile Glu Arg Asp Ile Lys Asp Arg Arg Leu Glu Phe Val Thr Ile Thr
25 30 35
gat gtg acc atg acc ggt gac ctg cac gat gca aag gtg ttt tac acc 259
Asp Val Thr Met Thr Gly Asp Leu His Asp Ala Lys Val Phe Tyr Thr
40 45 50
gtt cgt gga gct tcc att gaa gaa gaa cca gat ctt gag gca gca gca 307
Val Arg Gly Ala Ser Ile Glu Glu Glu Pro Asp Leu Glu Ala Ala Ala
55 60 65
gag gct ctt cac cga gca cgc ggc cag ctg agg aag atc gtt ggc cag 355
Glu Ala Leu His Arg Ala Arg Gly Gln Leu Arg Lys Ile Val Gly Gln
70 75 80 85
cag ctg ggt gtt cgg ttt acc ccg acc ctg act tac agc atc gat acc 403
Gln Leu Gly Val Arg Phe Thr Pro Thr Leu Thr Tyr Ser Ile Asp Thr
90 95 100
gtc cca gag gca tcc gca cac atg gaa gct ttg ttg gat cgt gct cgc 451
Val Pro Glu Ala Ser Ala His Met Glu Ala Leu Leu Asp Arg Ala Arg
105 110 115
aag cgc gat gag gag ctg gct aaa ttg cgc gaa ggt gca gcg cct gca 499
Lys Arg Asp Glu Glu Leu Ala Lys Leu Arg Glu Gly Ala Ala Pro Ala
120 125 130
ggt gat gca gat cct tac aag act tca tcc aag tct gaa tct gag gaa 547
Gly Asp Ala Asp Pro Tyr Lys Thr Ser Ser Lys Ser Glu Ser Glu Glu
135 140 145
taacaccagt gacggataat agt 570

<210> 262

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Ala Asp Asn Ala Arg Ala Ala Arg Met Ala Lys Arg Ile Gln Thr
1 5 10 15
Ile Val Ala Ser Ala Ile Glu Arg Asp Ile Lys Asp Arg Arg Leu Glu
20 25 30

Phe Val Thr Ile Thr Asp Val Thr Met Thr Gly Asp Leu His Asp Ala
 35 40 45
 Lys Val Phe Tyr Thr Val Arg Gly Ala Ser Ile Glu Glu Glu Pro Asp
 50 55 60
 Leu Glu Ala Ala Ala Glu Ala Leu His Arg Ala Arg Gly Gln Leu Arg
 65 70 75 80
 Lys Ile Val Gly Gln Gln Leu Gly Val Arg Phe Thr Pro Thr Leu Thr
 85 90 95
 Tyr Ser Ile Asp Thr Val Pro Glu Ala Ser Ala His Met Glu Ala Leu
 100 105 110
 Leu Asp Arg Ala Arg Lys Arg Asp Glu Glu Leu Ala Lys Leu Arg Glu
 115 120 125
 Gly Ala Ala Pro Ala Gly Asp Ala Asp Pro Tyr Lys Thr Ser Ser Lys
 130 135 140
 Ser Glu Ser Glu Glu
 145

<210> 263
 <211> 678
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(655)
 <223> RXA01893

<400> 263
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 atcagaatcc acgctgttag aaaaacacag gagtgaataa atg att gat gaa att 115
 Met Ile Asp Glu Ile
 1 5

 ctg ttc gaa gcg gaa gag cgc atg acc gca acg gtc gag cac acc cgc 163
 Leu Phe Glu Ala Glu Glu Arg Met Thr Ala Thr Val Glu His Thr Arg
 10 15 20

 gaa gac ttg acc acc att cgt acc ggt cgc gca aac ccg gct atg ttc 211
 Glu Asp Leu Thr Thr Ile Arg Thr Gly Arg Ala Asn Pro Ala Met Phe
 25 30 35

 aac ggt gtc atg gct gaa tac tac ggc gtg cct act cct att act cag 259
 Asn Gly Val Met Ala Glu Tyr Tyr Gly Val Pro Thr Pro Ile Thr Gln
 40 45 50

 atg tca ggc atc act gtt cca gag cct cgc atg ctg ctg atc aag cct 307
 Met Ser Gly Ile Thr Val Pro Glu Pro Arg Met Leu Leu Ile Lys Pro
 55 60 65

 tat gag atg tct tcc atg cag gtc att gag aat gct atc cgt aac tct 355
 Tyr Glu Met Ser Ser Met Gln Val Ile Glu Asn Ala Ile Arg Asn Ser

70	75	80	85	
gac ctt ggt gtt aac ccc acc aac gat ggc cag gtg ctg cgt gtg acc				403
Asp Leu Gly Val Asn Pro Thr Asn Asp Gly Gln Val Leu Arg Val Thr				
	90	95	100	
atc cca cag ctt act gaa gag cgt cgt aag gac atg gtc aag ctt gct				451
Ile Pro Gln Leu Thr Glu Glu Arg Arg Lys Asp Met Val Lys Leu Ala				
	105	110	115	
aag ggt aag ggc gaa gac ggc aag att gcc att cgt aac atc cgc cgc				499
Lys Gly Lys Gly Glu Asp Gly Lys Ile Ala Ile Arg Asn Ile Arg Arg				
	120	125	130	
aag ggc atg gac cag cta aag aag ctg caa aaa gat ggc gac gct ggc				547
Lys Gly Met Asp Gln Leu Lys Lys Leu Gln Lys Asp Gly Asp Ala Gly				
	135	140	145	
gaa gat gaa gta cag gca gca gaa aaa gaa cta gat aaa gtc acc gct				595
Glu Asp Glu Val Gln Ala Ala Glu Lys Glu Leu Asp Lys Val Thr Ala				
	150	155	160	165
ggt ttt gtt gcg cag gtc gat gaa gtc gtt gct cgc aag gaa aag gaa				643
Gly Phe Val Ala Gln Val Asp Glu Val Val Ala Arg Lys Glu Lys Glu				
	170	175	180	
ctg atg gag gtc tagaagacct ttatcgcaat ggc				678
Leu Met Glu Val				
	185			

<210> 264

<211> 185

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

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Val Glu His Thr Arg Glu Asp Leu Thr Thr Ile Arg Thr Gly Arg Ala				
	20	25		30
Asn Pro Ala Met Phe Asn Gly Val Met Ala Glu Tyr Tyr Gly Val Pro				
	35	40		45
Thr Pro Ile Thr Gln Met Ser Gly Ile Thr Val Pro Glu Pro Arg Met				
	50	55		60
Leu Leu Ile Lys Pro Tyr Glu Met Ser Ser Met Gln Val Ile Glu Asn				
	65	70		75
Ala Ile Arg Asn Ser Asp Leu Gly Val Asn Pro Thr Asn Asp Gly Gln				
	85	90		95
Val Leu Arg Val Thr Ile Pro Gln Leu Thr Glu Glu Arg Arg Lys Asp				
	100	105		110
Met Val Lys Leu Ala Lys Gly Lys Gly Glu Asp Gly Lys Ile Ala Ile				
	115	120		125

Arg Asn Ile Arg Arg Lys Gly Met Asp Gln Leu Lys Lys Leu Gln Lys
 130 135 140
 Asp Gly Asp Ala Gly Glu Asp Glu Val Gln Ala Ala Glu Lys Glu Leu
 145 150 155 160
 Asp Lys Val Thr Ala Gly Phe Val Ala Gln Val Asp Glu Val Val Ala
 165 170 175
 Arg Lys Glu Lys Glu Leu Met Glu Val
 180 185

<210> 265
 <211> 458
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(435)
 <223> RXA01568

<400> 265
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 Trp Asp Asn Ile Thr Tyr Leu Met Arg Ala Ala Arg Lys Gly Thr Val
 1 5 10 15
 gtt ccc atg gtc atc gag ttg gat ggc cgg ttc gtg ggg cag ttg act 96
 Val Pro Met Val Ile Glu Leu Asp Gly Arg Phe Val Gly Gln Leu Thr
 20 25 30
 atc ggc aac atc cag cac ggc ggc atc tcc gat gcc tgg att ggc tat 144
 Ile Gly Asn Ile Gln His Gly Gly Ile Ser Asp Ala Trp Ile Gly Tyr
 35 40 45
 tgg gtt tcc agc gcg gtg acg ggg cgc ggt atc gct acg gcc gcc tgc 192
 Trp Val Ser Ser Ala Val Thr Gly Arg Gly Ile Ala Thr Ala Ala Cys
 50 55 60
 gcg ctc ggc gtg gat cat gct ttt cga cgc ata ggt ctg cat cgc ctc 240
 Ala Leu Gly Val Asp His Ala Phe Arg Arg Ile Gly Leu His Arg Leu
 65 70 75 80
 acc gcc acc tat cta ccc agc aac cca gca tcc ggg aag gtg ctc gga 288
 Thr Ala Thr Tyr Leu Pro Ser Asn Pro Ala Ser Gly Lys Val Leu Gly
 85 90 95
 cac agc ggt ttc cgc cca gaa ggc tat ctc att aga aat ctg cat att 336
 His Ser Gly Phe Arg Pro Glu Gly Tyr Leu Ile Arg Asn Leu His Ile
 100 105 110
 gat gga caa tgg atg gat cac cat ttt gtg gca ttg ctg gcg gat gag 384
 Asp Gly Gln Trp Met Asp His His Phe Val Ala Leu Leu Ala Asp Glu
 115 120 125
 tat tca ata acc gcg gtg gaa cgt ctc act aga gag gga cga ttg cgc 432
 Tyr Ser Ile Thr Ala Val Glu Arg Leu Thr Arg Glu Gly Arg Leu Arg
 130 135 140
 cga tgattactaa tgcgaagaaa ttt 458

Arg
145

<210> 266
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 266
Trp Asp Asn Ile Thr Tyr Leu Met Arg Ala Ala Arg Lys Gly Thr Val
1 5 10 15
Val Pro Met Val Ile Glu Leu Asp Gly Arg Phe Val Gly Gln Leu Thr
20 25 30
Ile Gly Asn Ile Gln His Gly Gly Ile Ser Asp Ala Trp Ile Gly Tyr
35 40 45
Trp Val Ser Ser Ala Val Thr Gly Arg Gly Ile Ala Thr Ala Ala Cys
50 55 60
Ala Leu Gly Val Asp His Ala Phe Arg Arg Ile Gly Leu His Arg Leu
65 70 75 80
Thr Ala Thr Tyr Leu Pro Ser Asn Pro Ala Ser Gly Lys Val Leu Gly
85 90 95
His Ser Gly Phe Arg Pro Glu Gly Tyr Leu Ile Arg Asn Leu His Ile
100 105 110
Asp Gly Gln Trp Met Asp His His Phe Val Ala Leu Leu Ala Asp Glu
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Tyr Ser Ile Thr Ala Val Glu Arg Leu Thr Arg Glu Gly Arg Leu Arg
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Leu Asp Ser Thr Asn
1 5
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Thr Pro Gly Pro Thr Glu Trp Gly Glu Ser Arg Val Gly Lys Gly Pro
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Trp Glu Glu Glu Asn Pro Gly Val Pro Arg Pro Thr Ser Pro Leu Phe	
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Asp Val Thr Leu Leu Asn Glu Gly Asp Arg Arg Asn Val Val Asp Ala	
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Tyr Arg Tyr Trp Thr Arg Glu Ala Ile Val Glu Asp Ile Asp Thr Arg	
55 60 65	
cgc cac agc ctc cac gta gcg atc gaa aac ttt gaa aac gac gcc aac	355
Arg His Ser Leu His Val Ala Ile Glu Asn Phe Glu Asn Asp Ala Asn	
70 75 80 85	
atc ggc acc gtc gtg cgc acc gcc aac gcc ttt gcc gtg aac aca gtc	403
Ile Gly Thr Val Val Arg Thr Ala Asn Ala Phe Ala Val Asn Thr Val	
90 95 100	
cac att gtg ggc agg cgt cgg tgg aac cgc agg gga gcc atg gtg act	451
His Ile Val Gly Arg Arg Arg Trp Asn Arg Arg Gly Ala Met Val Thr	
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gac cgt tac cag cac ctc atg cac cac gaa gac gtt gat tcg ctg ctt	499
Asp Arg Tyr Gln His Leu Met His His Glu Asp Val Asp Ser Leu Leu	
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gcg tgg gca atc gcg gag cgg ctt acc atc gtc gcg atc gat aac acc	547
Ala Trp Ala Ile Ala Glu Arg Leu Thr Ile Val Ala Ile Asp Asn Thr	
135 140 145	
cca ggt tcc gtg cct ttg gaa acc gct gag ttg ccg aag aac tgc ctg	595
Pro Gly Ser Val Pro Leu Glu Thr Ala Glu Leu Pro Lys Asn Cys Leu	
150 155 160 165	
ttg ctg ttt ggt cag gaa ggc cca ggt gtc acc gaa gct gcg cgt gca	643
Leu Leu Phe Gly Gln Glu Gly Pro Gly Val Thr Glu Ala Ala Arg Ala	
170 175 180	
ggt gcg tta atg acc tgt tcg att gcc caa ttt ggt tcc act cga tcc	691
Gly Ala Leu Met Thr Cys Ser Ile Ala Gln Phe Gly Ser Thr Arg Ser	
185 190 195	
atc aac gcg ggt gta gct gct ggt att gca atg cat gca tgg att cgt	739
Ile Asn Ala Gly Val Ala Ala Gly Ile Ala Met His Ala Trp Ile Arg	
200 205 210	
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 35 40 45

Asn Val Val Asp Ala Tyr Arg Tyr Trp Thr Arg Glu Ala Ile Val Glu
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Asp Ile Asp Thr Arg Arg His Ser Leu His Val Ala Ile Glu Asn Phe
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Glu Asn Asp Ala Asn Ile Gly Thr Val Val Arg Thr Ala Asn Ala Phe
 85 90 95

Ala Val Asn Thr Val His Ile Val Gly Arg Arg Arg Trp Asn Arg Arg
 100 105 110

Gly Ala Met Val Thr Asp Arg Tyr Gln His Leu Met His His Glu Asp
 115 120 125

Val Asp Ser Leu Leu Ala Trp Ala Ile Ala Glu Arg Leu Thr Ile Val
 130 135 140

Ala Ile Asp Asn Thr Pro Gly Ser Val Pro Leu Glu Thr Ala Glu Leu
 145 150 155 160

Pro Lys Asn Cys Leu Leu Leu Phe Gly Gln Glu Gly Pro Gly Val Thr
 165 170 175

Glu Ala Ala Arg Ala Gly Ala Leu Met Thr Cys Ser Ile Ala Gln Phe
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Gly Ser Thr Arg Ser Ile Asn Ala Gly Val Ala Ala Gly Ile Ala Met
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His Ala Trp Ile Arg Gln His Ala Asp Leu Ser Gln Ala Trp
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<223> RXA01581

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 Met Ala Leu Asp Phe
 1 5

aat gag gcg ttt acc gaa cgc acc ccg cgc atc gtc aac gca gct aaa	163
Asn Glu Ala Phe Thr Glu Arg Thr Pro Arg Ile Val Asn Ala Ala Lys	
10 15 20	
ctg cat cgc gcc gcg cag cgc aaa aaa gat aag cgt ttt cta gtt gaa	211
Leu His Arg Ala Ala Gln Arg Lys Lys Asp Lys Arg Phe Leu Val Glu	
25 30 35	
ggc gaa aat tcc gtt gaa gca gct gtc gct acc ggc gca gca act gac	259
Gly Glu Asn Ser Val Glu Ala Ala Val Ala Thr Gly Ala Ala Thr Asp	
40 45 50	
ctc ttt gtc act gaa tcc gct gcg gag cgc ttc gag gaa atc gtc cgc	307
Leu Phe Val Thr Glu Ser Ala Ala Glu Arg Phe Glu Glu Ile Val Arg	
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Thr Ala Gly Tyr Met Asn Val Tyr Thr His Ala Ile Thr Asp Lys Ala	
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gcg aag cat ctt agc gac acc gtc acc acc acg ggc att ttt gcg ctt	403
Ala Lys His Leu Ser Asp Thr Val Thr Thr Thr Gly Ile Phe Ala Leu	
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Cys Asp Asp Val Leu Trp Ser Val Gly Lys Ala Ile Thr Gly Gln Pro	
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Arg Leu Val Ser Val Pro Val Glu Thr Arg Glu Pro Gly Asn Ala Gly	
120 125 130	
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Thr Leu Ile Arg Val Ser Asp Ala Val Gly Ala Asp Ala Val Val Phe	
135 140 145	
gct ggt gaa tca gta gat cca ctt ggc gca aaa gct gtg cgc tcc tca	595
Ala Gly Glu Ser Val Asp Pro Leu Gly Ala Lys Ala Val Arg Ser Ser	
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Ala Gly Ser Leu Phe His Ile Pro Val Ala Arg Asn Asn Asn Ile Ala	
170 175 180	
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Asp Val Leu Gly Gln Leu Arg Ser Lys Gly Leu Gln Ile Leu Ala Thr	
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Ser Ala Asp Gly Glu Val Asp Leu Asp Asp Ala Asp Glu Leu Leu Ala	
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Lys Pro Thr Ala Trp Leu Phe Gly Asn Glu Ala His Gly Leu Asp Glu	
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Ser Leu Leu Ala Gln Ala Asp His Arg Val Arg Ile Pro Ile Arg Gly	
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Ile	Thr	Asp	Lys	Ala	Ala	Lys	His	Leu	Ser	Asp	Thr	Val	Thr	Thr	Thr
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Gly	Ile	Phe	Ala	Leu	Cys	Asp	Asp	Val	Leu	Trp	Ser	Val	Gly	Lys	Ala
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Ala	Val	Arg	Ser	Ser	Ala	Gly	Ser	Leu	Phe	His	Ile	Pro	Val	Ala	Arg
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Asn	Asn	Asn	Ile	Ala	Asp	Val	Leu	Gly	Gln	Leu	Arg	Ser	Lys	Gly	Leu
			180					185					190		
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Met Ala Gly Asn Asp																1
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Ser Arg Arg Gly Gly Leu Arg Lys Thr Asn Lys Lys Gly Ala Thr Lys																10
15																
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ggc agt ggc gga cag gtt cgt cgc ggt ctg aaa ggt aag ggg cct acc																211
Gly Ser Gly Gly Gln Val Arg Arg Gly Leu Lys Gly Lys Gly Pro Thr																25
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Pro Lys Ala Glu Asp Arg Thr Tyr His Ala Ala His Lys Arg Lys Val																40
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Glu Arg Asp Arg Arg Asp Arg Gly Arg His Gln Arg Glu Met Pro Glu																55
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Leu Val Val Gly Arg Asn Pro Val Leu Glu Cys Leu His Ala Arg Val																70
75																
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cca gcg act gct ttg tat gtt gca gag ggt gcg gcg aac gat gag cgt																403
Pro Ala Thr Ala Leu Tyr Val Ala Glu Gly Ala Ala Asn Asp Glu Arg																90
95																
100																
ctg agc gag gca gtg cac act gcg gct ggc cga aat ctt cca gtg ctg																451
Leu Ser Glu Ala Val His Thr Ala Ala Gly Arg Asn Leu Pro Val Leu																105
110																
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125																
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cag ggc atc ggc ctg gcg atc cct cct tac gag tac gca gat gtt cat																547
Gln Gly Ile Gly Leu Ala Ile Pro Pro Tyr Glu Tyr Ala Asp Val His																135
140																
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Asp Leu Ile Ala Asn Ala Ala Ala Ser Lys Lys Pro Gly Met Phe Val
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 Ile Leu Asp Asn Ile Thr Asp Pro Arg Asn Leu Gly Ala Val Ile Arg
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 tcc gtc ggt gct ttc ggc ggc aac ggt gtc atc att ccg gag cgt cgt 691
 Ser Val Gly Ala Phe Gly Gly Asn Gly Val Ile Ile Pro Glu Arg Arg
 185 190 195
 tca gca tct gtg acc gct gtt gca tgg cgt act tct gct ggt acc gca 739
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 200 205 210
 gcg cgt gtg cca gtg gcg aag gaa acc aac atg act cgt gtc gtg aag 787
 Ala Arg Val Pro Val Ala Lys Glu Thr Asn Met Thr Arg Val Val Lys
 215 220 225
 gaa ttc cag caa aac ggt tac cag gtc gtc ggc ctt gac gct ggc ggc 835
 Glu Phe Gln Gln Asn Gly Tyr Gln Val Val Gly Leu Asp Ala Gly Gly
 230 235 240 245
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 Asp His Thr Leu Asp Thr Tyr Asp Gly Thr Asp Asn Val Val Ile Val
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 gtc ggt tct gag ggc aag gga att tcc cgt ctc gtt cgc gaa aac tgc 931
 Val Gly Ser Glu Gly Lys Gly Ile Ser Arg Leu Val Arg Glu Asn Cys
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 Asp Thr Ile Met Ser Ile Pro Thr Glu Gly Trp Val Glu Ser Leu Asn
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 gct tcg gtt gct gcc ggc gtc gtg ctg tcg gag ttc tcg cgc cag cgt 1027
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<211> 313

<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

His Lys Arg Lys Val Glu Arg Asp Arg Arg Asp Arg Gly Arg His Gln
 50 55 60

Arg Glu Met Pro Glu Leu Val Val Gly Arg Asn Pro Val Leu Glu Cys
65 70 75 80
Leu His Ala Arg Val Pro Ala Thr Ala Leu Tyr Val Ala Glu Gly Ala
85 90 95
Ala Asn Asp Glu Arg Leu Ser Glu Ala Val His Thr Ala Ala Gly Arg
100 105 110
Asn Leu Pro Val Leu Glu Val Asn Lys Leu Glu Leu Asp Arg Met Thr
115 120 125
Gly Asn Gly Met His Gln Gly Ile Gly Leu Ala Ile Pro Pro Tyr Glu
130 135 140
Tyr Ala Asp Val His Asp Leu Ile Ala Asn Ala Ala Ser Lys Lys
145 150 155 160
Pro Gly Met Phe Val Ile Leu Asp Asn Ile Thr Asp Pro Arg Asn Leu
165 170 175
Gly Ala Val Ile Arg Ser Val Gly Ala Phe Gly Gly Asn Gly Val Ile
180 185 190
Ile Pro Glu Arg Arg Ser Ala Ser Val Thr Ala Val Ala Trp Arg Thr
195 200 205
Ser Ala Gly Thr Ala Ala Arg Val Pro Val Ala Lys Glu Thr Asn Met
210 215 220
Thr Arg Val Val Lys Glu Phe Gln Gln Asn Gly Tyr Gln Val Val Gly
225 230 235 240
Leu Asp Ala Gly Gly Asp His Thr Leu Asp Thr Tyr Asp Gly Thr Asp
245 250 255
Asn Val Val Ile Val Val Gly Ser Glu Gly Lys Gly Ile Ser Arg Leu
260 265 270
Val Arg Glu Asn Cys Asp Thr Ile Met Ser Ile Pro Thr Glu Gly Trp
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<223> RXN00460

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          20              25              30

Leu  His  Leu  Val  Glu  Pro  Leu  Gly  Phe  Glu  Leu  Thr  Glu  Lys  His  Leu
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 Ala Thr Phe Asp Glu Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala
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 Phe Thr Thr Thr Ala Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro
 85 90 95
 Gly Asp Ala Leu Leu Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu
 100 105 110
 His Val Glu His Ser Arg Ile Thr Ser Glu Leu Arg Ile Pro Met Leu
 115 120 125
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 Met Pro Glu His Pro
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 ctt cac gtt atc ttc gac aat cct gtc atc cct ccc aac acc gga aac 163
 Leu His Val Ile Phe Asp Asn Pro Val Ile Pro Pro Asn Thr Gly Asn
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 Pro Leu Gly Phe Glu Leu Thr Glu Lys His Leu Arg Arg Ala Gly Leu
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Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro Gly Asp Ala Leu Leu
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Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu His Val Glu His Ser
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35 40 45

Arg Arg Ala Gly Leu Asp Tyr His Asp Leu Ala Asp Val Thr Val His
50 55 60

Ala Thr Phe Asp Glu Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala
65 70 75 80

Phe Thr Thr Thr Ala Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro
85 90 95

Gly Asp Ala Leu Leu Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu
100 105 110

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<210> 277

<211> 951

<212> DNA

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<222> (101)..(928)

<223> RXA02179

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Met Thr Thr Arg Thr
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